

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 8, 2005, 23:47:02 ; Search time 2534.83 Seconds
(without alignments)
1166.064 Million cell updates/sec

Title: US-10-624-932C-2_COPY_163_223

Perfect score: 326

Sequence: 1 EQGIVLPCRPPEGIPPAEVE.....HSLVVRQRLADTANYTCVA 61

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters: -DB=frame+ p2n.model -DEV=xlh

-Q=/cgn2.1/USPTO spool_h/US10624932/runat_08092005_161705_15773/app.query.fasta_1.1386
-DB=GenEmbl -QFMT=fastap -SUFFIX=erge -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10624932 @CNC 1.1 7509 @runat_08092005_161705_15773 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

10: gb.rc.*

11: gb.sts.*

12: gb.sv.*

13: gb.un.*

14: gb.vi.*

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	326	100.0	2230	6	CQ845766 Sequence
2	326	100.0	2230	9	AK131380 Homo sapi
3	326	100.0	2697	6	AX268596 Sequence
4	326	100.0	2697	6	AX451652 Sequence

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

5	326	100.0	2697	10	RNU87305	U87305 Rattus norv
6	326	100.0	2752	6	CQ449572	AX449572 Sequence
7	326	100.0	2784	6	CQ730306	CQ730306 Sequence
8	326	100.0	2881	6	AX527916	AX527916 Sequence
9	326	100.0	3014	6	BD057524	BD057524 Netrin re
10	326	100.0	3580	6	AX367094	AX367094 Sequence
11	326	100.0	3992	10	MMU487852	AJ487852 Mus muscu
12	326	100.0	4294	10	AK122575	AK122575 Mus muscu
13	321	98.5	3844	10	BC058084	BC058084 Mus muscu
14	295	90.5	171419	2	AC135142	AC135142 Rattus no
15	270.5	83.0	121282	9	AC027318	AC027318 Homo sapi
16	270.5	83.0	166534	2	AC034209	AC034209 Homo sapi
17	270.5	83.0	168168	2	AC012283	AC012283 Homo sapi
18	267	81.9	242128	5	AC123700	AC123700 Mus muscu
19	245	75.2	1482	5	AY764374	AY764374 Danio rer
20	245	75.2	9299	10	MMU72634	U72634 Mus musculu
21	242	74.2	2612	6	CQ881064	CQ881064 Sequence
22	242	74.2	2780	6	CQ881054	CQ881054 Sequence
23	242	74.2	2986	6	CQ881052	CQ881052 Sequence
24	242	74.2	3646	6	CQ881060	CQ881060 Sequence
25	242	74.2	3646	9	AF055634	AF055634 Homo sapi
26	242	74.2	9328	10	AB118026	AB118026 Rattus no
27	237	72.7	2962	5	AY187310	AY187310 Gallus ga
28	236	72.4	2270	9	BC041156	BC041156 Homo sapi
29	236	72.4	2832	5	AY099459	AY099459 Xenopus l
30	230	70.6	2625	6	CQ721377	CQ721377 Sequence
31	230	70.6	2831	6	BD057526	BD057526 Netrin re
32	230	70.6	2838	10	RNU87306	U87306 Rattus norv
33	230	70.6	2860	6	AX686445	AX686445 Sequence
34	230	70.6	2860	6	AX686447	AX686447 Sequence
35	230	70.6	2895	6	AX512281	AX512281 Sequence
36	230	70.6	2995	6	AX497288	AX497288 Sequence
37	230	70.6	3672	10	BC048162	BC048162 Mus muscu
38	230	70.6	3672	10	BC057560	BC057560 Mus muscu
39	230	70.6	3770	9	AY126437	AY126437 Homo sapi
40	230	70.6	3788	10	MMU487853	AJ487853 Mus muscu
41	230	70.6	3884	6	AR528525	AR528525 Sequence
42	230	70.6	3884	6	AX464012	AX464012 Sequence
43	230	70.6	3884	9	AY358351	AY358351 Homo sapi
44	230	70.6	3933	6	CQ850929	CQ850929 Sequence
45	230	70.6	3933	9	AK128132	AK128132 Homo sapi

ALIGNMENTS

RESULT 1	CQ845766	Sequence 4413 from Patent EP1440981.	2230 bp	DNA	linear	PAT 02-AUG-2004
LOCUS	CQ845766	Sequence 4413 from Patent EP1440981.				
DEFINITION	CQ845766					
ACCESSION	CQ845766					
VERSION	CQ845766.1	GI:50895365				
KEYWORDS						
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	1	Isogai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S., Yamamoto, J., Isono, Y., Nagai, K. and Irie, R.				
AUTHORS						
TITLE		Full-length human cdna				
JOURNAL		Patent: EP 1440981-A 4413 28-JUL-2004;				
FEATURES		Research Association for Biotechnology (JP)				
source		Location/Qualifiers				
		1..2230				
		/organism="Homo sapiens"				
		/mol_type="unassigned DNA"				
		/db_xref="taxon:9606"				

ORIGIN						
Alignment Scores:						
Pred. No.:	1.46e-29	Length:	2230			
Score:	326.00	Matches:	61			
Percent Similarity:	100.00%	Conservative:	0			

```

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x CQ845766 (1-2230)

QY 1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProProAlaGluValGlu 20
Db 556 GAGCAGGGCATCGTGCTCCCTGCGCTCCACCGGAGGCATCCCTCCAGCGAGGTGGAG 615

QY 21 TrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArg 40
Db 616 TGGCTCCGACGACGAGGACCTGGTGACCGCTCCCTGGACCCCAATGTATACATCACGGGG 675

QY 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
Db 676 GAGCACAGCGCTGGTGGTGGACGACCGCGCTTGTGTACAGCGGCCAACACTACACCTGCGTG 735

QY 61 Ala 61
Db 736 GCC 738

RESULT 2
AKI31380 2230 bp mRNA linear PRI 07-MAY-2004
LOCUS Homo sapiens cDNA FLJ16449 fis, clone BRAWH2006395, highly similar
to Rattus norvegicus transmembrane receptor Unc5H1.
ACCESSION AKI31380
VERSION AKI31380.1 GI:47077220
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Tanigami,A., Fujiwara,T., Shibahara,T., Goto,Y., Hirao,M.,
Shimizu,F., Wakebe,H., Ono,T., Hishigaki,H., Watanabe,T., Ozaki,K.,
Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Ota,T., Wakamatsu,A.,
Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K.,
Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y.,
Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K.,
Kanehori,K., Takahashi-Fujii,A., Oshima,A., Sugiyama,A.,
Kawakami,B., Suzuki,Y., Sugano,S., Nagahara,K., Masubo,Y., Nagai,K.
and Isogai,T.
NEBO human cDNA sequencing project
Unpublished
REFERENCE 2 (bases 1 to 2230)
AUTHORS Isogai,T. and Yamamoto,J.
TITLE Direct Submission
JOURNAL Submitted (01-MAR-2004) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEBO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.
FEATURES
Location/Qualifiers
1..2230
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="BRAWH2006395"
/tissue type="brain"
/clone_lib="BRAWH2"
/notes="cloning vector: pME18SFL3"
70..975
/notes="unnamed protein product"
/codon_start=1
/protein_id="BAD18531.1"

CDS

```

```

/db_xref="GI:47077221"
/translation="MAVRPGLWPAALLGIVLAAWLRGSGAQOSATVANPVGANPDLLP
HFLVNPEDVTVIKNKPVLLVCKAVPATQIFKCNQEWVRQVDHVIERTSDNSGLPTM
EVRINVSQVQKVFGLBEEYWCQVAMSSGTTKSKAYIRIAYLRKNFOEPLAKEV
SLQGIPLPCRPPEGIPPAEVEWLRNEDLDVPSLDPNVYITREHSLVVRQPLADTAN
YTCVAKNIVARRRSASAATVIVYVDGSMSPWSKWSACGLDCTHWRSECSDPAPRNGGE
ECQGTDLDTNRCTSDLCVHSESLP"

ORIGIN
Alignment Scores:
Pred. No.: 1,46e-29 Length: 2230
Score: 326.00 Matches: 61
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x AKI31380 (1-2230)

QY 1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProProAlaGluValGlu 20
Db 556 GAGCAGGGCATCGTGCTCCCTGCGCTCCACCGGAGGCATCCCTCCAGCGAGGTGGAG 615

QY 21 TrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArg 40
Db 616 TGGCTCCGACGACGAGGACCTGGTGACCGCTCCCTGGACCCCAATGTATACATCACGGGG 675

QY 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
Db 676 GAGCACAGCGCTGGTGGTGGACGACCGCGCTTGTGTACAGCGGCCAACACTACACCTGCGTG 735

QY 61 Ala 61
Db 736 GCC 738

RESULT 3
AX268596 2697 bp DNA linear PAT 29-OCT-2001
LOCUS AX268596 Sequence 15 from Patent WO01/5440.
DEFINITION AX268596
ACCESSION AX268596
VERSION AX268596.1 GI:16541710
KEYWORDS Rattus sp.
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1
AUTHORS Cochran,S.W., Paterson,G.Y., Ohashi,Y.W., Morris,B.Y. and
Pratt,J.Y.
TITLE Schizophrenia related genes
JOURNAL Patent: WO 01/5440-A 15 11-OCT-2001;
WELFIDE CORPORATION (JP)
FEATURES
Location/Qualifiers
source
1..2697
/organism="Rattus sp."
/mol_type="unassigned DNA"
/db_xref="taxon:10118"

ORIGIN
Alignment Scores:
Pred. No.: 1,74e-29 Length: 2697
Score: 326.00 Matches: 61
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x AX268596 (1-2697)

QY 1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProProAlaGluValGlu 20
Db 487 GAGCAGGCATTTGTACTACCTTGTGCGCCCCCAGAGGAATCCCCCAGCTGAGGTGGAG 546

```

REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE
1 (bases 1 to 2697)	Leonardo, E.D., Hinck, L., Maasu, M., Keino-Masu, K., Ackerman, S.L. and	Vertebrate homologues of <i>C. elegans</i> UNC-5 are candidate netrin	Nature 386 (6627), 833-838 (1997)	97271897

2. (bases 1 to 2597)
Leonardo, E. D., Hinck, L., Masu, M., Keino-Masu, K. and
Tessier-Lavigne, M.

JOURNAL
 Submitted (28-JAN-1997) Anatomy, UCSF, 513 Parnassus, San Francisco, CA 94143-0452, USA
 Location/Qualifiers
 1. .2697
 source
 /organism="Rattus norvegicus"
 /mol type="mRNA"

```

CDS
1. .2697 /codon start=1
/tissue type="brain and ventral spinal cord"
/dev stage="18 day embryo and 13 day embryo"

```

```

/protein_id="AAB57678.1"
/db_xref="GI:2055392"
/translation="MAVPEGLWPVLLGLVLAWLGRSGAQQSATVANPVPGANPDLLP
/protein_id="AAB57678.1"
/db_xref="GI:2055392"
/translation="MAVPEGLWPVLLGLVLAWLGRSGAQQSATVANPVPGANPDLLP

```

HYEYRINVSQVQVEKVLGEBEYWCQVWSSGTTQKQAYIRIAYLRKNEQPEQLAKEV
SLEOGIYVLCRPEEGIPAEVEWMLNEDLVPSLDPNVYITREHSLVUVRQARLADYAN
TTCVAKNIVARRRSTSAIVYVQVGSWSTWTSVSCSACGRGWKXRSSTNPAPLAN
YGACCEGQNVQKTACATCIVYVQVGSWSSKWSACGLDCTTHWBSBCSDPAPRNGBEEC

DVADSSILITSGPOPIVLIKPSKADNPILLITOPDLSTTTTYYQSGILCSRGDGPSPKPOL
 RNMHITSLGSGRHNILHSSPTSEAEDEFVSRILSTQNYFSLFRGCTSNMAYGTFNPFLLGG
 LMLITNGTSLILPDAIPRGKIYEILTLHPDEFVRLPACQITLLSNNYVSGCPGPGV
 LUTRIVLAMDHCGBSPDPSLTKKSCSEGSWEDVHLHBESPSHLTYCQLEAGC
 VYFTQGLRHCGLVBALSVAAATKRLRLILFAFVATSELYNRVYCLHDTIHALKEW
 QLEKQGLQIQEPLRHFDPKSHYLNLSIHDPVSLKSKULLVSYQEI.PFYHIWNGT
 QOYLCTHTTLERINASTDLACKVWVWQEGDQGFNFNFNTTKYTRFAELILALESEG
 GYPALVPSFAFKIPELIRQKIITASLDPPCPSRGADWRTLAQKLHLSHLSFFASFKPSPT
 AMILNLWAEHPFNGNLGOLAAAVAGLQPDAGLFTVSEAC.

Alignment Scores:	
Pred. No.:	1.74e-29
Score:	326.00
Percent Similarity:	100.00%
Length:	2697
Matches:	61
Conservative:	0

Best Local Similarity:	
Query Match:	100.00%
DB:	10
Gaps:	0
Indels:	0
Mismatches:	0

Qy 1 GluGlnGlyIyleValLeuProCysArgProGluGlyIleProProAlaGluValGlu 20

Qy 21 TrpLeuArgGlnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArg 40

41	QY	GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal	60
607	Db	GAGCACAGCCTAGTCGTGGCCGCCCTCAGGCCGACACGGCCAACTACACTGTGG	666

Qy 61 Ala 61
|||
Db 667 GCC 669

RESULT 6
AX449572

```
LOCUS      AX449572                2752 bp      DNA          linear      PAT 03-JUL-2002
DEFINITION Sequence 1 from Patent WO0210216.
ACCESSION  AX449572
VERSION    AX449572.1  GI:21698195
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Padigaru,M., Mezes,P., Mishra,V., Burgess,C., Cagman,S.,
            Grosse,W.M., Alsbrook,J.P., Lepley,D.M., Gerlach,V.L.,
            Macdonald,J.R. and Smithson,G.
TITLE     Proteins and nucleic acids encoding same
JOURNAL   Patent: WO 0210216-A 1 07-FEB-2002;
            Curagen Corporation (US)
FEATURES   Location/Qualifiers
            source
            1..2752
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.:      1.77e-29      Length:      2752
Score:          326.00      Matches:      61
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             6      Gaps:      0
US-10-624-932C-2_COPY_163_223 (1-61) x AX449572 (1-2752)
Qy 1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProProAlaGluValGlu 20
Db 532 GAGCAGGCGATCGTGCCTCCCTCCACCGGAGGCATCCCTCCAGCGAGGTGGAG 591
Qy 21 TrpLeuArgAnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArg 40
Db 592 TGGCTCCGGAACGAGGACCTGGTGACCGCGCTCCCTGGACCCCAATGTATATACATCACGCGG 651
Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
Db 652 GAGCACACCTGGTGGTGGACAGCGCCGCTTGCTGACACGGCCAACTACACCTCGGTG 711
Qy 61 Ala 61
Db 712 GCC 714
RESULT 7
LOCUS      CQ730306                2784 bp      DNA          linear      PAT 03-FEB-2004
DEFINITION Sequence 16240 from Patent WO02068579.
ACCESSION  CQ730306
VERSION    CQ730306.1  GI:42303801
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE     Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
JOURNAL   Patent: WO 02068579-A 16240 06-SEP-2002;
            PE Corporation (NY) (US)
FEATURES   Location/Qualifiers
            source
            1..2784
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
ORIGIN
```

```
Alignment Scores:
Pred. No.:      1.79e-29      Length:      2784
Score:          326.00      Matches:      61
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             6      Gaps:      0
US-10-624-932C-2_COPY_163_223 (1-61) x CQ730306 (1-2784)
Qy 1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProProAlaGluValGlu 20
Db 487 GAGCAGGCGATCGTGCCTCCCTCCACCGGAGGCATCCCTCCAGCGAGGTGGAG 546
Qy 21 TrpLeuArgAnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArg 40
Db 547 TGGCTCCGGAACGAGGACCTGGTGGACCGCTCCCTGGACCCCAATGTATATACATCACGCGG 606
Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
Db 607 GAGCACAGCCTGGTGGTGGACAGCGCCGCTTGCTGACACGGCCAACTACACCTCGGTG 666
Qy 61 Ala 61
Db 667 GCC 669
RESULT 8
LOCUS      AX527916                2881 bp      DNA          linear      PAT 21-NOV-2002
DEFINITION Sequence 1 from Patent WO0229038.
ACCESSION  AX527916
VERSION    AX527916.1  GI:25172359
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Herrmann,J.L., Rastelli,L. and Shinkets,R.A.
TITLE     Novel proteins and nucleic acids encoding same and antibodies
            directed against these proteins
JOURNAL   Patent: WO 0229038-A 1 11-APR-2002;
            Curagen Corporation (US)
FEATURES   Location/Qualifiers
            source
            1..2881
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.:      1.85e-29      Length:      2881
Score:          326.00      Matches:      61
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             6      Gaps:      0
US-10-624-932C-2_COPY_163_223 (1-61) x AX527916 (1-2881)
Qy 1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProProAlaGluValGlu 20
Db 573 GAGCAGGCGATCGTGCCTCCCTCCACCGGAGGCATCCCTCCAGCGAGGTGGAG 632
Qy 21 TrpLeuArgAnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArg 40
Db 633 TGGCTCCGGAACGAGGACCTGGTGGACCGCTCCCTGGACCCCAATGTATATACATCACGCGG 692
Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
Db 693 GAGCACAGCCTGGTGGTGGACAGCGCCGCTTGCTGACACGGCCAACTACACCTCGGTG 752
```



```

Qy      61 Ala 61
Db      753 GCC 755

RESULT 9
BD057524
LOCUS   BD057524
DEFINITION Netrin receptors.
ACCESSION BD057524
VERSION   BD057524.1 GI:22603130
KEYWORDS JP 2001505062-A/1.
SOURCE   synthetic construct
ORGANISM synthetic construct
REFERENCE
AUTHORS Lavigne,M.T., Leonardo,D.E., Hinck,L., Masu,M. and Masu,K.K.
TITLE    Netrin receptors
JOURNAL  Patent: JP 2001505062-A 1 17-APR-2001;
          THE REGENTS OF THE UNIV OF CALIFORNIA
COMMENT  PN JP 2001505062-A/1
          PD 17-APR-2001
          PF 19-FEB-1998 JP 1998536840
          PR 19-FEB-1997 US 08/808982
          PI MARC TESSIER LAVIGNE,DAVID E LEONARDO,LINDSAY HINCK,MASAYUKI
          PI MASU,
          PI KAZUKO KEINO MASU
          PC C07K1/00,C07K14/00,C07K17/00,C07H21/02,C07H21/04,G01N33/53 CC
          Strandedness: Double;
          CC Topology: Linear; Location/Qualifiers.
          FH Key Location/Qualifiers
FEATURES
    source
        1..3014
        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"

ORIGIN
Alignment Scores:
Pred. No.:      1.93e-29      Length:      3014
Score:          326.00      Matches:      61
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:    0
DB:             6      Gaps:      0

US-10-624-932C-2_COPY_163_223 (1-61) x BD057524 (1-3014)

Qy      1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProProAlaGluValGlu 20
Db      487 GAGCAAGGCATTGTACTACCTTGTGCGCCCGCCAGGAAGAAATCCCCCAGCTGAGGTGGAG 546

Qy      21 TrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArg 40
Db      547 TGGCTTCGAATGAGACCTGTGGACCCCTCCCTCGATCCCAATGTATATACATACACGGG 606

Qy      41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
Db      607 GAGCACACCTAGTGTGCGTCAGCGCCGCTGGCGGACACGGCCAACTACACCTGTGTG 666

Qy      61 Ala 61
Db      667 GCC 669

RESULT 10
AX367094
LOCUS   AX367094
DEFINITION Sequence 13 from Patent WO0198354.
ACCESSION AX367094
VERSION   AX367094.1 GI:18855296
KEYWORDS Homo sapiens (human)
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Griffin,J.A., Kallick,D.A., Tribouley,C.M., Yue,H., Nguyen,D.B.,
Tang,Y.T., Lal,P., Policky,J.L., Azimzai,Y., Lu,D.A., Graul,R.,
Yao,M.G., Burford,N., Hafalia,A.J., Baughn,M.R., Bandman,O.,
Patterson,C., Yang,J., Xu,Y., Warren,B.A., Ding,L. and
Sanjanwala,M.S.
Receptors
Patent: WO 0198354-A 13 27-DEC-2001;
Incyte Genomics, Inc. (US)
Location/Qualifiers
    source
        1..3580
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"
        /note="Incyte ID No: 6052371CBI"

ORIGIN
Alignment Scores:
Pred. No.:      2.26e-29      Length:      3580
Score:          326.00      Matches:      61
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:    0
DB:             6      Gaps:      0

US-10-624-932C-2_COPY_163_223 (1-61) x AX367094 (1-3580)

Qy      1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProProAlaGluValGlu 20
Db      490 GAGCAGGGCATCGTGCCTGCCCTGCCCGGAGGCGCATCCCTCCAGCGGTGGAG 549

Qy      21 TrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArg 40
Db      550 TGGCTCCGGACAGGAGACCTGTGGACCCGCTCCCTGACCCCATGTATATACATACACGGG 609

Qy      41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
Db      610 GAGCACACCTGTGTGGTGGCAGACGCGCCCTGCTGACACGGCCAACTACACCTGCGTG 669

Qy      61 Ala 61
Db      670 GCC 672

RESULT 11
MMU487852
LOCUS   MMU487852
DEFINITION Mus musculus mRNA for netrin receptor Unc5h1 (Unc5h1 gene).
ACCESSION AJ487852
VERSION   AJ487852.1 GI:22035783
KEYWORDS netrin receptor Unc5h1; Unc5h1 gene.
SOURCE   Mus musculus (house mouse)
ORGANISM Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
Engelkamp,D.
Cloning of three mouse Unc5 genes and their expression patterns at
mid-gestation
Mech. Dev. 118 (1-2), 191-197 (2002)
MEDLINE 22239710
PUBMED 12351186
REFERENCE 2 (bases 1 to 3992)
AUTHORS Engelkamp,D.
TITLE    Direct Submission
JOURNAL  Submitted (15-MAY-2002) Neuroanatomy, Max Planck Institute for
          Brain Research, Deutschordenstrasse 46, Frankfurt 60528, GERMANY
FEATURES
    source
        1..3992
        /organism="Mus musculus"
        /mol_type="mRNA"
        /db_xref="taxon:10090"
        1..3992
    gene

```

CDS	/gene="UncSh1"		Okazaki, N., Kikuno, R., Nagase, T., Ohara, O. and Koga, H.	
	232..2928		Direct Submission	
	/gene="UncSh1"		Submitted (07-FEB-2003) Hisashi Koga, Kazusa DNA Research	
	/codon_start=1		Institute, Laboratory for Genome Informatics; 2-6-7	
	/product="netrin receptor UncSh1"		Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan	
	/protein_id="CAD32250.1"		(E-mail: mouse@kazusa.or.jp, Tel: 81-438-52-3919, Fax: 81-438-52-3918)	
	/db_xref="GI:22035784"		The CREATE program supported by Japan science and technology	
	/db_xref="GOA:O8K1S4"		corperation, cDNA full insert sequencing: Kazusa DNA Research	
	/db_xref="UniProt/TrEMBL:O8K1S4"		institute; cDNA library construction, clone selection and 5'- &	
	/translation="MAVRPGLWPAALGIVLTAMLRGSGAQQSAVTANVPVGPANPDLLP		3'-end one pass sequencing.	
FEATURES	HFLVPEEDVTVTKNKPVLVCKVAPATQIFKCNGEWVRQVDHVERSTGGSSGLPTM		Location/Qualifiers	
	EVRINVRQGVKEVLEEVQCVAVSSGTTKSKAYIRIAYLRKNFQEPFLAKEV		1..4294	
	SLEGIIVLCPPEPGIIPAEVWELENEDLVDSLDPNVITREHSLVVRQARLADTAN		/organism="Mus musculus"	
	YTCVAKNIVARRSASAIVVYNGGSHSTWVSCASGCGKQKRSCTNPAPLN		/mol_type="mRNA"	
	GGAFCEGQVQKTCATLCPDVGSPWSKAGLVCLDTHWRSGCDPAPRNGGEEC		/db_xref="taxon:10090"	
	RGADLTRNCTSDLCITSSGPEDEVALYIGLVAVAGCLILLLVLIYCRKKEGLDS		/clone="mbh03993"	
	DVADSSILTSGFQVSIKPKADNPHELLTIQPDLSITTTTQYSGSLCPQDGPSPKFOL		/tissue_type="brain"	
	SNHLLSPGSGRHTLHSSPTSSEAFDFVSRSLSTONVFRSLPRGTSNMYGTNFTNFGG		/dev_stage="adult"	
	RLMTPTGISLIPPDALPRGKIYEIYLTJLHKPEDVRLPLAGCOTLLSPVSCGPGCV		/note="vector:modified pBC SK+"	
	LLTPVILAMDHCGEPSPDSWSLRKQSCGSEWEDVHLGEESPSHLYYCQLEAGAC		1..4294	
ORIGIN	YVFTQJLGRFALVGEALVAATKKRLILLFAPVACTSLEYNIRVYCIUHDTHDALKEVV		/gene="mKIAA1976"	
	QLEKQLGGQITQEPRLVHKDSYHNLRSLSDHVPSSLWKSLVSYQEIIFYHIWNGT		<2263..3249	
	QQYLHCTFTLERNVASTDLACKVWVWQVGGDGQSFNINFTKDTFAEMLALESEG		/gene="mKIAA1976"	
	GVPAIVGPSAPKIPFLIRQKIITSLDPPCSRGADWRTLAKLHLDSLSPFASKPSPT		/note="CDS is predicted by in silico analysis. Start codon	
	AMILNWEARHFPNGLQLAAAVAGLGQPDAGLFTVSEAC"		is not identified."	
			/codon_start=1	
			/evidences=not_experimental	
			/product="mKIAA1976 protein"	
			/protein_id="BAC65857.1"	
			/db_xref="GI:28972882"	
		/translation="SLYIPAILTKTSLAASSGPEDEVALYIGLVAVAVCLILLLVLV		
		LIYCRKKEGLDSVDVSSILTSGFQVSIKPKADNPHELLTIQPDLSITTTTQYSGSLC		
		PRODGPSPKFQLEKQGLQIOPRLVHKDSYHNLRSLSDHVPSSLWKSLVSYQEI		
		IPFYHIWNGTQQYLHCTFTLERNVASTDLACKVWVWQVGGDGQSFNINFTKDT		
		AEMLALESEGGVPALVGPSAPKIPFLIRQKIITSLDPPCSRGADWRTLAKLHLDSL		
		SPFASKPSPTAMILNWEARHFPNGLQLAAAVAGLGQPDAGLFTVSEAC"		
		</		

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 3844)

REFERENCE
AUTHORS

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.P., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusik, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullighy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Male, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettner, M., Madan, A., Rodriguez, S., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y., Bonfield, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257

12477932

2 (bases 1 to 3844)

Strausberg, R.

Direct Submission

Submitted (08-SEP-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa

cDNA Library Preparation: M. Bento Soares, University of Iowa

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada

info@bcgsc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kuteche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Farvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Teai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAP Plate: 126 Row: b Column: 11

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 23346570.

FEATURES

source

1..3844

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6"

/db_xref="taxon:10090"

/clone="MGC:66671 IMAGE:6813463"

/tissue_type="Brain, mouse, 13.5, 14.5, 16.5, 17.5 dpc"

/clone_lib="NIH BMAP_FW0"

/lab_host="DH10B"

/note="Vector: pYX-ASC"

1..3844

/gene="Unc5a"

/db_xref="LocusID:107448"

/db_xref="MGI:894682"

252..2780

gene

CDS

/gene="Unc5a"

/codon_start=1

/product="Unc5a protein"

/protein_id="AAHS8084.1"

/db_xref="GI:34784159"

/db_xref="LocusID:107448"

/db_xref="MGI:894682"

/translation="MAVRPGLPALLGLVLTAWLRGSAQOASATVANPVGANPDLLP
HFLINVRQOVKVFLEEVKCVKAVPAQIFPKCKGKWWQVQDVHVIERTSDGSSGLPTM
EVRPEPDEVIVKKNPVLLVCVAVPAQIFPKCKGKWWQVQDVHVIERTSDGSSGLPTM
SLEQIVLPCRPPEGIPPAEVEWLNEDLVDPISLDPNVYITREHSLVVRQARLADTPN
TVAKNIIVARRSASAVIVYDGSWSPWMSKACGLDCTHWRSDPAPRNGGE
ECRGADLTNCTSDALHTSSGDEVALYIGLVAVCLILLVLLVLIYCRKEGL
DSVDASISLTSGFPVSIKPSKADNPHLLTIQDLSITTTTQOGLCPROGSPKPF
QLSNGHLLPLSGSRHTLHSSPTSEAEQFVRLSTQNYFRSLPRGTSNMAVGTNFLL
GRLMIPNTGISLLIPDAIPRGKIYEIYTLKPEDVRLPLAGCOTLLSIVSCGPP
GVLLITRUVILAMDHCGSPSDSLSRLKKQSCGSMEDVLHGESPSHLVYCOLEAG
ACYFTQLGRFALVGEALSVAATKRLRLLLFAPVACTSLSEYNIYVCLHHTHALKE
VVQLEKGGQLIQSPRVLPKDSYHNLRSIHDPVPSLWKSLLVSYQEIYFFHYMN
GTQOYLCTFTLERVNSTDLACKVWVWQVGEQGSFNFINFTKDTFRFAEMLALES
EGVPALVGPSPAFKIPFLIROKIITSLDPPCSRGADWRTLAQKHLHLSLFFASKPS
PTMILNLWEARHPNGLQAAAAVAGLQPDAGLFTVSEAC"

714..926

/misc_feature

/gene="Unc5a"

/note="IG; Region: Immunoglobulin"

/db_xref="CDD:smart00409"

984..1130

/misc_feature

/gene="Unc5a"

/note="TSPI; Region: Thrombospondin type 1 repeats"

/db_xref="CDD:smart00209"

1566..1877

/misc_feature

/gene="Unc5a"

/note="ZUS; Region: Domain present in ZO-1 and Unc5-like netrin receptors"

/db_xref="CDD:smart00218"

2496..2684

/misc_feature

/gene="Unc5a"

/note="DEATH; Region: DEATH domain, found in proteins involved in cell death (apoptosis). Alpha-helical domain present in a variety of proteins with apoptotic functions. Some (but not all) of these domains form homotypic and heterotypic dimers"

/db_xref="CDD:smart00005"

ORIGIN

Alignment Scores:

Pred. No.: 9,7e-29 Length: 3844

Score: 321.00 Matches: 60

Percent Similarity: 98.36% Conservative: 0

Best Local Similarity: 98.36% Mismatches: 1

Query Match: 98.47% Indels: 0

DB: 10 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x BC058084 (1-3844)

Qy 1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProAlaGluValGlu 20

Db 738 GAGCAAGGCATTGTGCTACCTTGTGCGCCCGGAGGAATCCCCCAGCTGAGTGGAG 797

Qy 21 TrpLeuArgAnGluAAspLeuValAspProSerLeuAspProAsnValTyrIleThrArg 40

Db 798 TGGCTCCGAAATGAGGACCTCGTGACCCCTCCCTCGACCCCAATGTGTATCATCACGG 857

Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60

Db 858 GAGCACACGCTAGTGTGCGGACGCCCGCTCGCCGACACTCCCACTACACTCGCTGTG 917

Qy 61 Ala 61

Db 918 GCC 920

RESULT 14

AC135142/c

LOCUS	AC135142	171419 bp	DNA	linear	HTG 15-NOV-2002
DEFINITION	Rattus norvegicus clone CH230-169P5, *** SEQUENCING IN PROGRESS				
ACCESSION	AC135142				
VERSION	AC135142.2 GI:25007239				
KEYWORDS	HTG; HTGS PHASE1; HTGS DRAFT; HTGS_ENRICHED.				
SOURCE	Rattus norvegicus (Norway rat)				
ORGANISM	Rattus norvegicus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
REFERENCE	1 (bases 1 to 171419)				
AUTHORS	Muzny D, Marie, Metzker M, Lee, Abramson S, Adams C, Alder J, Allen C, Allen H, Albrooks S, Amin A, Anguiano D, Anyalbechi V, Aoyagi A, Ayodeji M, Baca E, Baden H, Baldwin D, Bandaranaike D, Barber M, Barnstead M, Benahmed F, Biswal K, Blair J, Blankenburg K, Blyth P, Brown M, Bryant N, Buhay C, Burch P, Burrell K, Calderon E, Cardenas V, Carter K, Cavazos I, Ceasar H, Center A, Chacko J, Chavez D, Chen G, Chen R, Chen Y, Chen Z, Chu J, Cleveland C, Cockrell R, Cox C, Coyle M, Cree A, D'Souza L, Davila M, Davis C, Davy-Carroll L, De Anda C, Dederich D, Delgado O, Denson S, Deramo C, Ding Y, Dinh H, Divya K, Draper H, Dugan-Rocha S, Dunn A, Durbin K, Duval B, Eaves K, Egan A, Escotto M, Eugene C, Evans C, Falls T, Fan G, Fernandez S, Finley M, Flagg N, Forbes L, Foster M, Foster P, Fraser C, Gabisi A, Ganta R, Garcia A, Garner T, Garza M, Gebregiorgis E, Geer K, Gill R, Grady M, Guerra M, Guevara W, Gunaratne P, Haaland W, Hamill C, Hamilton C, Hamilton K, Harvey J, Havlak P, Hawes A, Henderson N, Hernandez J, Hernandez R, Hines S, Hladun S, Hodgson A, Hogues M, Hollins B, Howells S, Hulyk S, Hume J, Idlebird D, Jackson A, Jackson L, Jacob L, Jiang H, Johnson B, Johnson R, Jolivet A, Karpathy S, Kelly S, Kelly S, Khan Z, King L, Kovac C, Kowis C, Kraft C, Lebow H, Levan J, Lewis L, Li Z, Liu J, Liu J, Liu W, Liu J, London P, Longacre S, Lopez J, Lorensuewa L, Loulseghe H, Lozado R, Lu X, Ma J, Maheshwari M, Mahindratne M, Mahmoud M, Malloy K, Mangum A, Mangum B, Mapua P, Martin K, Martin R, Martinez E, Mawhinney S, McLeod M, McNeill T, Meenen E, Milosavljevic A, Miner G, Minja E, Montemayor J, Moore S, Morgan M, Morris K, Morris S, Munidasa M, Murphy M, Nair L, Nankervis C, Neal D, Newton N, Nguyen N, Norris S, Nwakoileme O, Okwuonu G, Olarnpusagoon A, Pal S, Parke K, Pasternak S, Paul H, Perez A, Perez J, Pfamkoch C, Plopper F, Poindecker A, Popovic D, Primus E, Pu L, Pu L, Puazo M, Quiroz J, Rachlin E, Reeves K, Regier M, Reigh R, Reilly B, Reilly M, Ren Y, Reuter M, Richards S, Riggs F, Rives C, Rodkey T, Rojas A, Rose M, Rose R, Ruiz S, Sanders W, Savery G, Scherer S, Scott G, Shateman S, Shen H, Shetty J, Shvartsbeyn A, Sison I, Sitter C, Smajs D, Sneed A, Sodergren E, Song X, Sorelle R, Sosa J, Steimle M, Strong R, Sutton A, Svatek A, Taber P, Taylor C, Taylor T, Thomas N, Thomas S, Tingey A, Trejos Z, Usmani K, Valas R, Vega V, Villasana D, Waldron L, Walker B, Wang J, Wang Q, Wang S, Warren J, Warren R, Wei X, White F, Williams G, Willson R, Wleczyk R, Wooden H, Worley K, Wright D, Wright R, Wu J, Yakub S, Yen J, Yoon L, Yoon V, Yu F, Zhang J, Zhou J, Zhou X, Zhao S, Dunn D, von Weinstock G, and Gibbs R.A.				
	Direct Submission				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 171419)				
AUTHORS	Rat Genome Sequencing Consortium.				
TITLE	Direct Submission				
JOURNAL	Submitted (08-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA				
REFERENCE	3 (bases 1 to 171419)				
AUTHORS	Rat Genome Sequencing Consortium.				
TITLE	Direct Submission				
JOURNAL	Submitted (15-NOV-2002) Human Genome Sequencing Center, Department				
COMMENT	<p>of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA</p> <p>On Nov 15, 2002 this sequence version replaced gi:23578050. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.</p> <p>----- Genome Center Center: Baylor College of Medicine Center code: BCM Web site: http://www.hgsc.bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu</p> <p>----- Project Information Center project name: KCMS Center clone name: CH230-169P5 ----- Summary Statistics Assembly program: Phrap; version 0.990329 Consensus quality: 127081 bases at least Q40 Consensus quality: 131254 bases at least Q30 Consensus quality: 131849 bases at least Q20 Estimated insert size: 128800; sum-of-contigs estimation Quality coverage: 5x in Q20 bases; sum-of-contigs estimation</p> <p>----- * NOTE: Estimated insert size may differ from sequence length * (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html). * NOTE: This is a 'working draft' sequence. It currently * consists of 9 contigs. The true order of the pieces * is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.</p> <p>1 18754: contig of 18754 bp in length 18854: gap of unknown length 18855: contig of 129006 bp in length 147861: gap of unknown length 147960: contig of 11875 bp in length 159835: gap of unknown length 159936: contig of 1150 bp in length 161086: gap of unknown length 161185: contig of 1304 bp in length 162489: gap of unknown length 162589: contig of 1459 bp in length 164048: gap of unknown length 164148: contig of 1170 bp in length 165318: gap of unknown length 165418: contig of 2149 bp in length 165419: gap of unknown length 167667: contig of 3752 bp in length. 167668: Location/Qualifiers 1.171419 /organism="Rattus norvegicus" /mol_type="genomic DNA" /db_xref="taxon:10116" /clone="CH230-169P5"</p>				
FEATURES	source				
ORIGIN	<p>Alignment Scores:</p> <p>Pred. No.: 4,45e-24 Length: 171419</p> <p>Score: 295.00 Matches: 61</p> <p>Percent Similarity: 59.22% Conservative: 0</p> <p>Best Local Similarity: 59.22% Mismatches: 0</p> <p>Query Match: 90.49% Indels: 42</p> <p>DB: 2 Gaps: 1</p>				

```

misc_feature      13700..15000
/notes=NOTE: Shatter libraries failed to verify number of
repeat copies 13700-15000. Unsure number of repeat copies
13700-15000."

ORIGIN

Alignment Scores:
Pred. No.:          2,97e-21          Length:      121282
Score:              270.50            Matches:      60
Percent Similarity: 59.41%            Conservative: 0
Best Local Similarity: 59.41%          Mismatches:   1
Query Match:        82.98%            Indels:       41
DB:                 9                  Gaps:         1

US-10-624-932C-2_COPY_163_223 (1-61) x AC027318 (1-121282)

Qy      1  GluGlnGlyIleValLeuProCysArgProGluGlyIleProProAlaGluVal--- 19
Db      11386 GAGCAGGGCATCGTGTGCCCTGCGCTCCACGGAGGGGCATCCCTCCAGCCGAGGT-GAG 11444
Qy      19  ----- 19
Db      11445 GGCTCCTCTAGTAGCCCAACGCTGGACCTGGGCTCTGCTGCTGCTCACCTGGCAGGGGCCA 11504
Qy      20  -----Glu 20
Db      11505 CTCTGGCGAGGGCCAGCATGGGGCTGGCAGTACATGGCAGGGCTCCCTCCCTAGTGGAG 11566
Qy      21  TrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArg 40
Db      11565 TGGCTCCGGAACGAGACACCTGGTGGAGCCCGTCCCTGGACCCCAATGTATACATCACGGCG 11627
Qy      41  GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
Db      11625 GAGCAGAGCCTGGTGGTGACAGAGCCCGCCTTGCTGACACGGCCCACTACACCTGCGTG 11687
Qy      61  Ala 61
Db      11685 GCC 11687

Search completed: September 9, 2005, 09:39:41
Job time : 2571.83 secs

```

US-10-624-932C-2_COPY_163_223 (1-61) x AC135142 (1-171419)

Qy	1	GlulnclnlyileValLeuProCyArsgProProGluGlyileProProAlaGlu	----- 18
Db	27265	GAGCAAGGCATTCTACTACCTTGTGCGCCCCCAGAGGAATCCCCAGCTGAGGTGAGT	27206
Qy	18	-----	18
Db	27205	AGGGGTACCGGGTTCCAGACCTCTGCTCTACTAAAGCTCAGACTCTCGCTTCCCCC	27146
Qy	18	-----	18
Db	27145	TCCCCAGTCTCACTCTGTACCTCTGTCAGGCCAGCATGGCTTCTCCCCCTAG	27086
Qy	19	ValgluTriLeuArghenGluAepLeuValAepProSerLeuAepProAsnValTyrlle	38
Db	27085	GTGAGTGGCTTCGAAATCAGGACCTCTGTGGACCCCTCCCTCGATCCCAATGTGTACATC	27026
Qy	39	ThrArgGluHisSerLeuValValArgGlnAlaAArgLeuAlaAsnThrAlaAsnTyThr	58
Db	27025	ACCCGGAGCACAGCCTGTGCTGCGCTCAGGCCCGCTGGCCGACACGGCCAACCTACACC	26966
Qy	59	CysValAla 61	
Db	26965	TGTGTGCC 26957	
RESULT 15			
LOCUS	AC027318	121282 bp DNA linear PRI 01-DEC-2002	
DEFINITION	Homo sapiens chromosome 5 clone CTC-347K15, complete sequence.		
ACCESSION	AC027318		
VERSION	AC027318.5	GI:25989047	
KEYWORDS	HTG.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 121282)		
AUTHORS	DOE Joint Genome Institute and Stanford Human Genome Center.		
TITLE	Direct Submission		
REFERENCE	2 (bases 1 to 121282)		
AUTHORS	DOE Joint Genome Institute.		
TITLE	Direct Submission		
JOURNAL	Submitted (30-MAR-2000) Production Sequencing Facility, DOE Joint		
	Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA		
REFERENCE	3 (bases 1 to 121282)		
AUTHORS	DOE Joint Genome Institute.		
TITLE	Direct Submission		
JOURNAL	Submitted (07-MAR-2002) Production Sequencing Facility, DOE Joint		
	Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA		
REFERENCE	4 (bases 1 to 121282)		
AUTHORS	DOE Joint Genome Institute and Stanford Human Genome Center.		
TITLE	Direct Submission		
JOURNAL	Submitted (01-DEC-2002) DOE Joint Genome Institute, 2800 Mitchell		
	Drive, Walnut Creek, CA 94598, USA		
COMMENT	On Dec 1, 2002 this sequence version replaced gi:19224786.		
	Draft Sequence Produced by DOE Joint Genome Institute		
	www.jgi.doe.gov		
	Finishing Completed at Stanford Human Genome Center		
	www.ehgc.stanford.edu		
	Quality: Phrap Quality >=40 99.9% of Sequence;		
	Estimated Total Number of Errors is 0.1.		
	NOTE: Shatter libraries failed to verify number of repeat copies		
	13700-15000. Unsure number of repeat copies 13700-15000.		
FEATURES	Location/Qualifiers		
source	1. .121282		
	/organism="Homo sapiens"		
	/mol_type="genomic DNA"		
	/db_xref="taxon:9606"		
	/chromosome="5"		
	/clone="CTC-347K15"		

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 8, 2005, 20:54:46 ; Search time 315.473 Seconds
(without alignments)
1144.643 Million cell updates/sec

Title: US-10-624-932C-2_COPY_163_223

Perfect score: 326

Sequence: 1 EQGIVLPCRPPGPIPAEVE.....HSLVVRQARLADTANYTCVA 61

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool_h/US10624932/runat_08092005_161705_15766/app_query.fasta_1.1386
-DB=N Geneseq -QFMT=fastcap -SUFFIX=rng -MINMATCH=0 -LORFEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORW=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USBR=US10624932 @CGN 1 1 1052 @runat_08092005_161705_15766 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq_16Dec04.*

- 1: geneseqn1980s.*
- 2: geneseqn1990s.*
- 3: geneseqn2000s.*
- 4: geneseqn2001as.*
- 5: geneseqn2001bs.*
- 6: geneseqn2002as.*
- 7: geneseqn2002bs.*
- 8: geneseqn2003as.*
- 9: geneseqn2003bs.*
- 10: geneseqn2003cs.*
- 11: geneseqn2003ds.*
- 12: geneseqn2004as.*
- 13: geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	326	100.0	993	12 ADH71611	Adh71611 Human gen
2	326	100.0	1002	12 ADH71619	Adh71619 Human gen
3	326	100.0	1009	12 ADH71615	Adh71615 Human gen
4	326	100.0	1009	12 ADH71613	Adh71613 Human gen
5	326	100.0	2230	12 ADQ67252	Adq67252 Novel hum

6	326	100.0	2463	12 ADH71623	Adh71623 Human gen
7	326	100.0	2575	12 ADH71621	Adh71621 Human gen
8	326	100.0	2697	6 AAS16843	Aas16843 Rat netri
9	326	100.0	2697	6 ABK52891	Abk52891 Human net
10	326	100.0	2752	6 ABK37922	Abk37922 cDNA enco
11	326	100.0	2752	12 ADH71617	Adh71617 Human gen
12	326	100.0	2880	12 ADH71633	Adh71633 Human gen
13	326	100.0	2881	6 ABK49422	Abk49422 DNA enco
14	326	100.0	2881	10 ADG42568	Adg42568 Novel hum
15	326	100.0	2881	12 ADH71649	Adh71649 Human gen
16	326	100.0	2881	12 ADH71635	Adh71635 Human gen
17	326	100.0	2881	12 ADH71637	Adh71637 Human gen
18	326	100.0	2881	12 ADH71641	Adh71641 Human gen
19	326	100.0	2881	12 ADH71609	Adh71609 Human gen
20	326	100.0	2881	12 ADH71629	Adh71629 Human gen
21	326	100.0	2881	12 ADH71631	Adh71631 Human gen
22	326	100.0	2881	12 ADH71645	Adh71645 Human gen
23	326	100.0	2881	12 ADH71627	Adh71627 Human gen
24	326	100.0	2881	12 ADH71639	Adh71639 Human gen
25	326	100.0	2881	12 ADH71643	Adh71643 Human gen
26	326	100.0	2881	12 ADH71625	Adh71625 Human gen
27	326	100.0	2881	12 ADH71647	Adh71647 Human gen
28	326	100.0	2907	4 AAK52261	Aak52261 Human pol
29	326	100.0	3014	2 AAV52940	Av52940 Rat UNC-5
30	326	100.0	3561	12 ADL06497	Adl06497 Human tum
31	326	100.0	3580	6 ABK15169	Abk15169 Human RBP
32	242	74.2	2612	13 ADR99261	Adr99261 Splice va
33	242	74.2	2780	13 ADR99251	Adr99251 Human sRO
34	242	74.2	2796	10 AAL56266	Aal56266 Human thr
35	242	74.2	2986	13 ADR99249	Adr99249 Human lRO
36	242	74.2	3646	5 AAS75738	Aas75738 DNA enco
37	242	74.2	3646	13 ADR99257	Adr99257 Human unc
38	230	70.6	2831	2 AAV52942	Av52942 Rat UNC-5
39	230	70.6	2838	12 ADO09501	Ado09501 Rat trans
40	230	70.6	2860	6 ABT06279	Abt06279 Human NOV
41	230	70.6	2860	6 ABT06280	Abt06280 Human NOV
42	230	70.6	2895	6 ABQ33898	Abq33898 Human tra
43	230	70.6	2995	6 ABK92062	Abk92062 DNA enco
44	230	70.6	3501	11 ADN39805	Adn39805 Cancer/an
45	230	70.6	3884	4 AAS21316	Aas21316 Human cDN

ALIGNMENTS

RESULT 1
ADH71611
ID ADH71611 standard; DNA; 993 BP.
XX
AC ADH71611;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human gene of the invention NOV21b SEQ ID NO:507.
XX

ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
anorectic; antidiabetic; antimicrobial; antipaemic; gene therapy;
vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
obesity; diabetes; infectious disease; metabolic syndrome X;
dyslipidaemia.

OS Homo sapiens.
XX
FN WO2003102155-A2.
XX
PD 11-DEC-2003.
XX

XX 03-JUN-2003; 2003WO-US017430.
XX
PF 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 05-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.

XX ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipaeamic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.

XX Homo sapiens.

XX WO2003102155-A2.

XX 11-DEC-2003.

XX 03-JUN-2003; 2003WO-US017430.

XX 03-JUN-2002; 2002US-0385120P.

XX 04-JUN-2002; 2002US-0385784P.

XX 05-JUN-2002; 2002US-0386041P.

XX 05-JUN-2002; 2002US-0386047P.

XX 06-JUN-2002; 2002US-0386453P.

XX 06-JUN-2002; 2002US-0387016P.

XX 07-JUN-2002; 2002US-0387969P.

XX 07-JUN-2002; 2002US-0386931P.

XX 07-JUN-2002; 2002US-0386942P.

XX 07-JUN-2002; 2002US-0386971P.

XX 07-JUN-2002; 2002US-0387262P.

XX 08-JUN-2002; 2002US-0296960P.

XX 10-JUN-2002; 2002US-0387400P.

XX 10-JUN-2002; 2002US-0387535P.

XX 11-JUN-2002; 2002US-0387610P.

XX 11-JUN-2002; 2002US-0387625P.

XX 11-JUN-2002; 2002US-0387634P.

XX 11-JUN-2002; 2002US-0387668P.

XX 11-JUN-2002; 2002US-0387702P.

XX 11-JUN-2002; 2002US-0387836P.

XX 11-JUN-2002; 2002US-0387859P.

XX 12-JUN-2002; 2002US-0387933P.

XX 12-JUN-2002; 2002US-0387934P.

XX 12-JUN-2002; 2002US-0387960P.

XX 12-JUN-2002; 2002US-0388022P.

XX 12-JUN-2002; 2002US-0388096P.

XX 13-JUN-2002; 2002US-0389123P.

XX 14-JUN-2002; 2002US-0389118P.

XX 14-JUN-2002; 2002US-0389120P.

XX 14-JUN-2002; 2002US-0389144P.

XX 14-JUN-2002; 2002US-0389146P.

XX 17-JUN-2002; 2002US-0389729P.

XX 17-JUN-2002; 2002US-0389742P.

XX 18-JUN-2002; 2002US-0389884P.

XX 19-JUN-2002; 2002US-0390068P.

XX 19-JUN-2002; 2002US-0390209P.

XX 21-JUN-2002; 2002US-0390763P.

XX 17-JUL-2002; 2002US-0396706P.

XX 06-AUG-2002; 2002US-0401628P.

XX 09-AUG-2002; 2002US-0402156P.

XX 09-AUG-2002; 2002US-0402256P.

XX 09-AUG-2002; 2002US-0402389P.

XX 12-AUG-2002; 2002US-0402786P.

XX 12-AUG-2002; 2002US-0402816P.

XX 12-AUG-2002; 2002US-0402821P.

XX 12-AUG-2002; 2002US-0402832P.

XX 13-AUG-2002; 2002US-0403448P.

XX 13-AUG-2002; 2002US-0403459P.

XX 13-AUG-2002; 2002US-0403531P.

XX 13-AUG-2002; 2002US-0403532P.

XX 13-AUG-2002; 2002US-0403563P.

XX 13-AUG-2002; 2002US-0406317P.

XX 15-AUG-2002; 2002US-0403617P.

XX 26-AUG-2002; 2002US-0406182P.

PR 26-AUG-2002; 2002US-0406355P.

PR 27-AUG-2002; 2002US-0406240P.

PR 12-SEP-2002; 2002US-0410084P.

PR 20-SEP-2002; 2002US-0412528P.

PR 23-SEP-2002; 2002US-0412731P.

PR 30-SEP-2002; 2002US-0414801P.

PR 30-SEP-2002; 2002US-0414839P.

PR 30-SEP-2002; 2002US-0414840P.

PR 09-OCT-2002; 2002US-0417186P.

PR 09-OCT-2002; 2002US-0417406P.

PR 23-OCT-2002; 2002US-0420639P.

PR 28-OCT-2002; 2002US-0421156P.

PR 31-OCT-2002; 2002US-0422690P.

PR 01-NOV-2002; 2002US-0423130P.

PR 05-NOV-2002; 2002US-00423798.

PR 05-NOV-2002; 2002US-0423798P.

PR 12-NOV-2002; 2002US-0425453P.

XX (CURA-) CURAGEN CORP.

XX Alsbrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;

XX Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;

XX Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;

XX Gusev VI, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;

XX MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;

XX Padigaru M, Patturajan M, Pena CE, Peyman JA, Raha D, Rastelli L;

XX Rieger DK, Rotherberg ME, Sciore P, Shenoy SG, Shimkets RA;

XX Smithson G, Spytek KA, Stone DJ, Vernet CM, Voss EZ, Zhong M;

XX Zhong H;

XX WPI; 2004-081935/08.

XX P-PSDB; ADH71620.

XX New NOVX polypeptides and nucleic acid molecules useful for preventing or

XX creating NOVX-associated disorders, e.g. cancer, diabetes, infection or

XX obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

XX Example 21; SEQ ID NO 515; 1880pp; English.

XX The invention relates to a novel isolated polypeptide (NOVX). A

XX polypeptide of the invention has cytostatic, immunomodulator,

XX neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and

XX antilipaeamic activity, and may have a use in gene therapy, and as a

XX vaccine. The polypeptides are encoded by NOVX polynucleotides comprising

XX any of the 303 fully defined nucleotide sequences given in the

XX specification. The polypeptide is useful in the manufacture of a

XX medicament for treating a syndrome associated with a human disease. The

XX polypeptide, polynucleotide and antibody are useful in diagnosing,

XX treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,

XX Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious

XX diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are

XX further used as hybridisation probes, in chromosome mapping, tissue

XX typing, preventive medicine, and pharmacogenomics. The present sequence

XX encodes a NOVX polypeptide of the invention.

XX SQ Sequence 1002 BP; 193 A; 311 C; 335 G; 163 T; 0 U; 0 Other;

XX Alignment Scores:

XX Pred. No.: 9.76e-35 Length: 1002

XX Score: 326.00 Matches: 61

XX Percent Similarity: 100.00% Conservative: 0

XX Best Local Similarity: 100.00% Mismatches: 0

XX Query Match: 100.00% Indels: 0

XX DB: 12 Gaps: 0

XX US-10-624-932C-2_COPY_163_223 (1-61) x ADH71619 (1-1002)

XX Qy 1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProGluValGlu 20

XX Db 418 GAGCAGGGCATCGTGGCTCCCTCCACCGAGGGGCATCCCTCCAGCGAGGTGGAG 477

XX Qy 21 TriLeuArgAenGluAspLeuValAspProSerLeuAspProAenValTyrIleThrArg 40

XX New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
XX Example 21; SEQ ID NO 509; 1880pp; English.
XX
XX The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipidemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.
XX
SQ Sequence 1009 BP; 195 A; 314 C; 336 G; 164 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9.85e-35 Length: 1009
Score: 326.00 Matches: 61
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-10-624-932c-2_COPY_163_223 (1-61) x ADH71613 (1-1009)
Qy 1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProAlaGluValGlu 20
Db 422 GAGCAGGGCATCGTGTGCTGCCCTCCACCGAGGGCATCCCTCCAGCGAGGTGGAG 481

Qy 21 TrpLeuArgAsnGluAspLeuValAspProSerLeuAspProLeuValTyrIleThrArg 40
Db 482 TGGCTCCGGAAACGAGGACCTGGTGGACCCGCTCCCTGGACCCCAATGTATACATCAGCGG 541

Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAspThrCysVal 60
Db 542 GAGCACAGCCTGGTGGTGACAGGCCCGCTTCTGACACGGCCCACTACCTCGGTG 601

Qy 61 Ala 61
Db 602 GCC 604

RESULT 5
AD067252
ID ADQ67252 standard; cDNA; 2230 BP.
XX
AC ADQ67252;
XX
DT 07-OCT-2004 (first entry)
XX
XX Novel human cDNA sequence #2225.
XX
ss; gene; osteopathic; neuroprotective; nootropic; antiparkinsonian;
KW cytostatic; gene therapy; diagnostic marker; morbid state; osteoporosis;
KW neurological disease; Alzheimer's disease; Parkinson's disease; dementia;
KW cancer.
XX
XX Homo sapiens.
OS
XX
PN EP1440981-A2.
XX
PD 28-JUL-2004.
XX
XX 21-JAN-2004; 2004EP-00001196.

XX 21-JAN-2003; 2003JP-00102206.
PR 03-MAY-2003; 2003JP-00131392.
XX
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Nagai K, Irie R;
XX
DR WPI; 2004-535376/52.
DR P-PSDB; ADQ67559.
XX
XX Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,
PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
XX
XX Claim 1; SEQ ID NO 4413; 2449pp; English.
XX
XX The invention relates to 2495 novel polynucleotides (I) and their encoded
CC polypeptides, sequences hybridizing to these nucleotides, sequences
CC encoding partial polypeptides and sequences having 70% or 90% identity to
CC the nucleotide and protein sequences. The nucleotides and polypeptides
CC are useful as diagnostic markers or therapeutic target for the diseases
CC or morbid states. They are also useful for treating osteoporosis,
CC neurological diseases, Alzheimer's diseases, Parkinson's diseases,
CC dementia and various cancers. This sequence corresponds to a nucleotide
CC sequence of the invention.
XX
SQ Sequence 2230 BP; 458 A; 947 C; 462 G; 363 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.78e-34 Length: 2230
Score: 326.00 Matches: 61
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-10-624-932c-2_COPY_163_223 (1-61) x ADQ67252 (1-2230)
Qy 1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProAlaGluValGlu 20
Db 556 GAGCAGGGCATCGTGTGCTGCCCTCCACCGAGGGCATCCCTCCAGCGAGGTGGAG 615

Qy 21 TrpLeuArgAsnGluAspLeuValAspProSerLeuAspProLeuValTyrIleThrArg 40
Db 616 TGGCTCCGGAAACGAGGACCTGGTGGACCCGCTCCCTGGACCCCAATGTATACATCAGCGG 675

Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAspThrCysVal 60
Db 676 GAGCACAGCCTGGTGGTGACAGGCCCGCTTCTGACACGGCCCACTACCTCGGTG 735

Qy 61 Ala 61
Db 736 GCC 738

RESULT 6
ADH71623
ID ADH71623 standard; DNA; 2463 BP.
XX
AC ADH71623;
XX
XX 25-MAR-2004 (first entry)
DT
XX Human gene of the invention NOV21h SEQ ID NO:519.
DE
XX
KW ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipidemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX
OS Homo sapiens.
XX

Db 598 GCC 600
RESULT 7
ADH71621
ID ADH71621 standard; DNA; 2575 BP.
XX AC ADH71621;
XX AC ADH71621;
XX 25-MAR-2004 (first entry)
XX Human gene of the invention NOV21g SEQ ID NO:517.
DE
KW ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipaeamic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX
OS Homo sapiens.
XX
PN W02003102155-A2.
XX
XX 11-DEC-2003.
XX 03-JUN-2003; 2003WO-US017430.
XX
PR 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 05-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 06-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-0386796P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0295960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 10-JUN-2002; 2002US-0387535P.
PR 10-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390066P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.

PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
XX
XX (CURA-) CURAGEN CORP.
XX
PI Alsbrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Btenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigar M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg MB, Sciore P, Shenoy SG, Shinkets RA;
PI Smithson G, Spytek KA, Stone DU, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;
XX
XX WPI; 2004-081935/08.
DR P-PSDB; ADH71622.
DR
XX
XX
PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
XX Example 21; SEQ ID NO 517; 1880pp; English.
XX
XX The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaeamic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.
XX
SQ Sequence 2575 BP; 490 A; 873 C; 754 G; 458 T; 0 U; 0 Other;
Alignment Scores: 3.35e-34 Length: 2575
Pred. No.: 326.00 Matches: 61
Score: 100.00% Conservative: 0
Percent Similarity:

```
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x ADH71621 (1-2575)

Qy 1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProProAlaGluValGlu 20
Db 462 GAGCAGGCGCATCGTGCCTGCCCTCCACCGGAGGCGCATCCCTCCAGCGGAGTGGAG 521

Qy 21 TrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArg 40
Db 522 TGGCTCCGGAACGAGGACCTGGTGACCCCGCTGGACCCCAATGTATATACATCACGCGG 581

Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
Db 582 GAGCAGACCTGGTGGTGCGACAGCCCGCTTGTGACAGGCGCAACTACACCTGGGTG 641

Qy 61 Ala 61
Db 642 GCC 644

RESULT 8
AAS16843
ID AAS16843 standard; cDNA; 2697 BP.
AC AAS16843;
XX
DT 14-FEB-2002 (first entry)
XX
DE Rat netrin receptor UNC5H1 (YSG7) cDNA.
XX
XX YSG; YSG7; schizophrenia; chronic animal model; LCGU; netrin receptor;
XX local cerebral glucose utilisation; phosphodiesterase 1-alpha; UNC5H1;
XX calcium-independent alpha-latrotoxin receptor; CIRL; trkB; synapsin 1A;
XX epithelial discoidin domain receptor 1; synapsin 1B; neuroleptic; ss;
XX tumour necrosis factor alpha; TNF-alpha; rat.
XX
OS Rattus sp.
XX
XX
XX Key Location/Qualifiers
XX CDS 1..2697
XX FT /*tag= a
XX FT /product= "Rat netrin receptor UNC5H1"
XX
XX PN WO200175440-A2.
XX
XX PD 11-OCT-2001.
XX
XX PF 02-APR-2001; 2001WO-GB001486.
XX
XX PR 31-MAR-2000; 2000GB-00007880.
XX
XX PR 26-MAY-2000; 2000GB-00012768.
XX
XX PA (WELF-) WELFIDE CORP.
XX
XX PI Cochran S, Paterson G, Ohashi Y, Morris B, Pratt J;
XX
XX WPI; 2002-010813/01.
XX
XX DR P-PSDB; AAU10543.
XX
XX Novel chronic animal model of schizophrenia, useful for identifying anti-
XX psychotic drugs and genes that are associated with schizophrenia.
XX
XX PS Claim 1; Fig 8a; 79pp; English.
XX
XX The invention relates to YSG polynucleotide fragments for use in
XX diagnosing and/or developing treatments for schizophrenia using chronic
XX animal models. The polynucleotides and their encoded polypeptides are
XX used for identification of compounds which modulate the expression of YSG
XX molecules, leading to the manufacture of schizophrenia medications. The
XX sequences can also be used for testing candidate compounds for any effect
XX on the polypeptides. Anti-schizophrenic effects of a compound can be
```

```
CC determined by measuring local cerebral glucose utilisation (LCGU) or
CC comparing its expression level with that of a control group. The
CC sequences are useful in the identification of genes associated with
CC schizophrenic states and in the development of an antibody. The sequences
CC of the invention include phosphodiesterase 1-alpha, calcium-independent
CC alpha-latrotoxin receptors (CIRL)-1,2k3, epithelial discoidin domain
CC receptor 1 (trkB), netrin receptor (UNC5H1), synapsins 1A and 1B and
CC tumour necrosis factor (TNF) alpha. This sequence represents rat netrin
CC receptor UNC5H1 (YSG7) DNA
XX
SQ Sequence 2697 BP; 541 A; 864 C; 766 G; 526 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 3.56e-34 Length: 2697
Score: 326.00 Matches: 61
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
XX
US-10-624-932C-2_COPY_163_223 (1-61) x AAS16843 (1-2697)

Qy 1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProProAlaGluValGlu 20
Db 487 GAGCAGGCGCATCGTGCCTGCCCTCCACCGGAGGCGCATCCCTCCAGCGGAGTGGAG 546

Qy 21 TrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArg 40
Db 547 TGGCTTCGGAATGAGGACCTGGTGACCCCGCTCCCTCCGATCCCAATGTATATACATCACGCGG 606

Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
Db 607 GAGCAGACCTAGTGCCTGCGTGCAGCCCGCTGGCGGACGCGCAACTACACCTGTGTG 666

Qy 61 Ala 61
Db 667 GCC 669

RESULT 9
ABK52891
ID ABK52891 standard; DNA; 2697 BP.
XX
XX AC ABK52891;
XX
XX DT 27-AUG-2002 (first entry)
XX
XX DE Human netrin binding membrane receptor UNC5H-1 DNA sequence #1.
XX
XX KW Netrin binding membrane receptor; receptor; UNC5H-1; gene; ds; human;
XX neotropic; neuroprotective; cytosolic; antiparkinsonian;
XX cerebroprotective; cancer; central nervous system; CNS; stroke;
XX Parkinson's disease; multiple sclerosis; Alzheimer's disease.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX CDS 1..2697
XX FT /*tag= a
XX FT /product= "Netrin binding membrane receptor UNC5H-1"
XX
XX PN WO200233080-A2.
XX
XX XX 25-APR-2002.
XX
XX PF 15-OCT-2001; 2001WO-EP011891.
XX
XX PR 16-OCT-2000; 2000US-0240061P.
XX
XX PA (FARB ) BAYER AG.
XX
XX PI Koehler RH;
XX
XX WPI; 2002-463314/49.
XX
XX DR
```

DR P-PSDB; AAU97899.
XX Novel human netrin binding membrane receptor polypeptide and
PT polynucleotides for identifying modulating agents useful in treating
PT diseases e.g. Parkinson's disease, multiple sclerosis, stroke,
PT Alzheimer's disease.
XX
XX
PS Claim 1; Fig 1; 94pp; English.
CC This invention relates to the DNA and protein sequences of a novel
CC purified human netrin binding membrane receptor, UNC5H-1. The DNA
CC sequence of the invention is useful as a probe for detecting a nucleic
CC acid encoding the UNC5H-1 protein in a biological sample. The sequences
CC of the invention are useful to screen for agents which decrease the
CC activity of the UNC5H-1 protein. The sequences are also useful for
CC screening agents which regulate (modulate) the activity of the protein of
CC the invention. A pharmaceutical composition containing the protein of the
CC invention or a reagent that modulates the activity of the UNC5H-1 protein
CC may be useful for treating a UNC5H-1 dysfunction related disease such as
CC cancer or a central nervous system (CNS) disorders (e.g. Parkinson's
CC disease, multiple sclerosis, stroke and Alzheimer's disease). Fusion
CC proteins comprising the UNC5H-1 protein are useful for generating
CC antibodies and for in various assay systems, and the protein can be used
CC as a bait protein in a two-hybrid assay or three-hybrid assay. The method
CC of the invention is useful for detecting a coding sequence for the UNC5H-
CC 1 protein. The present sequence represents a DNA sequence encoding the
CC human netrin binding membrane receptor UNC5H-1 protein of the invention
XX
SQ Sequence 2697 BP; 503 A; 906 C; 807 G; 481 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3,56e-34 Length: 2697
Score: 326.00 Matches: 61
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-624-932c-2_COPY_163_223 (1-61) x ABK52891 (1-2697)

QY 1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProGluAlaGluValGlu 20
DB 487 GAGCAGGCGCATCGTGTGCTGCTGCGTCCACCGAGGCGCATCCTCCAGCGAGGTGGAG 546
QY 21 TrpleuArgAnGluApLeuValAspProSerleuAspProAnValTyrIleThrArg 40
DB 547 TGGCTCCGGAACGAGGACCTGGTGGACCGCTCCCTGGACCCCAATGTATACATCACGCGG 606
QY 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
DB 607 GAGCAGAGCTGTGTGTGGCAGACGCCCGCTTGTGTACAGCGCCAACTACACTGCTGCTG 666
QY 61 Ala 61
DB 667 GCC 669

RESULT 10
ABK37922
ID ABK37922 standard; cDNA; 2752 BP.
XX
AC ABK37922;
XX
DT 21-MAY-2002 (first entry)
XX
DE cDNA encoding Human protein NOV1.
XX
KW Human; NOVX; ss; Gene; cardiomyopathy; atherosclerosis; diabetes;
KW cell signal processing disorder; metabolic disorder; obesity; infection;
KW anorexia; cancer-associated cachexia; cancer; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorders; dyslipidaemia; pain; asthma; hypertension;
KW osteoporosis; Crohn's disease; multiple sclerosis; angina pectoris;
KW myocardial infarction; ulcer; allergy; benign prostatic hypertrophy;

KW psychosis; neurological disorder; anxiety; schizophrenia;
KW manic depression; dementia; dyskinesia; Huntington's disease;
KW Gilles de la Tourette's syndrome; gene therapy.
XX
OS Homo sapiens.
XX
PN WC200210216-A2.
XX
PD 07-FEB-2002.
XX
XX 30-JUL-2001; 2001WO-US024225.
XX
XX 28-JUL-2000; 2000US-0221409P.
XX 04-AUG-2000; 2000US-0222840P.
PR 04-AUG-2000; 2000US-0223752P.
PR 04-AUG-2000; 2000US-0223762P.
PR 04-AUG-2000; 2000US-0223769P.
PR 04-AUG-2000; 2000US-0223770P.
PR 14-AUG-2000; 2000US-0225146P.
PR 15-AUG-2000; 2000US-0225392P.
PR 15-AUG-2000; 2000US-0225470P.
PR 16-AUG-2000; 2000US-0225697P.
PR 01-FEB-2001; 2001US-0263662P.
PR 05-APR-2001; 2001US-0281645P.
XX (CURA-) CURAGEN CORP.
XX
XX Padigaru M, Mezes P, Mishra V, Burgess C, Caeman S, Grosse WM;
PI Alsobrook JP, Lepley DM, Gerlach VL, Macdougall JR, Smithson G;
XX
DR WPI; 2002-180074/23.
DR P-PSDB; AAU85403.
XX
XX New isolated cytoplasmic, nuclear, membrane bound, or secreted
PT polypeptide, useful for treating cardiomyopathy, atherosclerosis,
PT infections, cancer, neurodegenerative, metabolic, hematopoietic and
PT immune disorders.
XX
PS Claim 9; Page 9-10; 213pp; English.

CC The invention relates to an isolated cytoplasmic, nuclear, membrane
CC bound, or secreted polypeptide (NOVX, x= 1-14) their variants or mature
CC form. Also included are the nucleic acids encoding the NOVX proteins, a
CC vector comprising the nucleic acid, a cell comprising the vector, an anti
CC -NOVX antibody and modulators of NOVX. NOVX, the nucleic acid and the
CC antibody are useful for treating or preventing a NOVX-associated
CC disorder, where the disorder is selected from cardiomyopathy,
CC atherosclerosis, diabetes, a disorder related to cell signal processing
CC and metabolic pathway modulation, metabolic disorders, obesity,
CC infectious disease, anorexia, cancer-associated cachexia, cancer,
CC neurodegenerative disorders, Alzheimer's disease, Parkinson's disease,
CC immune disorders, haematopoietic disorders, and the various
CC dyslipidaemias, metabolic disturbances associated with obesity, the
CC metabolic syndrome X and wasting disorders associated with chronic
CC diseases, bacterial, fungal, protozoal and viral infections, pain,
CC bulimia, asthma, hypertension, urinary retention, osteoporosis, Crohn's
CC disease, multiple sclerosis, Albright Hereditary Osteodystrophy, angina
CC pectoris, myocardial infarction, ulcer, allergy, benign prostatic
CC hypertrophy, and psychotic and neurological disorders, including anxiety,
CC schizophrenia, manic depression, delirium, dementia, and dyskinesias,
CC such as Huntington's disease and Gilles de la Tourette's syndrome. The
CC nucleic acid is useful in gene therapy. The present sequence encodes a
CC NOVX protein
XX
SQ Sequence 2752 BP; 505 A; 937 C; 829 G; 481 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3,56e-34 Length: 2752
Score: 326.00 Matches: 61
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-624-932c-2_copy_163_223 (1-61) x ABK37922 (1-2752)

QY 1 GluGlnGlyIleValLeuProCysArgProProGluGlyIleProProAlaGluValGlu 20

Db 532 GAGCAGGGGATCGTCTGCCCTCCCTCCACGAGGGATCCCTCCAGCCGAGGTGGAG 591

QY 21 TrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTrpIleThrArg 40

Db 592 TGGCTCCGGAACGAGGACCTGGTGGACCGTCCCTGGACCCCAATGTATACATCAGCGG 651

QY 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTrpThrCysVal 60

Db 652 GAGCAGCGCTGGTGGCAGAGCCCGCTTGTGTGACGCGCAACTACACCTGCGGTG 711

QY 61 Ala 61

Db 712 GCC 714

RESULT 11

ID ADH71617

XX ADH71617 standard; DNA; 2752 BP.

AC ADH71617;

XX 25-MAR-2004 (first entry)

XX Human gene of the invention NOV21e SEQ ID NO:513.

XX ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;

KW anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;

KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;

KW obesity; diabetes; infectious disease; metabolic syndrome X;

XX dyslipidaemia.

XX Homo sapiens.

XX WO2003102155-A2.

XX 11-DEC-2003.

XX 03-JUN-2003; 2003WO-US017430.

XX 03-JUN-2002; 2002US-0385120P.

PR 04-JUN-2002; 2002US-0385784P.

PR 05-JUN-2002; 2002US-0386041P.

PR 05-JUN-2002; 2002US-0386047P.

PR 06-JUN-2002; 2002US-0386376P.

PR 06-JUN-2002; 2002US-0386664P.

PR 07-JUN-2002; 2002US-0387016P.

PR 07-JUN-2002; 2002US-0387969P.

PR 07-JUN-2002; 2002US-0388631P.

PR 07-JUN-2002; 2002US-0388942P.

PR 07-JUN-2002; 2002US-0388971P.

PR 07-JUN-2002; 2002US-0387262P.

PR 08-JUN-2002; 2002US-0296960P.

PR 10-JUN-2002; 2002US-0387400P.

PR 10-JUN-2002; 2002US-0387535P.

PR 11-JUN-2002; 2002US-0387610P.

PR 11-JUN-2002; 2002US-0387625P.

PR 11-JUN-2002; 2002US-0387634P.

PR 11-JUN-2002; 2002US-0387668P.

PR 11-JUN-2002; 2002US-0387696P.

PR 11-JUN-2002; 2002US-0387702P.

PR 11-JUN-2002; 2002US-0387836P.

PR 11-JUN-2002; 2002US-0387859P.

PR 12-JUN-2002; 2002US-0387933P.

PR 12-JUN-2002; 2002US-0387934P.

PR 12-JUN-2002; 2002US-0387960P.

PR 12-JUN-2002; 2002US-0388022P.

PR 12-JUN-2002; 2002US-0388096P.

PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-039006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 15-AUG-2002; 2002US-0406317P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.

(CURA-) CURAGEN CORP.

PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kakuda R, Li L, Liu X, Macdougall JR;
PI Maciachian T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigaru M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shinkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;

WPI; 2004-081935/08.

P-PSDB; ADH71618.

New NOVX polypeptides and nucleic acid molecules useful for preventing or treating NOVX-associated disorders, e.g. cancer, diabetes, infection or obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

Example 21; SEQ ID NO 513; 1880pp; English.

The invention relates to a novel isolated polypeptide (NOVX). A

polypeptide of the invention has cytostatic, immunomodulator,

neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and

antilipemic activity, and may have a use in gene therapy, and as a

vaccine. The polypeptides are encoded by NOVX polynucleotides comprising

CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOX polypeptide of the invention.
XX
SQ Sequence 2752 BP; 505 A; 937 C; 829 G; 481 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3.66e-34 Length: 2752
Score: 326.00 Matches: 61
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-10-624-932c-2_copy_163_223 (1-61) x ADH71617 (1-2752)

Qy 1 GluGlnGlyIleValLeuProCysArgProProGluGlyIleProProAlaGluValGlu 20
|||
Db 532 GAGCAGGCGCATCGTCTGCCCTGCCCTCCACCGAGGGCATCCCTCCAGCGAGTGGAG 591
|||
Qy 21 TrpLeuArgAenGluAppLeuValAspProSerLeuAspProAenValTyrIleThrArg 40
|||
Db 592 TGGCTCCGGAACAGGAGCACCTGGTGGACCCGCTCCCTGGAGCCCAATGTATACATCACGCGG 651
|||
Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAenTyrThrCysVal 60
|||
Db 652 GAGCACACGCTGGTGGTGGCGACAGGCGCCGCTTGTGACACGGCCAACTACACCTGGGTG 711
|||
Qy 61 Ala 61
|||
Db 712 GCC 714

RESULT 12
ADH71633
ID ADH71633 standard; DNA; 2880 BP.
XX AC ADH71633;
XX DT 25-MAR-2004 (first entry)
XX DE Human gene of the invention NOV21m SEQ ID NO:529.
XX ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
XX anorectic; antidiabetic; antimicrobial; antilipaeamic; gene therapy;
XX vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
XX obesity; diabetes; infectious disease; metabolic syndrome X;
XX dyslipidaemia.
XX OS Homo sapiens.
XX WO2003102155-A2.
XX 11-DEC-2003.
XX 03-JUN-2003; 2003WO-US017430.
XX 03-JUN-2002; 2002US-0385120P.
XX 04-JUN-2002; 2002US-0385784P.
XX 05-JUN-2002; 2002US-0386041P.
XX 05-JUN-2002; 2002US-0386047P.
XX 06-JUN-2002; 2002US-0386376P.
XX 06-JUN-2002; 2002US-0386453P.
XX 06-JUN-2002; 2002US-0386864P.
XX 06-JUN-2002; 2002US-0387016P.
XX 07-JUN-2002; 2002US-0386796P.
XX 07-JUN-2002; 2002US-0386816P.

PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 08-JUN-2002; 2002US-0387262P.
PR 10-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387658P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390066P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-040617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-0423798P.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
XX
PA (CURA-) CURAGEN CORP.
XX
XX Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Caterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Eitenberg S, Gangoli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;


```
AC ADG42568;
XX
XX 26-FEB-2004 (first entry)
XX AC
XX ADH71649;
XX
XX DE
XX Novel human NOV1 cDNA.
XX
XX cytostatic; gene therapy; NOVX-agonist; NOVX-antagonist; pharmaceutical;
XX NOVX-associated disorder; cancer; human; gene; ss.
XX
XX Homo sapiens.
XX
XX US2003204052-A1.
XX
XX 30-OCT-2003.
XX
XX 04-OCT-2001; 2001US-00970944.
XX
XX 04-OCT-2000; 2000US-0237862P.
XX
XX (HERR/) HERRMANN J L.
XX (RAST/) RASTELLI L.
XX (SHIM/) SHIMKETS R A.
XX
XX Herrmann JL, Rastelli L, Shimkets RA;
XX
XX WPI; 2003-900673/82.
XX
XX P-PSDB; ADG42569.
XX
XX New NOVX gene or NOVX-specific antibody, useful for preparing a
XX composition for treating or preventing a NOVX-associated disorder, e.g.,
XX cancer.
XX
XX Claim 9; SEQ ID NO 1; 118pp; English.
XX
XX The invention describes a new isolated polypeptide comprising: a
XX polypeptide or its mature form comprising a sequence not given in the
XX specification; or a variant of (A) where one or more amino acid residues
XX in the variant differs in no more than 15% from the amino acid sequence
XX of the mature form. The pharmaceutical composition may be administered
XX via oral, transdermal, rectal or parenteral route. The polypeptide,
XX nucleic acid or antibody is useful for preparing a composition for
XX treating or preventing a NOVX-associated disorder, e.g., cancer. This
XX sequence encodes a human NOVX protein.
XX
XX Sequence 2881 BP; 526 A; 987 C; 866 G; 502 T; 0 U; 0 Other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 3.89e-34 Length: 2881
XX Score: 326.00 Matches: 61
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 10 Gaps: 0
XX
XX US-10-624-932C-2_COPY_163_223 (1-61) x ADG42568 (1-2881)
XX
XX Qy 1 GluGinglylleValLeuProCysArgProGluGlylleProProAlaGluValGlu 20
XX Db 573 GAGCAGGGCATCGTGTGCTGCCCTGCCCTCCACCGAGGGCATCCCTCCACGGGTGGAG 632
XX
XX Qy 21 TrpLeuArgGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArg 40
XX Db 633 TGGCTCCGGACAGAGACCTGGTGGACCCGTCCTGGACCCCAATGTATCATCACGGG 692
XX
XX Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
XX Db 693 GAGCACAGCCTGGTGGTGGCGACAGCCCGCTTGTGACACGGCCAACTACACCTGGGTG 752
XX
XX Qy 61 Ala 61
XX Db 753 GCC 755
XX
XX RESULT 15
```


THIS PAGE BLANK (03/20)

THIS PAGE BLANK (03/20)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 8, 2005, 23:51:22 ; Search time 97.232 Seconds
(without alignments)
1026.543 Million cell updates/sec

Title: US-10-624-932C-2_COPY_163_223

Perfect score: 326
Sequence: 1 EQGIVLPCRPPEGIPPAEVE.....HSLVVRQARLADTANYTCVA 61

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-O=/cgn2_1/USPTO_spool_b/US10624932/runat_08092005_161706_15822/app_query.fasta_1.1386
-DB=Issued_Patents_NA -QWTF=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=Blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10624932 @CGN 1 1 187 @runat_08092005_161706_15822 -NCPUS=6 -ICPU=3
-NO MMAP -LARGEOURY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PTCUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	326	100.0	3014	2	US-08-808-982-1
2	326	100.0	3014	3	US-09-306-902A-1
3	242	74.2	3008	4	US-09-949-016-4794
4	230	70.6	2831	2	US-08-808-982-3
5	230	70.6	2831	3	US-09-306-902A-3
6	201	61.7	1659	4	US-09-969-532-7
7	201	61.7	1692	4	US-09-969-532-5
8	201	61.7	1701	4	US-09-969-532-3
9	201	61.7	1734	4	US-09-969-532-1
10	201	61.7	2661	4	US-09-969-532-15
11	201	61.7	2694	4	US-09-969-532-13
12	201	61.7	2703	4	US-09-969-532-11

13	201	61.7	2736	4	US-09-969-532-9
14	201	61.7	3411	4	US-09-969-532-33
15	170	52.1	114139	4	US-09-949-016-16536
16	105	32.2	7647	4	US-09-566-921-75
17	94	28.8	3991	3	US-08-506-296B-3
18	92.5	28.4	4548	4	US-08-571-479C-5
19	88.5	27.1	5506	4	US-09-976-594-530
20	87	26.7	5905	4	US-09-949-016-5625
21	87	26.7	6218	4	US-09-949-016-706
22	87	26.7	6384	4	US-09-976-594-724
23	87	26.7	6384	4	US-09-919-039-279
24	85	26.1	6599	4	US-09-799-451-350
25	82	25.2	601	4	US-09-949-016-31727
26	82	25.2	601	4	US-09-949-016-31728
27	82	25.2	601	4	US-09-949-016-199440
28	82	25.2	601	4	US-09-949-016-199441
29	82	25.2	1896	3	US-09-412-554A-8
30	82	25.2	3192	3	US-09-412-554A-1
31	82	25.2	102520	4	US-09-949-016-17367
32	82	25.2	102526	4	US-09-949-016-12448
33	79.5	24.4	3551	4	US-09-620-312D-760
34	76.5	23.5	6814	3	US-09-484-970B-66
35	76	23.3	3318	4	US-09-949-016-4450
36	76	23.3	3360	1	US-08-408-093-5
37	76	23.3	3360	1	US-08-408-420A-5
38	76	23.3	3360	1	US-08-714-901-5
39	76	23.3	3360	3	US-08-040-741-5
40	76	23.3	4597	4	US-09-949-016-5173
41	75.5	23.2	1574	4	US-09-270-767-12428
42	75.5	23.2	4078	4	US-09-016-434-1120
43	75.5	23.2	5926	4	US-09-917-254-41
44	75.5	22.9	5999	4	US-09-949-016-4676
45	74	22.7	2264	1	US-08-232-538-16

ALIGNMENTS

RESULT 1

US-08-808-982-1
; Sequence 1, Application US/08808982
; Patent No. 5939271
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; APPLICANT: Leonardo, E. David
; APPLICANT: Hink, Lindsey
; APPLICANT: Masu, Masayuki
; APPLICANT: Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,982
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:

```
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3014 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-808-982-1
Alignment Scores:
Pred. No.: 6.23e-38 Length: 3014
Score: 326.00 Matches: 61
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
US-10-624-932C-2_COPY_163_223 (1-61) x US-08-808-982-1 (1-3014)
Qy 1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProAlaGluValGlu 20
Db 487 GAGCAGGCATTGTACTACCTTGTGCGCCCCCAGAGGAATCCCCCAGCTGAGGTGGAG 546
Qy 21 TrpLeuArgAnGluAspLeuValAspProSerLeuAspProAnValTyrIleThrArg 40
Db 547 TGGCTTCGAATGAGGACCTCGTGACCCCTCCCTCGATCCCAATGTGTACATCACGCGG 606
Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
Db 607 GAGCACAGCCTAGTGTGCGTGCAGCGCGCGCTGGCCGACACGCGGCAACTACACCTGTGTG 666
Qy 61 Ala 61
Db 667 GCC 669
RESULT 2
US-09-306-902A-1
; Sequence 1, Application US/09306902A
; Patent No. 6277585
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindaey
; Masu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/306,902A
; FILING DATE: 07-May-1999
; CLASSIFICATION: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3014 base pairs
; TYPE: nucleic acid
```

```
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-306-902A-1
Alignment Scores:
Pred. No.: 6.23e-38 Length: 3014
Score: 326.00 Matches: 61
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-10-624-932C-2_COPY_163_223 (1-61) x US-09-306-902A-1 (1-3014)
Qy 1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProAlaGluValGlu 20
Db 487 GAGCAGGCATTGTACTACCTTGTGCGCCCCCAGAGGAATCCCCCAGCTGAGGTGGAG 546
Qy 21 TrpLeuArgAnGluAspLeuValAspProSerLeuAspProAnValTyrIleThrArg 40
Db 547 TGGCTTCGAATGAGGACCTCGTGACCCCTCCCTCGATCCCAATGTGTACATCACGCGG 606
Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
Db 607 GAGCACAGCCTAGTGTGCGTGCAGCGCGCGCTGGCCGACACGCGGCAACTACACCTGTGTG 666
Qy 61 Ala 61
Db 667 GCC 669
RESULT 3
US-09-949-016-4794
; Sequence 4794, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4794
; LENGTH: 3008
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4794
Alignment Scores:
Pred. No.: 1.73e-25 Length: 3008
Score: 242.00 Matches: 42
Percent Similarity: 86.89% Conservative: 11
Best Local Similarity: 68.85% Mismatches: 8
Query Match: 74.23% Indels: 0
DB: 4 Gaps: 0
US-10-624-932C-2_COPY_163_223 (1-61) x US-09-949-016-4794 (1-3008)
Qy 1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProAlaGluValGlu 20
Db 57 GAACAGGAAGTCTTACTTCAGTGTCCAGCCACCTGAAGGGATCCAGTGGCTGAGGTGGAA 116
Qy 21 TrpLeuArgAnGluAspLeuValAspProSerLeuAspProAnValTyrIleThrArg 40
Db 667 GCC 669
```


Db 117 TGGTTGAAATGAAGACATATTCATCCCGTTGAAGATCGGAATTTTATATTAATTAAT 176
Qy 41 GluHisSerLeuValValArgGlnAlaAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
Db 177 GATCACAACCTCATCATTAAGCAGGCGCGACTCTCTGATACTGCAAAATTACACCTGTGT 236
Qy 61 Ala 61
Db 237 GCC 239
RESULT 4
US-08-808-982-3
; Sequence 3, Application US/08808982
; Patent No. 5939271
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; APPLICANT: Leonardo, E. David
; APPLICANT: Hink, Lindsey
; APPLICANT: Masu, Masayuki
; APPLICANT: Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,982
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2831 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-808-982-3
Alignment Scores:
Pred. No.: 9.54e-24 Length: 2831
Score: 230.00 Matches: 38
Percent Similarity: 87.93% Conservative: 13
Best Local Similarity: 65.52% Mismatches: 7
Query Match: 70.55% Indels: 0
DB: 2 Gaps: 0
US-10-624-932C-2_COPY_163_223 (1-61) x US-08-808-982-3 (1-2831)
Qy 4 IleValLeuProCysArgProGluGlyIleProAlaGluValGluTyrLeuArg 23
Db 502 GTCTTCTGCGAGTCCCGCCACAGAGGAGTGCTGTGGCTGAGGTGAATGCTCAAG 561
Qy 24 AsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArgGluHisSer 43
Db 562 AATGAGATGTCATCGATCCCGCTCAGGACACTAACTTCCTGCTCACCATTGACCAAC 621
Qy 44 LeuValValArgGlnAlaAlaArgLeuAlaAspThrAlaAsnTyrThrCysValAla 61
Db 562 AATGAGATGTCATCGATCCCGCTCAGGACACTAACTTCCTGCTCACCATTGACCAAC 621
Qy 44 LeuValValArgGlnAlaAlaArgLeuAlaAspThrAlaAsnTyrThrCysValAla 61

Db 622 CTCATCATCCGCGAGCGCGCTCTCAGACACACCACTACACCTGTGTGGCA 675
RESULT 5
US-09-306-902A-3
; Sequence 3, Application US/09306902A
; Patent No. 6277585
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; APPLICANT: Leonardo, E. David
; APPLICANT: Hink, Lindsey
; APPLICANT: Masu, Masayuki
; APPLICANT: Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/306,902A
; FILING DATE: 07-May-1999
; CLASSIFICATION: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2831 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-306-902A-3
Alignment Scores:
Pred. No.: 9.54e-24 Length: 2831
Score: 230.00 Matches: 38
Percent Similarity: 87.93% Conservative: 13
Best Local Similarity: 65.52% Mismatches: 7
Query Match: 70.55% Indels: 0
DB: 3 Gaps: 0
US-10-624-932C-2_COPY_163_223 (1-61) x US-09-306-902A-3 (1-2831)
Qy 4 IleValLeuProCysArgProGluGlyIleProAlaGluValGluTyrLeuArg 23
Db 502 GTCTTCTGCGAGTCCCGCCACAGAGGAGTGCTGTGGCTGAGGTGAATGCTCAAG 561
Qy 24 AsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArgGluHisSer 43
Db 562 AATGAGATGTCATCGATCCCGCTCAGGACACTAACTTCCTGCTCACCATTGACCAAC 621
Qy 44 LeuValValArgGlnAlaAlaArgLeuAlaAspThrAlaAsnTyrThrCysValAla 61
Db 622 CTCATCATCCGCGAGCGCGCTCTCAGACACACCACTACACCTGTGTGGCA 675
RESULT 6
US-09-969-532-7
; Sequence 7, Application US/09969532

```
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encoding
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1659
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-7

Alignment Scores:
Pred. No.:          9,06e-20      Length:      1659
Score:              201.00        Matches:      34
Percent Similarity: 79.31%        Conservative: 12
Best Local Similarity: 58.62%     Mismatches:  12
Query Match:        61.66%        Indels:       0
DB:                 4             Gaps:         0

US-10-624-932C-2_COPY_163_223 (1-61) x US-09-969-532-7 (1-1659)
Qy      4 IleValLeuProCysArgProProGluGlyIleProProAlaGluValGluTrpLeuArg 23
Db      526 ATTGTACTGCACCTGCCGCCACCAGAGGAGTCCCTGCTGCCGAGGTGGAATGGCTGAAA 585
Qy      24 AsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArgGluHisSer 43
Db      586 AATGAAGAGCCCATTTGACTCTGAACAGACGAGAACATTGACACCCAGGGCTGACCATTAAC 645
Qy      44 LeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysValAla 61
Db      646 CTGATCATCAGGAGGACGGCTCTCGGACTCAGGAATAATTACCTGCATGGCA 699

RESULT 7
US-09-969-532-5
; Sequence 5, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encoding
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1692
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-5

Alignment Scores:
Pred. No.:          9,3e-20      Length:      1692
Score:              201.00        Matches:      34
Percent Similarity: 79.31%        Conservative: 12
Best Local Similarity: 58.62%     Mismatches:  12
Query Match:        61.66%        Indels:       0
DB:                 4             Gaps:         0

US-10-624-932C-2_COPY_163_223 (1-61) x US-09-969-532-5 (1-1692)
Qy      4 IleValLeuProCysArgProProGluGlyIleProProAlaGluValGluTrpLeuArg 23
Db      526 ATTGTACTGCACCTGCCGCCACCAGAGGAGTCCCTGCTGCCGAGGTGGAATGGCTGAAA 585
Qy      24 AsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArgGluHisSer 43
Db      586 AATGAAGAGCCCATTTGACTCTGAACAGACGAGAACATTGACACCCAGGGCTGACCATTAAC 645
Qy      44 LeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysValAla 61
Db      646 CTGATCATCAGGAGGACGGCTCTCGGACTCAGGAATAATTACCTGCATGGCA 699

RESULT 7
US-09-969-532-5
; Sequence 5, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encoding
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1692
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-5

Alignment Scores:
Pred. No.:          9,3e-20      Length:      1692
Score:              201.00        Matches:      34
Percent Similarity: 79.31%        Conservative: 12
Best Local Similarity: 58.62%     Mismatches:  12
Query Match:        61.66%        Indels:       0
DB:                 4             Gaps:         0

US-10-624-932C-2_COPY_163_223 (1-61) x US-09-969-532-5 (1-1692)
Qy      4 IleValLeuProCysArgProProGluGlyIleProProAlaGluValGluTrpLeuArg 23
Db      526 ATTGTACTGCACCTGCCGCCACCAGAGGAGTCCCTGCTGCCGAGGTGGAATGGCTGAAA 585
Qy      24 AsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArgGluHisSer 43
Db      586 AATGAAGAGCCCATTTGACTCTGAACAGACGAGAACATTGACACCCAGGGCTGACCATTAAC 645
Qy      44 LeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysValAla 61
Db      646 CTGATCATCAGGAGGACGGCTCTCGGACTCAGGAATAATTACCTGCATGGCA 699

RESULT 7
US-09-969-532-5
; Sequence 5, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encoding
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1692
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-5

Alignment Scores:
Pred. No.:          9,37e-20     Length:      1701
Score:              201.00        Matches:      34
Percent Similarity: 79.31%        Conservative: 12
Best Local Similarity: 58.62%     Mismatches:  12
Query Match:        61.66%        Indels:       0
DB:                 4             Gaps:         0

US-10-624-932C-2_COPY_163_223 (1-61) x US-09-969-532-3 (1-1701)
Qy      4 IleValLeuProCysArgProProGluGlyIleProProAlaGluValGluTrpLeuArg 23
Db      526 ATTGTACTGCACCTGCCGCCACCAGAGGAGTCCCTGCTGCCGAGGTGGAATGGCTGAAA 585
Qy      24 AsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArgGluHisSer 43
Db      586 AATGAAGAGCCCATTTGACTCTGAACAGACGAGAACATTGACACCCAGGGCTGACCATTAAC 645
Qy      44 LeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysValAla 61
Db      646 CTGATCATCAGGAGGACGGCTCTCGGACTCAGGAATAATTACCTGCATGGCA 699

RESULT 9
US-09-969-532-1
; Sequence 1, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encoding
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1734
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-1
```

```
Alignment Scores:
Pred. No.: 9.62e-20 Length: 1734
Score: 201.00 Matches: 34
Percent Similarity: 79.31% Conservative: 12
Best Local Similarity: 58.62% Mismatches: 12
Query Match: 61.66% Indels: 0
DB: 4 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x US-09-969-532-1 (1-1734)

Qy 4 IleValLeuProCysArgProProGluGlyIleProProAlaGluValGluTrpLeuArg 23
Db 526 ATTGTACTGCACCTGCCGCCACACAGAGGAGTCCCTGCTGCCGAGGTGGAATGGCTGAAA 585

Qy 24 AsnGluAspLeuValAspProSerLeuAspProAnValTyrIleThrArgGluHisSer 43
Db 586 AATGAAGAGCCCATGTGCTGAACAAGACAGAACATTGACACAGGGCTGACCATTAAC 645

Qy 44 LeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysValAla 61
Db 646 CTGATCATCAGCAGGACGGCTCTCGGACTCAGGAAATTACCTGCATGGCA 699

RESULT 10
US-09-969-532-15
; Sequence 15, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 2661
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-15

Alignment Scores:
Pred. No.: 1.73e-19 Length: 2661
Score: 201.00 Matches: 34
Percent Similarity: 79.31% Conservative: 12
Best Local Similarity: 58.62% Mismatches: 12
Query Match: 61.66% Indels: 0
DB: 4 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x US-09-969-532-15 (1-2661)

Qy 4 IleValLeuProCysArgProProGluGlyIleProProAlaGluValGluTrpLeuArg 23
Db 526 ATTGTACTGCACCTGCCGCCACACAGAGGAGTCCCTGCTGCCGAGGTGGAATGGCTGAAA 585

Qy 24 AsnGluAspLeuValAspProSerLeuAspProAnValTyrIleThrArgGluHisSer 43
Db 586 AATGAAGAGCCCATGTGCTGAACAAGACAGAACATTGACACAGGGCTGACCATTAAC 645

Qy 44 LeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysValAla 61
Db 646 CTGATCATCAGCAGGACGGCTCTCGGACTCAGGAAATTACCTGCATGGCA 699

RESULT 11
US-09-969-532-13
; Sequence 13, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
```

```
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 2694
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-13

Alignment Scores:
Pred. No.: 1.76e-19 Length: 2694
Score: 201.00 Matches: 34
Percent Similarity: 79.31% Conservative: 12
Best Local Similarity: 58.62% Mismatches: 12
Query Match: 61.66% Indels: 0
DB: 4 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x US-09-969-532-13 (1-2694)

Qy 4 IleValLeuProCysArgProProGluGlyIleProProAlaGluValGluTrpLeuArg 23
Db 526 ATTGTACTGCACCTGCCGCCACACAGAGGAGTCCCTGCTGCCGAGGTGGAATGGCTGAAA 585

Qy 24 AsnGluAspLeuValAspProSerLeuAspProAnValTyrIleThrArgGluHisSer 43
Db 586 AATGAAGAGCCCATGTGCTGAACAAGACAGAACATTGACACAGGGCTGACCATTAAC 645

Qy 44 LeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysValAla 61
Db 646 CTGATCATCAGCAGGACGGCTCTCGGACTCAGGAAATTACCTGCATGGCA 699

RESULT 12
US-09-969-532-11
; Sequence 11, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 2703
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-11

Alignment Scores:
Pred. No.: 1.77e-19 Length: 2703
Score: 201.00 Matches: 34
Percent Similarity: 79.31% Conservative: 12
Best Local Similarity: 58.62% Mismatches: 12
Query Match: 61.66% Indels: 0
DB: 4 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x US-09-969-532-11 (1-2703)

Qy 4 IleValLeuProCysArgProProGluGlyIleProProAlaGluValGluTrpLeuArg 23
Db 526 ATTGTACTGCACCTGCCGCCACACAGAGGAGTCCCTGCTGCCGAGGTGGAATGGCTGAAA 585

Qy 24 AsnGluAspLeuValAspProSerLeuAspProAnValTyrIleThrArgGluHisSer 43
Db 586 AATGAAGAGCCCATGTGCTGAACAAGACAGAACATTGACACAGGGCTGACCATTAAC 645
```

```
Db      586 AATGAAGAGCCATTGACTCTGACAAAGACAGAAACATTGACACAGGGCTGACCATTAAC 645
Qy      44  LeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysValAla 61
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      646 CTGATCATCAGCGCAGGACGGCTCTCGGACTCAGGAAATTAACCTGCATGGCA 699

RESULT 13
; Sequence 9, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2736
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-9

Alignment Scores:
Pred. No.:      1.8e-19      Length:      2736
Score:          201.00      Matches:      34
Percent Similarity: 79.31%      Conservative: 12
Best Local Similarity: 58.62%      Mismatches: 12
Query Match:    61.66%      Indels:      0
DB:            4          Gaps:      0

US-10-624-932C-2_COPY_163_223 (1-61) x US-09-969-532-9 (1-2736)

Qy      4  IleValLeuProCysArgProGluGlyLeProGluValGluValGluTrpLeuArg 23
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      526 ATTGTACTGACTGCCGCCACCCAGAGGAGTCCCTGCTGCCGAGGTGGAATGCTGAAA 585

Qy      24 AsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArgGluHisSer 43
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      586 AATGAAGAGCCATTGACTCTGACAAAGACAGAAACATTGACACAGGGCTGACCATTAAC 645

Qy      44  LeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysValAla 61
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      646 CTGATCATCAGCGCAGGACGGCTCTCGGACTCAGGAAATTAACCTGCATGGCA 699

RESULT 14
US-09-969-532-33
; Sequence 33, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 3411
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-33

Alignment Scores:
Pred. No.:      2.44e-19      Length:      3411
Score:          201.00      Matches:      34
```

```
Percent Similarity: 79.31%      Conservative: 12
Best Local Similarity: 58.62%      Mismatches: 12
Query Match:    61.66%      Indels:      0
DB:            4          Gaps:      0

US-10-624-932C-2_COPY_163_223 (1-61) x US-09-969-532-33 (1-3411)

Qy      4  IleValLeuProCysArgProGluGlyLeProGluValGluValGluTrpLeuArg 23
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      640 ATTGTACTGACTGCCGCCACCCAGAGGAGTCCCTGCTGCCGAGGTGGAATGCTGAAA 699

Qy      24 AsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArgGluHisSer 43
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      700 AATGAAGAGCCATTGACTCTGACAAAGACAGAAACATTGACACAGGGCTGACCATTAAC 759

Qy      44  LeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysValAla 61
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      760 CTGATCATCAGCGCAGGACGGCTCTCGGACTCAGGAAATTAACCTGCATGGCA 813

RESULT 15
US-09-949-016-16536
; Sequence 16536, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16536
; LENGTH: 114139
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(114139)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16536

Alignment Scores:
Pred. No.:      1.19e-12      Length:      114139
Score:          170.00      Matches:      29
Percent Similarity: 88.37%      Conservative: 9
Best Local Similarity: 67.44%      Mismatches: 5
Query Match:    52.15%      Indels:      0
DB:            4          Gaps:      0

US-10-624-932C-2_COPY_163_223 (1-61) x US-09-949-016-16536 (1-114139)

Qy      19  ValGluTrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIle 38
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      29702 GTGGAATGGTTGAAAAATGAAGACATAAATATGATCCCGTTGAAGATCGGAATTTTATATT 29761

Qy      39  ThrArgGluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThr 58
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      29762 ACTATTGATCACAACCTCATCATTAAGACAGCCGCGACTCTCTGTACTGCAATTAACACC 29821

Qy      59  CysValAla 61
      |||:|||||:
Db      29822 TGTGTTGCC 29830

Search completed: September 9, 2005, 09:50:52
Job time : 112.232 secs
```


THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 9, 2005, 04:41:16 ; Search time 608.726 Seconds
(without alignments)
658.098 Million cell updates/sec

Title: US-10-624-932C-2_COPY_163_223
Perfect score: 326
Sequence: 1 EQGIVLPCRPPEGIPPAEVE.....HSLVVRQARLADTANYTCVA 61

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 7351250 seqs, 3283620254 residues

Total number of hits satisfying chosen parameters: 14702500

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool_h/US10624932/runat_08092005_161709_15882/app_query.fasta_1.1386
-DB=Published_Applications_NA -Qfmt=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPECL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10624932 @cgn 1 1 989 @runat_08092005_161709_15882
-NCPU=6 -ICPU=3 -NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	326	100.0	2697	16	US-10-240-154-15
2	326	100.0	2752	10	US-09-918-779-1
3	326	100.0	2752	18	US-10-624-932-1
4	326	100.0	2881	10	US-09-970-944-1
5	326	100.0	3014	10	US-09-933-261-1
6	326	100.0	3014	14	US-10-256-702-1
7	326	100.0	3561	20	US-10-643-795A-77
8	326	100.0	3561	21	US-10-948-518-77
9	326	100.0	3580	17	US-10-311-623-13
10	230	70.6	2831	10	US-09-933-261-3
11	230	70.6	2831	14	US-10-256-702-3
12	230	70.6	2860	17	US-10-087-684-1
13	230	70.6	2860	17	US-10-087-684-3
14	230	70.6	2860	17	US-10-218-779-1
15	230	70.6	2860	17	US-10-218-779-3
16	230	70.6	2895	18	US-10-037-417-37
17	230	70.6	2995	11	US-09-972-211-55
18	230	70.6	2995	18	US-10-096-625-55
19	230	70.6	3485	9	US-09-816-828-18
20	230	70.6	3501	17	US-10-295-027-1123
21	230	70.6	3866	21	US-10-764-420-2213
22	230	70.6	3884	14	US-10-028-072-145
23	230	70.6	3884	14	US-10-140-808-145
24	230	70.6	3884	14	US-10-121-049-145
25	230	70.6	3884	14	US-10-123-904-145
26	230	70.6	3884	14	US-10-140-470-145
27	230	70.6	3884	14	US-10-175-746-145
28	230	70.6	3884	14	US-10-176-918-145
29	230	70.6	3884	14	US-10-176-921-145
30	230	70.6	3884	14	US-10-137-865-145
31	230	70.6	3884	14	US-10-140-474-145
32	230	70.6	3884	14	US-10-142-431-145
33	230	70.6	3884	14	US-10-143-114-145
34	230	70.6	3884	14	US-10-142-419-145
35	230	70.6	3884	14	US-10-123-262-145
36	230	70.6	3884	14	US-10-142-423-145
37	230	70.6	3884	14	US-10-121-050-145
38	230	70.6	3884	14	US-10-141-755-145
39	230	70.6	3884	14	US-10-143-032-145
40	230	70.6	3884	14	US-10-123-108-145
41	230	70.6	3884	14	US-10-123-236-145
42	230	70.6	3884	14	US-10-123-261-145
43	230	70.6	3884	14	US-10-140-921-145
44	230	70.6	3884	14	US-10-140-928-145
45	230	70.6	3884	14	US-10-121-045-145

ALIGNMENTS

RESULT 1
US-10-240-154-15
; Sequence 15, Application US/10240154
; Publication No. US20030175741A1
; GENERAL INFORMATION:
; APPLICANT: Cochran et al.
; TITLE OF INVENTION: SCHIZOPHRENIA RELATED GENES
; FILE REFERENCE: CKEW-P01-006
; CURRENT APPLICATION NUMBER: US/10/240,154
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: PCT/GB01/01486
; PRIOR FILING DATE: 2001-04-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 2697


```
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: 09/918,779
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/221,409
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/222,840
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,752
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,762
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,770
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,769
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/225,146
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/225,392
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/225,470
; PRIOR FILING DATE: 2000-08-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2752
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-624-932-1

Alignment Scores:
Pred. No.: 8.13e-37 Length: 2752
Score: 326.00 Matches: 61
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x US-10-624-932-1 (1-2752)

Qy 1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProAlaGluValGlu 20
Db 532 GAGCAGGGCATCGTGGCTGCCCTCCACCGAGGGCATCCCTCCAGCCGAGGTGGAG 591

Qy 21 TrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArg 40
Db 592 TGGCTCCGGACGAGGACCTGGTGGACCCGTCCTGGACCCCAATGTATACATCACGGG 651

Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
Db 652 GAGCACAGCCTGGTGGTGGACAGCGCCGCTTGTGTGACAGCGCCCAACTACACCTGCGTG 711

Qy 61 Ala 61
Db 712 GCC 714

RESULT 4
US-09-970-944-1
; Sequence 1, Application US/09970944
; Publication No. US20030204052A1
; GENERAL INFORMATION:
; APPLICANT: Herrman, John L
; APPLICANT: Rastelli, Luca
; APPLICANT: Shimkets, Richard A
; TITLE OF INVENTION: No. US20030204052A1el Proteins and Nucleic Acids Encoding Same an
; FILE REFERENCE: 21402-138
; CURRENT APPLICATION NUMBER: US/09/970,944
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 60/237,862
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
```

```
; SEQ ID NO 1
; LENGTH: 2881
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-970-944-1

Alignment Scores:
Pred. No.: 8.58e-37 Length: 2881
Score: 326.00 Matches: 61
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x US-09-970-944-1 (1-2881)

Qy 1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProAlaGluValGlu 20
Db 573 GAGCAGGGCATCGTGGCTGCCCTCCACCGAGGGCATCCCTCCAGCCGAGGTGGAG 632

Qy 21 TrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArg 40
Db 633 TGGCTCCGGACGAGGACCTGGTGGACCCGTCCTGGACCCCAATGTATACATCACGGG 692

Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
Db 693 GAGCACAGCCTGGTGGTGGACAGCGCCGCTTGTGTGACAGCGCCCAACTACACCTGCGTG 752

Qy 61 Ala 61
Db 753 GCC 755

RESULT 5
US-09-933-261-1
; Sequence 1, Application US/09933261
; Publication No. US20030040046A1
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; APPLICANT: Leonardo, E. David
; APPLICANT: Hink, Lindsey
; APPLICANT: Masu, Masayuki
; APPLICANT: Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/933,261
; FILING DATE: 20-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/808,982
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3014 base pairs
```

```
;
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-933-261-1
Alignment Scores:
Pred. No.: 9.05e-37 Length: 3014
Score: 326.00 Matches: 61
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
US-10-624-932C-2_COPY_163_223 (1-61) x US-09-933-261-1 (1-3014)
QY 1 GluGlnGlyLeValLeuProCysArgProGluGlyLeProProAlaGluValGlu 20
DB 487 GAGCAAGGCATTGTACTACCTTGTGCGCCCCCAGAGAGATCCCCCAGCTGAGTGGAG 546
QY 21 TrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArg 40
DB 547 TGGCTTCGAATGAGGACCTCGTGGACCCCTCCCTCGATCCCAATGTGTACATCACGCGG 606
QY 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
DB 607 GAGCACAGCCTAGTGTGCGGTGAGCGCCGCTGCGCCGACACGCGCAACTACACTGTGTG 666
QY 61 Ala 61
DB 667 GCC 669
RESULT 6
US-10-256-702-1
; Sequence 1, Application US/10256702
; Publication No. US20030059859A1
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindsey
; Masu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/256,702
; FILING DATE: 27-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/933,261
; FILING DATE: 20-Aug-2001
; APPLICATION NUMBER: 08/808,982
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
;
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3014 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-256-702-1
Alignment Scores:
Pred. No.: 9.05e-37 Length: 3014
Score: 326.00 Matches: 61
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0
US-10-624-932C-2_COPY_163_223 (1-61) x US-10-256-702-1 (1-3014)
QY 1 GluGlnGlyLeValLeuProCysArgProGluGlyLeProProAlaGluValGlu 20
DB 487 GAGCAAGGCATTGTACTACCTTGTGCGCCCCCAGAGAGATCCCCCAGCTGAGTGGAG 546
QY 21 TrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArg 40
DB 547 TGGCTTCGAATGAGGACCTCGTGGACCCCTCCCTCGATCCCAATGTGTACATCACGCGG 606
QY 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
DB 607 GAGCACAGCCTAGTGTGCGGTGAGCGCCGCTGCGCCGACACGCGCAACTACACTGTGTG 666
QY 61 Ala 61
DB 667 GCC 669
RESULT 7
US-10-643-795A-77
; Sequence 77, Application US/10643795A
; Publication No. US20040241703A1
; GENERAL INFORMATION:
; APPLICANT: FREDERIC J. DESAUVAGE
; APPLICANT: GRETCHEN FRANTZ
; APPLICANT: KENNETH J. HILLAN
; APPLICANT: PAUL POLAKIS
; APPLICANT: ANDREW POLSON
; APPLICANT: VICTORIA SMITH
; APPLICANT: SUSAN D. SPENCER
; APPLICANT: THOMAS D. WU
; APPLICANT: ZEMIN ZHANG
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF TUMOR
; FILE REFERENCE: P5026R1-US
; CURRENT APPLICATION NUMBER: US/10/643,795A
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405,645
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/413,192
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: US 60/419,008
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/426,847
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/484,959
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 158
; SEQ ID NO 77
; LENGTH: 3561
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-643-795A-77
```

Alignment Scores: 1.1e-36 Length: 3561
Pred. No.: 326.00 Matches: 61
Score: 326.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 20 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x US-10-643-795A-77 (1-3561)

Qy 1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProAlaGluValGlu 20
Dy 490 GAGCAGGCGCATCGTGGCTGCCCTCCACCGGAGGCGCATCCCTCCACGCGGAGGTGGAG 549
Qy 21 TrpLeuArgAenGluAspLeuValAspProSerLeuAspProAenValTyrIleThrArg 40
Dy 550 TGGCTCCGGACGAGGACCTGGTGGACCCGCTCCCTGGACCCCAATGTATACATCACGCGG 609
Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAenTyrThrCysVal 60
Dy 610 GAGCACAGCCTGGTGGTGGCGACAGCGCGCTTGTGTGACACGGCCAACTACACCTGGGTG 669
Qy 61 Ala 61
Dy 670 GCC 672

RESULT 8
US-10-948-518-77
; Sequence 77, Application US/10948518
; Publication No. US20050064492A1
; GENERAL INFORMATION:
; APPLICANT: FREDERIC J. DESAUVAGE
; APPLICANT: GRETCHEN FRANTZ
; APPLICANT: KENNETH J. HILLAN
; APPLICANT: PAUL POLAKIS
; APPLICANT: ANDREW POLSON
; APPLICANT: VICTORIA SMITH
; APPLICANT: SUSAN D. SPENCER
; APPLICANT: THOMAS D. WU
; APPLICANT: ZEMIN ZHANG
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5026R1-US
; CURRENT APPLICATION NUMBER: US/10/948,518
; CURRENT FILING DATE: 2004-09-22
; PRIOR FILING DATE: 2004-09-22
; PRIOR APPLICATION NUMBER: US/10/643,795
; PRIOR FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405,645
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/413,192
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: US 60/419,008
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/426,847
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/484,959
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 158
; SEQ ID NO 77
; LENGTH: 3561
; TYPE: DNA
; ORGANISM: Homo sapien

US-10-948-518-77

Alignment Scores: 1.1e-36 Length: 3561
Pred. No.: 326.00 Matches: 61
Score: 326.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

DB: 21 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x US-10-948-518-77 (1-3561)

Qy 1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProAlaGluValGlu 20
Dy 490 GAGCAGGCGCATCGTGGCTGCCCTCCACCGGAGGCGCATCCCTCCACGCGGAGGTGGAG 549
Qy 21 TrpLeuArgAenGluAspLeuValAspProSerLeuAspProAenValTyrIleThrArg 40
Dy 550 TGGCTCCGGACGAGGACCTGGTGGACCCGCTCCCTGGACCCCAATGTATACATCACGCGG 609
Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAenTyrThrCysVal 60
Dy 610 GAGCACAGCCTGGTGGTGGCGACAGCGCGCTTGTGTGACACGGCCAACTACACCTGGGTG 669
Qy 61 Ala 61
Dy 670 GCC 672

RESULT 9
US-10-311-623-13
; Sequence 13, Application US/10311623
; Publication No. US20040023244A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; GRIFFIN, Jennifer A.
; APPLICANT: KALLICK, Deborah A.; TRIBOULEY, Catherine M.
; APPLICANT: YUE, Henry; NGUYEN, Dannel B.
; APPLICANT: TANG, Y. Tom; LAL, Preeti G.
; APPLICANT: POLICKY, Jennifer L.; AZIMZAI, Yalda
; APPLICANT: LU, Dyung Alina M.; GRAUL, Richard C.
; APPLICANT: YAO, Monique G.; BURFORD, Neil
; APPLICANT: HAFALIA, April J. A.; BAUGHN, Mariah R.
; APPLICANT: BANDMAN, Olga; ARVIZU, Chandra S.
; APPLICANT: YANG, Junming; XU, Yuming
; APPLICANT: GANDHI, Ameena R.; WARREN, Bridget A.
; APPLICANT: DING, Li; SANJANWALA, Madhusudan M.
; APPLICANT: DUGGAN, Brendan M.; LU, Yan
; TITLE OF INVENTION: RECEPTORS
; FILE REFERENCE: PF-0793 USN
; CURRENT APPLICATION NUMBER: US/10/311,623
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 01/19942
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/214,027
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: US 60/228,045
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/255,104
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PERL Program
; SEQ ID NO 13
; LENGTH: 3580
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040023244A1 6052371CB1

US-10-311-623-13

Alignment Scores: 1.11e-36 Length: 3580
Pred. No.: 326.00 Matches: 61
Score: 326.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x US-10-311-623-13 (1-3580)

Qy 1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProAlaGluValGlu 20
Dy 670 GCC 672

Db 490 GAGCAGGGCATGCTGCTGCCCTCCAGCGGGCATCCCTCCAGCGGGTGGAG 549
Qy 21 TrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArg 40
Db 550 TGGCTCCGGAACAGGAGACCTGGTGGACCGCTCCCTGGACCCCAATGTATACATCAGCGG 609
Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
Db 610 GAGCAGACGCTGGTGGTGGCAGAGCGCCGCTTGTCTGACACGGCCAACTACACCTGGGTG 669
Qy 61 Ala 61
Db 670 GCC 672
RESULT 10
US-09-933-261-3
; Sequence 3, Application US/09933261
; Publication No. US20030040046A1
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindsey
; Masu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/933,261
; FILING DATE: 20-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/808,982
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2831 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-933-261-3
Alignment Scores:
Pred. No.: 8,33e-23 Length: 2831
Score: 230.00 Matches: 38
Percent Similarity: 87.93% Conservative: 13
Best Local Similarity: 65.52% Mismatches: 7
Query Match: 70.55% Indels: 0
DB: 10 Gaps: 0
US-10-624-932C-2_COPY_163_223 (1-61) x US-09-933-261-3 (1-2831)
Qy 4 IleValLeuProCysArgProProGluGlyIleProProAlaGluValGluTrpLeuArg 23

Db 502 GTCTTCTGCGAGTCCGCCCCACAGAGGGAGTGGCTGTGCTGAGTGGATGGCTCAAG 561
Qy 24 AsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArgGluHisSer 43
Db 562 AATGAAGATGTCATCGATCCGCTCAGGACACTAACTTCCTGCTCACCATTGACCAAC 621
Qy 44 LeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysValAla 61
Db 622 CTCATCATCCGCGAGCGCGCTCTCAGACACAGCCAACTACACCTGTGTGGCA 675
RESULT 11
US-10-256-702-3
; Sequence 3, Application US/10256702
; Publication No. US20030059859A1
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindsey
; Masu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/256,702
; FILING DATE: 27-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/933,261
; FILING DATE: 20-Aug-2001
; APPLICATION NUMBER: 08/808,982
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2831 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-256-702-3
Alignment Scores:
Pred. No.: 8,33e-23 Length: 2831
Score: 230.00 Matches: 38
Percent Similarity: 87.93% Conservative: 13
Best Local Similarity: 65.52% Mismatches: 7
Query Match: 70.55% Indels: 0
DB: 14 Gaps: 0
US-10-624-932C-2_COPY_163_223 (1-61) x US-10-256-702-3 (1-2831)
Qy 4 IleValLeuProCysArgProProGluGlyIleProProAlaGluValGluTrpLeuArg 23


```
Score: 230.00 Matches: 38
Percent Similarity: 87.93% Conservative: 13
Best Local Similarity: 65.52% Mismatches: 7
Query Match: 70.55% Indels: 0
DB: 17 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x US-10-087-684-3 (1-2860)

Qy 4 IleValLeuProCysArgProGluGlyLeProAlaGluValGluTrpLeuArg 23
Db 566 GTTCTCTGAGTGCCTGCGGAGGGGTGCTGTGGCCGAGGTGAATGGCTCAAG 625

Qy 24 AsnGluAspLeuValAspProSerLeuAspProAlaGluValGluTrpLeuArg 43
Db 626 AATGAGGATGTCATCGACCCACCAGGACACCAACTTCCTGCTCACCATCGACCAAC 685

Qy 44 LeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysValAla 61
Db 686 CTCATCATCGCCAGGCGCGCTGTGCGACACTGCCAACTATACCTGCGTGGCC 739

RESULT 14
US-10-218-779-1
; Sequence 1, Application US/10218779
; Publication No. US20040029222A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit
; APPLICANT: MacDougall, John
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David
; APPLICANT: Gerlach, Valerie
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook II, John
; APPLICANT: Lepley, Denise
; APPLICANT: Rieger, Daniel
; APPLICANT: Burgess, Catherine
; APPLICANT: Casman, Stacie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Patturajan, Meera
; APPLICANT: Shenoy, Suresh
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zerkhusen, Bryan
; APPLICANT: Malyankar, Uriel
; APPLICANT: Guo, Xiaojia
; APPLICANT: Miller, Charles
; APPLICANT: Gangolli, Esha
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; CURRENT APPLICATION NUMBER: US/10/218,779
; PRIOR FILING DATE: 2002-08-14
; PRIOR FILING DATE: 2000-11-29
; PRIOR FILING DATE: 2000-11-29
; PRIOR FILING DATE: 2000-11-29
; PRIOR FILING DATE: 2000-11-29
; PRIOR FILING DATE: 2001-01-25
; PRIOR FILING DATE: 2001-08-20
; PRIOR FILING DATE: 2001-08-20
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2860
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-218-779-1

Score: 230.00 Matches: 38
Percent Similarity: 87.93% Conservative: 13
Best Local Similarity: 65.52% Mismatches: 7
Query Match: 70.55% Indels: 0
DB: 17 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x US-10-218-779-1 (1-2860)

Qy 4 IleValLeuProCysArgProGluGlyLeProAlaGluValGluTrpLeuArg 23
Db 566 GTTCTCTGAGTGCCTGCGGAGGGGTGCTGTGGCCGAGGTGAATGGCTCAAG 625

Qy 24 AsnGluAspLeuValAspProSerLeuAspProAlaGluValGluTrpLeuArg 43
Db 626 AATGAGGATGTCATCGACCCACCAGGACACCAACTTCCTGCTCACCATCGACCAAC 685

Qy 44 LeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysValAla 61
Db 686 CTCATCATCGCCAGGCGCGCTGTGCGACACTGCCAACTATACCTGCGTGGCC 739

RESULT 15
US-10-218-779-3
; Sequence 3, Application US/10218779
; Publication No. US20040029222A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit
; APPLICANT: MacDougall, John
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David
; APPLICANT: Gerlach, Valerie
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook II, John
; APPLICANT: Lepley, Denise
; APPLICANT: Rieger, Daniel
; APPLICANT: Burgess, Catherine
; APPLICANT: Casman, Stacie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Patturajan, Meera
; APPLICANT: Shenoy, Suresh
; APPLICANT: Rastelli, Luca
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zerkhusen, Bryan
; APPLICANT: Malyankar, Uriel
; APPLICANT: Guo, Xiaojia
; APPLICANT: Miller, Charles
; APPLICANT: Gangolli, Esha
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-214
; CURRENT APPLICATION NUMBER: US/10/218,779
; CURRENT FILING DATE: 2002-08-14
; PRIOR FILING DATE: 2000-11-29
; PRIOR FILING DATE: 2000-11-29
; PRIOR FILING DATE: 2000-11-29
; PRIOR FILING DATE: 2000-11-29
; PRIOR FILING DATE: 2000-11-29
; PRIOR FILING DATE: 2001-01-25
; PRIOR FILING DATE: 2001-08-20
; PRIOR FILING DATE: 2001-08-20
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2860
```

; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-218-779-3

Alignment Scores:
Pred. No.: 8,43e-23 Length: 2860
Score: 230.00 Matches: 38
Percent Similarity: 87.93% Conservative: 13
Best Local Similarity: 65.52% Mismatches: 7
Query Match: 70.55% Indels: 0
DB: 17 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x US-10-218-779-3 (1-2860)

Qy	4	IleValLeuProCysArgProGluGlyIleProProAlaGluValGluTrpLeuArg	23
Db	566	GTTCCTCTGCAGTGCCTGCGCGAGGGGTGCTGTGGCCGAGGTGGAATGGCTCAAG	625
Qy	24	AsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArgGluHisSer	43
Db	626	AATGAGGATGTCATCGACCCGCCAGGACACCAACTTCTCTGCTCACCATCGACCAAC	685
Qy	44	LeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysValAla	61
Db	686	CTCATCATCCCGCCAGCCCGCTGTGCGACACTGCCCAACTATACCTGGTGCC	739

Search completed: September 9, 2005, 18:52:05
Job time : 616.726 secs

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 8, 2005, 22:38:37; Search time 2007.62 Seconds
(without alignments)
1156.553 Million cell updates/sec

Title: US-10-624-932C-2_COPY_163_223
Perfect score: 326
Sequence: 1 EQGIVLPCRPPEGIPPAEVE.....HSLVVRQARLADTANYTCVA 61

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame, p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool_h/US10624932/runat_08092005_161706_15792/app_query.fasta_1.1386
-DB=EST -OFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=bloum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10624932 @CEN 1.1 8180 @runat_08092005_161706_15792 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -TRANS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_hic: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gssi: *
9: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	326	100.0	421	6	CB764405 AMGNNUC:N
2	326	100.0	445	6	CB744716 AMGNNUC:N
3	326	100.0	471	5	BX282095 BX282095
4	326	100.0	514	5	BX522364 BX522364
5	326	100.0	749	7	CF735417 UI-M-HBO-
6	326	100.0	751	7	CF735550 UI-M-HBO-
7	326	100.0	818	4	BI818609 60303362
8	326	100.0	1175	2	BF530640 602071931
9	326	100.0	1532	3	BC033727 Homo sapi

10	322	98.8	485	6	CB727042
11	320	98.2	1034	4	BI758231
12	318	97.5	853	5	BX364574
13	313	96.0	276	1	AA288582
14	313	96.0	723	5	BU613458
15	299	91.7	843	4	BG913440
16	283	86.8	900	5	BX345406
17	270	82.8	548	5	BX452510
18	245	75.2	3790	3	AK031655
19	242	74.2	459	2	BE700724
20	242	74.2	841	5	BP435136
21	242	74.2	856	7	CN164143
22	242	74.2	1843	3	BC034747
23	242	74.2	2802	9	AY406491
24	241	73.9	720	1	AI959236
25	236	72.4	351	1	AJ729962
26	230	70.6	403	2	AW357482
27	230	70.6	517	1	AI508226
28	230	70.6	523	5	BX526679
29	230	70.6	679	7	CO045001
30	230	70.6	2532	9	AY411747
31	230	70.6	2532	9	AY411749
32	230	70.6	3866	3	AK018177
33	223	68.4	594	6	CA771550
34	221	67.8	977	5	BX345407
35	215	66.0	373	1	AA020206
36	215	66.0	1072	5	BX422753
37	213	65.3	2802	9	AY406492
38	208	63.8	774	5	BU365958
39	202	62.0	2791	9	AY408493
40	201	61.7	733	5	BX920046
41	201	61.7	2775	9	AY401469
42	201	61.7	2775	9	AY401471
43	195	59.8	2507	9	AY401470
44	192	58.9	445	5	BX291669
45	190	58.3	693	6	CB246544

ALIGNMENTS

RESULT 1

CB764405

LOCUS

DEFINITION

AMGNNUC:NRHY7-00021-F2-A nrhy7 (10850) Rattus norvegicus cDNA clone

nrhy7-00021-f2 5', mRNA sequence.

ACCESSION

CB764405

VERSION

CB764405.1

KEYWORDS

EST.

SOURCE

Rattus norvegicus (Norway rat)

ORGANISM

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

REFERENCE

1 (bases 1 to 421)

AUTHORS

Amgen EST Program.

TITLE

Amgen Rat EST Program

JOURNAL

Unpublished (2003)

COMMENT

Contact: Dan Fitzpatrick

Amgen, Inc.

One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA

Tel: 805 447-4881

Plate: 00021 row: f column: 2.

Location/Qualifiers

1. 421

/organism="Rattus norvegicus"

/mol_type="mRNA"

/db_xref="taxon:10116"

/clone="nrhy7-00021-f2"

/note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; W Rat

hypothenamus adult female Wistar rat avg. Insert size 2.3

kb fraction 6 and 7"

ORIGIN

```

Alignment Scores:
Pred. No.: 7,85e-31 Length: 421
Score: 326.00 Matches: 61
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x CB7644405 (1-421)

Qy 1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProProAlaGluValGlu 20
Db 191 GAGCAAGGCATTGTACTACCTTGTGCGCCCGCCAGAGGAATCCCCCAGCTGAGGTGGAG 240

Qy 21 TrpLeuArgAnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArg 40
Db 241 TGGCTTCGAAATGAGGACCTCGTGACCCCTCCCTCGATCCCAATGTGTACATCACGCGG 300

Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
Db 301 GAGCACAGCCCTAGTGTGCGTCAGCGCCGCTGGCCGACACGGCCAACTACACCTGTGTG 360

Qy 61 Ala 61
Db 361 GCC 363

RESULT 2
CB744716
LOCUS CB744716 445 bp mRNA linear EST 11-APR-2003
DEFINITION AMGNNUC:NRH21-00003-e12-A nrh21 (10741) Rattus norvegicus CDNA
ACCESSION CB744716
VERSION CB744716.1 GI:29812016
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 445)
AUTHORS Angen EST Program
TITLE Angen Rat EST Program
JOURNAL Unpublished (2003)
COMMENT Contact: Dan Fitzpatrick
Angen, Inc
One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00003 row: e column: 12.
FEATURES
Location/Qualifiers
source 1..445
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="nrh21-00003-e12"
/tissue_type="hypothalamus"
/clone_lib="nrh21 (10741)"
/note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI;
hypothalamus"

ORIGIN
Alignment Scores:
Pred. No.: 8,36e-31 Length: 445
Score: 326.00 Matches: 61
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x CB744716 (1-445)

Qy 1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProProAlaGluValGlu 20
Db 191 GAGCAAGGCATTGTACTACCTTGTGCGCCCGCCAGAGGAATCCCCCAGCTGAGGTGGAG 240

```

```

Db 246 GAGCAAGGCATTGTACTACCTTGTGCGCCCGCCAGAGGAATCCCCCAGCTGAGGTGGAG 305

Qy 21 TrpLeuArgAnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArg 40
Db 306 TGGCTTCGAAATGAGGACCTCGTGACCCCTCCCTCGATCCCAATGTGTACATCACGCGG 365

Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
Db 366 GAGCACAGCCCTAGTGTGCGTCAGCGCCGCTGGCCGACACGGCCAACTACACCTGTGTG 425

Qy 61 Ala 61
Db 426 GCC 428

RESULT 3
BX282095
LOCUS BX282095 471 bp mRNA linear EST 04-MAR-2003
DEFINITION IMAGE:4943333, mRNA sequence.
ACCESSION BX282095
VERSION BX282095.1 GI:28612897
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 471)
AUTHORS Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
Radelof,U., Schneider,D. and Korn,B.
TITLE Human UnigeneSet - RZPD3
JOURNAL Unpublished (2003)
COMMENT Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGP998J0610886.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human UnigeneSet - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-
bin/showlib.pl/cgi/response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13u, Primer sequence: CGTTGTAACGACGCGCCAGT.
FEATURES
Location/Qualifiers
source 1..471
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGP998J0610886 ; IMAGE:4943333"
/tissue_type="anaplastic oligodendroglioma with lp/19q
loss"
/lab host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP_Brn67"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI CGAP Library."

ORIGIN
Alignment Scores:
Pred. No.: 8,93e-31 Length: 471
Score: 326.00 Matches: 61
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x BX282095 (1-471)

```

QY 1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProGluGlyIleProAlaGluValGlu 20
 |||||
 Db 183 GAGCAGGGCATCGTCTGCCCTGCCCTCCACCGAGGGCATCCCTCCAGCGAGGTGGAG 242
 |||||
 QY 21 TrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArg 40
 |||||
 Db 243 TGGCTCCCGAAGCAGAGCATGTGTGACCGCGCTCCCTCGGACCCCAATGTATACATCACGCGG 302
 |||||
 QY 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
 |||||
 Db 303 GAGCACACGCTGTGTGTGGACAGCGCCGCTTGTGTGACAGCGGCACTACACCTGCGGTG 362
 |||||
 QY 61 Ala 61
 |||||
 Db 363 GCC 365

RESULT 4
 BX522364
 LOCUS BX522364 Life Tech mouse embryo 8 5dpc 10664019 Mus musculus cDNA
 DEFINITION clone IMAGE:569336, mRNA sequence.
 ACCESSION BX522364
 VERSION BX522364.1 GI:32302310
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 514)
 REFERENCE Heil, O., Ebert, L., Neubert, P., Peters, M., Radelof, U., Schneider, D.
 and Korn, B.
 AUTHORS Mouse Unigeneset - RZPD2
 TITLE Mouse Unigeneset - RZPD2
 JOURNAL Unpublished (2003)
 COMMENT Contact: Ina Rolfs
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
 RZPD; IMAGE:569336

RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
 Mouse Unigeneset - RZPD2 (RZPDLIB No.981)
 http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi?response?libNo=981 Contact: Ina Rolfs
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Heubnerweg 6, D-14059 Berlin, Germany
 Tel: +49 30 32639 101
 Fax: +49 30 32639 111
 www.rzpd.de

This clone is available royalty-free from RZPD;
 contact RZPD (clone@rzpd.de) for further information. Seq primer:
 SP6, Primer sequence: ATTAGGTGACACTATAG.

FEATURES

Location/Qualifiers
 1..514
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:569336"
 /tissue_type="embryo"
 /dev_stage="8.5dpc embryos"
 /lab_host="DH10B"
 /clone_lib="Life Tech mouse embryo 8 5dpc 10664019"
 /note="Organ: whole embryo; Vector: pCMV-SPORT2; Site_1:
 SalI; Site_2: NotI; Cloned unidirectionally. Primer:
 Oligo dt. 8.5dpc embryos. pCMV-SPORT2 vector."

ORIGIN

Alignment Scores:
 Pred. No.: 9.88e-31 Length: 514
 Score: 326.00 Matches: 61
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 5 Gaps: 0

US-10-624-932c-2_COPY_163_223 (1-61) x BX522364 (1-514)
 QY 1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProGluGlyIleProAlaGluValGlu 20
 |||||
 Db 5 GAGCAGGGCATGTGTGCTACCTTGTGCGCCCCCGGAGGAATCCCCAGCTGAGGTGGAG 64
 |||||
 QY 21 TrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArg 40
 |||||
 Db 65 TGGCTCCGAAATGAGGACCTCGTGACCCCTCCCTCGAGCCCAATGTGTATACATCACGCG 124
 |||||
 QY 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
 |||||
 Db 125 GAGCACACGCTAGTGTGTGGCAGCGCCGCTGCGCGACACTGCCCACTACACCTGCGGTG 184
 |||||
 QY 61 Ala 61
 |||||
 Db 185 GCC 187

RESULT 5
 CF735417
 LOCUS CF735417
 DEFINITION UI-M-HB0-cke-a-07-0-UI.r1 NIH_BMAP_HB0 Mus musculus cDNA clone
 IMAGE:30549030 5', mRNA sequence.
 ACCESSION CF735417
 VERSION CF735417
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 749)
 REFERENCE NIH-MGC http://mgc.nci.nih.gov/
 AUTHORS NIH-MGC
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 Tissue Procurement: Dr. James Lin University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
 http://genome.uiowa.edu/distribution/mousefl.html
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)

Seq primer: pYX-5.

Location/Qualifiers
 1..749
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="IMAGE:30549030"
 /tissue_type="whole eye"
 /dev_stage="embryo 12.5,13.5,14.5 dpc"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="NIH_BMAP_HB0"
 /note="Organ: Eye; Vector: pYX-Asc; Site_1: EcoR I;
 Site_2: Not I; The library was constructed according
 Bernaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured RNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with oligo-dt
 primer containing a Not I site. Double strand cDNA was
 size selected according to mRNA size fraction, ligated
 with EcoR I adaptor, digested with NotI and then cloned
 directionally into pYX-Asc vector. The library tag
 sequence located between the Not I site and the polyA tail
 is TTAATGAAGT. This library was created for the University
 of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
 Developing Mouse Nervous System', supported by National
 Institute of Mental Health (NIMH)."

FEATURES

source

ORIGIN

Alignment Scores:

Pred. No.: 1.53e-30 Length: 749
 Score: 326.00 Matches: 61
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0

US-10-624-932c-2_COPY_163_223 (1-61) x CF735417 (1-749)

Qy 1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProGluGlyIleProAlaGluValGlu 20
 Db 258 GAGCAAGGCAATGTGTACCTTGTCTGCGCCCGGAGGAATCCCCAGCTGAGGTGGAG 317
 Qy 21 TrpLeuArgAnGluAspLeuValAspProSerLeuAspProAnValTyrIleThrArg 40
 Db 318 TGGCTCCGAAATGAGGACCTCGTGACCCCTCCCTCGACCCCAATGTGTACATCACACGG 377
 Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
 Db 378 GAGCACAGCCTAGTGTGCGGAGGCCCGCTGCGGACACTGCCAACTACACTGCGTG 437
 Qy 61 Ala 61
 Db 438 GCC 440

RESULT 6
 LOCUS CF735550 751 bp mRNA linear EST 10-OCT-2003
 DEFINITION UI-M-HB0-cke-i-06-0-UI.r1 NIH_BMAP_HB0 Mus musculus cDNA clone IMAGE:30549221 5', mRNA sequence.
 ACCESSION CF735550
 VERSION CF735550.1 GI:37631886
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 751)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. James Lin University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at <http://genome.uiowa.edu/distribution/mousef1.html>
 This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
 Seq primer: pYX-5.
 Location/Qualifiers
 1. 751
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:30549221"
 /tissue_type="whole eye"
 /dev_stages="embryo 12.5,13.5,14.5 dpc"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="NIH_BMAP_HB0"
 /note="Organ: Eye; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail

is TTATTGAAGT. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH)."
 ORIGIN
 Alignment Scores:
 Pred. No.: 1.53e-30 Length: 751
 Score: 326.00 Matches: 61
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0

US-10-624-932c-2_COPY_163_223 (1-61) x CF735550 (1-751)

Qy 1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProGluGlyIleProAlaGluValGlu 20
 Db 257 GAGCAAGGCAATGTGTACCTTGTCTGCGCCCGGAGGAATCCCCAGCTGAGGTGGAG 316
 Qy 21 TrpLeuArgAnGluAspLeuValAspProSerLeuAspProAnValTyrIleThrArg 40
 Db 317 TGGCTCCGAAATGAGGACCTCGTGACCCCTCCCTCGACCCCAATGTGTACATCACACGG 376
 Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
 Db 377 GAGCACAGCCTAGTGTGCGGAGGCCCGCTGCGGACACTGCCAACTACACTGCGTG 436
 Qy 61 Ala 61
 Db 437 GCC 439

RESULT 7
 LOCUS B1818609 818 bp mRNA linear EST 04-OCT-2001
 DEFINITION 603033362F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5174559 5', mRNA sequence.
 ACCESSION B1818609
 VERSION B1818609.1 GI:15929902
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 818)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LUAM1434 row: 1 column: 16
 High quality sequence stop: 744.
 Location/Qualifiers
 1. 818
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5174559"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_115"
 /note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb,

FEATURES
 source

insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."

```

ORIGIN
Alignment Scores:
Pred. No.: 1.69e-30 Length: 818
Score: 326.00 Matches: 61
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x BI818609 (1-818)

Qy 1 GluGlnGlylleValLeuProCysArgProGluGlylleProAlaGluValGlu 20
Dy 490 GAGCAGGCGCATCGTCTGCCCTCCACCGAGGCGCATCCCTCCAGCGAGGTGGAG 549

Qy 21 TrpLeuArgAenGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArg 40
Dy 550 TGGCTCCGACGACGAGGACTGGTGGACCGCTCCCTGGACCCCAATGTATATACATCA 609

Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
Dy 610 GAGCACAGCCTGGTGGTGGACAGCGCGCTTGTGACAGCGGCAACTACACCTGGCTG 669

Qy 61 Ala 61
Dy 670 GCC 672

RESULT 8
BF530640 1175 bp mRNA linear EST 11-DEC-2000
LOCUS 602071931F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4214959
DEFINITION 5', mRNA sequence.
ACCESSION BF530640
VERSION BF530640.1 GI:11618003
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1175)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L16A9789 row: m column: 08
High quality sequence stop: 665.
Location/Qualifiers
1. .1175
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4214959"
/tissue_type="anaplastic oligodendroglioma with lp/19q
loss"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Brn67"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

```

```

ORIGIN
Alignment Scores:
Pred. No.: 2.57e-30 Length: 1175
Score: 326.00 Matches: 61
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x BF530640 (1-1175)

Qy 1 GluGlnGlylleValLeuProCysArgProGluGlylleProAlaGluValGlu 20
Dy 333 GAGCAGGCGCATCGTCTGCCCTCCACCGAGGCGCATCCCTCCAGCGAGGTGGAG 392

Qy 21 TrpLeuArgAenGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArg 40
Dy 393 TGGCTCCGGAACGAGGACCTGGTGGACCGCTCCCTGGACCCCAATGTATATACATCAC 452

Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
Dy 453 GAGCACAGCCTGGTGGTGGACAGCGCGCTTGTGACAGCGGCAACTACACCTGGTG 512

Qy 61 Ala 61
Dy 513 GCC 515

RESULT 9
BC033727 1532 bp mRNA linear HTC 25-MAR-2004
LOCUS Homo sapiens unc-5 homolog A (C. elegans), mRNA (cDNA clone
DEFINITION IMAGE:5166762), containing frame-shift errors.
ACCESSION BC033727
VERSION BC033727.1 GI:21707230
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1532)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Heieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahy,J., Hulton,E., Kettman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shavchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalka,U., Smailus,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 1532)
Strausberg,R.
Direct Submission
Submitted (02-JUL-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov

```

Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc_mgc@nhgri.nih.gov
 Akhtar, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
 Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., Legaspi, R.,
 Maduro, Q.L., Masiello, C., Maekeri, B., Mastrian, S.D., McCloskey, J.C.,
 McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
 Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
 Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 68 Row: i Column: 2
 This clone was selected for full length sequencing because it
 passed the following selection criteria: GenomesScan gene prediction
 This clone has the following problem: frame shifted.

FEATURES

source
 1..1532
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5166762"
 /tissue types="Brain, adult medulla"
 /clone_lib="NIH_MGC_119"
 /lab_host="DH10B"
 /note="vector: pCMV-SPORT6"

ORIGIN

Alignment Scores:
 Pred. No.: 3..49e-30 Length: 1532
 Score: 326.00 Matches: 61
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x BC033727 (1-1532)

Qy 1 GluGlnGlyLeValLeuProCysArgProGluGlyLeProProAlaGluValGlu 20
 |||||
 Db 807 GAGCAGGCGCATCGTGTGCGCTGCGCTCCACCGGAGGCGCATCCCTCCAGCGCGAGGTGGAG 865
 |||||
 Qy 21 TrpLeuArgGlnAspLeuValAspProSerLeuAspProAsnValTyrIleThrArg 40
 |||||
 Db 867 TGGCTCCGGACAGGAGGACCTGGTGGACCGCTCCCTGGACCCCAATGATATACATCACCGGG 926
 |||||
 Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
 |||||
 Db 927 GAGCACAGCCTGGTGGTGGCGACAGCGCGCTTCTGACACGCGCAACTACACCTGGTG 986
 |||||
 Qy 61 Ala 61
 |||||
 Db 987 GCC 989

RESULT 10

LOCUS CB727042 485 bp mRNA linear EST 11-APR-2003
 DEFINITION AMGNNUC:NRHVS-00009-C10-A W Rat hypothalamus (10471) Rattus
 norvegicus cDNA clone nrhvs-00009-c10 5', mRNA sequence.
 ACCESSION CB727042
 VERSION CB727042.1 GI:29794027
 KEYWORDS EST.
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 485)
 Angen EST Program.
 TITLE Angen Rat EST Program
 JOURNAL Unpublished (2003)
 COMMENT Contact: Dan Fitzpatrick
 Angen, Inc
 One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA
 Tel: 805 447-4881
 Plate: 00009 row: c column: 10.
 Location/Qualifiers
 source
 1..485
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /db_xref="taxon:10116"
 /clone="nrhvs-00009-c10"
 /notes="Vector: pSPORT1, Site 1: SalI; Site 2: NotI; W Rat
 hypothalamus adult female WiStar rat avg. Insert size 2.3
 kb fraction 6 and 7"

FEATURES

source
 1..485
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /db_xref="taxon:10116"
 /clone="nrhvs-00009-c10"
 /notes="Vector: pSPORT1, Site 1: SalI; Site 2: NotI; W Rat
 hypothalamus adult female WiStar rat avg. Insert size 2.3
 kb fraction 6 and 7"

ORIGIN

Alignment Scores:
 Pred. No.: 2..94e-30 Length: 485
 Score: 322.00 Matches: 60
 Percent Similarity: 98.36% Conservative: 0
 Best Local Similarity: 98.36% Mismatches: 1
 Query Match: 98.77% Indels: 0
 DB: 6 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x CB727042 (1-485)

Qy 1 GluGlnGlyLeValLeuProCysArgProGluGlyLeProProAlaGluValGlu 20
 |||||
 Db 236 GAGCAAGGCATTGTACTACCTTGTGCCCCCAGAGGAATCCCCCAGCTGAGGTGGAG 295
 |||||
 Qy 21 TrpLeuArgGlnAspLeuValAspProSerLeuAspProAsnValTyrIleThrArg 40
 |||||
 Db 296 TGGCTTCGAATGAGGACCTCGTGGACCCCTCCCTCGATCCCAATGTGTACATCACCGG 355
 |||||
 Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
 |||||
 Db 356 GAGCACAGCCTAGTGTGCGTGTGAGCCCGCTGTCGACACGCGCAACTACACCTGTGTG 415
 |||||
 Qy 61 Ala 61
 |||||
 Db 416 GCC 418

RESULT 11

LOCUS BI758231 1034 bp mRNA linear EST 25-SEP-2001
 DEFINITION 603029876F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5200171 5',
 mRNA sequence.
 ACCESSION BI758231
 VERSION BI758231.1 GI:15749809
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1034)
 TITLE NIH-MGC <http://mgc.nci.nih.gov/>.
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: sgapsb-rc@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

```
Plate: L1AM11501 row: g column: 20
High quality sequence stop: 793.
FEATURES
  source
    1..1034
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="IMAGE:5200171"
      /lab_host="DH10B"
      /clone_lib="NIH_MGC_114"
      /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
      Site 2: EcoRV (destroyed); RNA source anonymous pool of 6
      male brains, age range 23-27 yo. Library is oligo-dT
      primed and directionally cloned (EcoRV site is destroyed
      upon cloning). Average insert size 1.5 kb, insert size
      range 1-3 kb. Library is normalized and enriched for
      full-length clones and was constructed by C. Gruber
      (Invitrogen). Research Genetics tracking code 019. Note:
      this is a NIH_MGC Library."
ORIGIN
Alignment Scores:
Pred. No.: 1.26e-29 Length: 1034
Score: 320.00 Matches: 60
Percent Similarity: 98.36% Conservative: 0
Best Local Similarity: 98.36% Mismatches: 1
Query Match: 98.16% Indels: 0
DB: 4 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x B1758231 (1-1034)

Qy 1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProAlaGluValGlu 20
Db 383 GAGCAGGCGCATCGTGTCCCTGCGGTCCACCGGAGGCGCATCCCTCCAGCGAGTGGAG 442

Qy 21 TrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArg 40
Db 443 TGGCTCCGGAAACGAGGACCTGTGTGACCGCTCCCTGGACCCCAATGTATACATCACGCGG 502

Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
Db 503 GAGCAGACGCTTGGTGTGCGACGCGCCGCTTGTGTGACGCGCAACTACACTACCTGCGTG 562

Qy 61 Ala 61
Db 563 GCC 565

RESULT 12
BX364574 853 bp mRNA linear EST 08-APR-2004
LOCUS BX364574 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
DEFINITION cDNA clone CS0DC023YB10 5-PRIME, mRNA sequence.
ACCESSION BX364574
VERSION BX364574.2 GI:46286957
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 853)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 5, 2003 this sequence version replaced gi:30368812.
COMMENT Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
```

```
3529.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS1AC006ZF06QPI&c=3529.f.
FEATURES
  source
    1..853
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="CS0DC023YB10"
      /tissue="NEUROBLASTOMA COT 25-NORMALIZED"
      /clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
      /note="1st strand cDNA was primed with a NotI-oligo(dT)
      primer. Five prime end enriched, double-strand cDNA was
      digested with Not I and cloned into the Not I and EcoR V
      sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Alignment Scores:
Pred. No.: 1.79e-29 Length: 853
Score: 318.00 Matches: 59
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 97.55% Indels: 0
DB: 5 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x BX364574 (1-853)

Qy 1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProAlaGluValGlu 20
Db 675 GAGCAGGCGCATCGTGTCCCTGCGGTCCACCGGAGGCGCATCCCTCCAGCGAGTGGAG 734

Qy 21 TrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArg 40
Db 735 TGGCTCCGGAAACGAGGACCTGTGTGACCGCTCCCTGGACCCCAATGTATACATCACGCGG 794

Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCys 59
Db 795 GAGCAGACGCTTGGTGTGCGACGCGCGCTTGTGTGACGCGCAACTACACTGTC 851

RESULT 13
AA288582 276 bp mRNA linear EST 14-APR-1997
LOCUS AA288582
DEFINITION mp15g05.r1 Life Tech mouse embryo 8 5dpc 10664019 Mus musculus CDNA
clone IMAGE:569336 5', similar to TR:E67610 E67610 UNC-5 ;, mRNA
sequence.
ACCESSION AA288582
VERSION AA288582.1 GI:1937649
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1. (bases 1 to 276)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WASHU-HMI Mouse EST Project
Washington University School of Medicine#
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:343984
Seq primer: -28m13 rev1 ET from Amersham
High quality sequence stop: 271.
Location/Qualifiers
```

```

source
1. .276
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:569336"
/tissue_type="embryo"
/dev_stage="8.5dpc embryos"
/lab_host="DRI0B"
/notes="Organ: brain; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is GTGGTGGAA. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemlin Chin, Ph.D., program coordinator."

ORIGIN

Alignment Scores:
Pred. No.: 2,07e-29 Length: 276
Score: 313.00 Matches: 61
Percent Similarity: 98.39% Conservatives: 0
Best Local Similarity: 98.39% Mismatches: 0
Query Match: 96.01% Indels: 1
DB: 1 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x AA288582 (1-276)

Qy 1 GluGlnGlyLeuValLeuProCysArgProGluGlyLeuProAlaGluValGlu 20
Db 4 GAGCAGGCGATTGCTGCTACCTTGTGCGCCCGCGAAGGAATCCCCCAGCTGAGGTGGAG 63
Qy 21 TrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValThrArg 40
Db 64 TGGCTCCGAATGAGACCTGCTGACCCCTCCCTCGACCCCATGTGTACATCACACGG 123
Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAsp-ThrAlaAsnValThrCysVa 60
Db 124 GAGCACAGCCTAGTGTGTGCGCGAGCGCGCTGCGCGACTACTGCCAACTACACCTCGT 183
Qy 60 lAla 61
Db 184 GGCC 187

RESULT 14
BU613458 723 bp mRNA linear EST 20-FEB-2003
LOCUS UI-M-EW0-caz-d-10-0-UI.r1 NIH_BMAP_EW0 Mus musculus cDNA clone
DEFINITION UI-M-EW0-caz-d-10-0-UI 5', mRNA sequence.
ACCESSION BU613458
VERSION BU613458.1 GI:23279673
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 723)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
Seq primer: pYX-5.
Location/Qualifiers
1. .723
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"

FEATURES
source
/db_xref="taxon:10090"
/clone="UI-M-EW0-caz-d-10-0-UI"
/tissue_type="whole brain"
/dev_stage="embryo 15.5 dpc"
/lab_host="DHI0B (T1 phage resistant)"
/clone_lib="NIH_BMAP_EW0"
/notes="Organ: brain; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is GTGGTGGAA. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemlin Chin, Ph.D., program coordinator."

ORIGIN

Alignment Scores:
Pred. No.: 6,29e-29 Length: 723
Score: 313.00 Matches: 61
Percent Similarity: 98.39% Conservatives: 0
Best Local Similarity: 98.39% Mismatches: 0
Query Match: 96.01% Indels: 1
DB: 5 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x BU613458 (1-723)

Qy 1 GluGlnGlyLeuValLeuProCysArgProPro-GluGlyLeuProAlaGluValGlu 20
Db 149 GAGCAGGCGATTGCTGCTACCTTGTGCGCCCGCGAAGGAATCCCCCAGCTGAGGTGGGA 208
Qy 20 uTrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValThrArg 40
Db 209 GTGGCTCCGAATGAGACCTGCTGACCCCTCCCTCGACCCCATGTGTACATCACACG 268
Qy 40 GluHisSerLeuValValArgGlnAlaArgLeuAlaAsp-ThrAlaAsnValThrCysVa 60
Db 269 GGAGCACAGCCTAGTGTGTGCGCGAGCGCGCTGCGCGACTACTGCCAACTACACCTCGT 328
Qy 60 lAla 61
Db 329 GGCC 332

RESULT 15
BU613440 843 bp mRNA linear EST 05-JUN-2001
LOCUS 602811321F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4943333
DEFINITION 5', mRNA sequence.
ACCESSION BU613440
VERSION BU613440.1 GI:14293916
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 843)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

```


http://image.llnl.gov
Plate: LLAM10886 row: j column: 06
High quality sequence stop: 769.
FEATURES
Location/Qualifiers
1..843
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:494333"
/tissue_type="anaplastic oligodendroglioma with 1p/19q loss"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Brn67"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.3 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
ORIGIN

Alignment Scores:
Pred. No.: 4.31e-27 Length: 843
Score: 299.00 Matches: 60
Percent Similarity: 98.36% Conservative: 0
Best Local Similarity: 98.36% Mismatches: 1
Query Match: 91.72% Indels: 1
DB: 4 Gaps: 0
US-10-624-932C-2_COPY_163_223 (1-61) x BG913440 (1-843)
Qy 1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProProAlaGluValGlu 20
Db 194 GAGCAGGGGCATCGTCTGCCCTTCACCGAGGGCATCCCTCCAGCCGAGGTGGAG 253
Qy 21 TrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArg 40
Db 254 TGGCTCCGGAGAGAGGACCTGGTGACCCGCTCCCTGGACCCCAATGTATATACACGCGG 313
Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
Db 314 GAGCACAGCCTGGTGGTGGACAGCGCCGCTTGTGTGACACGGC-AACTACACCTGCGTG 372
Qy 61 Ala 61
Db 373 GCC 375

Search completed: September 9, 2005, 04:40:32
Job time : 2013.62 secs

THIS PAGE BLANK (uspto)

THIS PAGE BLANK (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 8, 2005, 23:47:02 ; Search time 4861.88 Seconds
(without alignments)
1166.064 Million cell updates/sec

Title: US-10-624-932C-2_COPY_232_348

Perfect score: 682
Sequence: 1 SASAAVIVYVVGWSTWTEW.....NGBECQGTDLDRNCTSDL 117

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters: -MODEL=frame+p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool_h/US10624932/runat_08092005_161705_15773/app_query.fasta_1.1386
-DB=GenEmbl -QFMT=fastcap -SUFFIX=rge -MINMATCH=0.1 -LOOPEXT=0 -DOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blom62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=spect -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10624932 @CGN 1 1 7509 @runat_08092005_161705_15773 -NCPU=6 -ICPU=3
-NO.MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*
1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sv.*
13: gb.un.*
14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	682	100.0	2697	6	AX451652 Sequence
2	682	100.0	2752	6	AX449572 Sequence
3	673	98.7	3992	10	MMU487852 Mus muscu
4	673	98.7	4294	10	AK122575 Mus muscu

5	661	96.9	2697	6	AX268596 Sequence
6	661	96.9	2697	10	RNU87305
7	661	96.9	3014	6	BD057524 Netrin re
8	657.5	96.4	2784	6	CQ730306 Sequence
9	622.5	91.3	2881	6	AX527916 Sequence
10	539	79.0	2270	9	BC041156 Homo sapi
11	539	79.0	2612	6	CQ881064 Sequence
12	539	79.0	2780	6	CQ881054 Sequence
13	539	79.0	2986	6	CQ881052 Sequence
14	539	79.0	3646	6	CQ881060 Sequence
15	539	78.0	3646	9	AF055634 Homo sapi
16	535	78.4	121282	9	AC027318 Homo sapi
c 17	535	78.4	166534	2	AC034209 Homo sapi
c 18	535	78.4	168168	2	AC012283 Homo sapi
19	534	78.3	2962	5	AY187310 Gallus ga
c 20	531.5	77.9	242128	2	AC123700 Mus muscu
21	531	77.9	9299	10	MMU72634
22	526	77.1	9328	10	AB118026 Rattus no
23	523	76.7	2860	6	AX686445 Sequence
24	523	76.7	2860	6	AX686447 Sequence
25	523	76.7	2895	6	AX512281 Sequence
26	523	76.7	2895	6	AX497288 Sequence
27	523	76.7	3770	9	AY126437 Homo sapi
28	523	76.7	3884	6	AX528525 Sequence
29	523	76.7	3884	6	AX464012 Sequence
30	523	76.7	3884	9	AY358351 Homo sapi
31	523	76.7	3933	6	CQ850929 Sequence
32	523	76.7	3933	9	AK128132 Homo sapi
33	523	76.7	3935	9	AB096256 Homo sapi
34	522	76.5	2831	6	BD057526 Netrin re
35	522	76.5	2838	10	RNU87306
36	522	76.5	3672	10	BC048162 Mus muscu
37	522	76.5	3672	10	BC057560 Mus muscu
38	522	76.5	3788	10	MMU487853
c 39	511	74.9	231407	2	AC139592 Rattus no
40	507	74.3	1482	5	AY764274 Danio rer
41	502	73.6	2832	5	AY099459 Xenopus l
42	488	71.6	4330	5	AY744919 Petromyzo
43	485	71.1	2585	6	CQ842137 Sequence
44	485	71.1	2585	9	AK122615 Homo sapi
45	485	71.1	2661	6	AX800717 Sequence

ALIGNMENTS

RESULT 1	AX451652	Sequence 1 from Patent WO0233080.	2697 bp	DNA	linear	PAT 03-JUL-2002
LOCUS	AX451652	Sequence 1 from Patent WO0233080.				
DEFINITION	AX451652					
ACCESSION	AX451652					
VERSION	AX451652.1	GI:21698587				
KEYWORDS						
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	1	Koehler,R.H.				
AUTHORS		Regulation of human netrin binding membrane receptor unc5h-1				
TITLE		Patent: WO 0233080-A 1 25-APR-2002;				
JOURNAL		Bayer Aktiengesellschaft (DE)				
FEATURES		Location/Qualifiers				
source		1. 2697				
		/organism="Homo sapiens"				
		/mol_type="unassigned DNA"				
		/db_xref="taxon:9606"				

ORIGIN	Alignment Scores:					
	Pred. No.:	5.72e-36	Length:	2697		
	Score:	682.00	Matches:	117		
	Percent Similarity:	100.00%	Conservative:	0		
	Best Local Similarity:	100.00%	Mismatches:	0		

Query Match:	100.00%	Indels:	0				
DB:	6	Gaps:	0				
US-10-624-932C-2_COPY_232_348 (1-117) x AX451652 (1-2697)							
Qy	1	SerAlaSerAlaAlaValIleValTyrValAsnGlyGlyTTPSerThrTTPThrGluTTP	20				
Db	694	AGCGCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGTGGTGCAGCTGACCGAGTGG	753				
Qy	21	SerValCysSerAlaSerCysGlyArgGlyTTPGlnLysArgSerArgSerCysThrAsn	40				
Db	754	TCCGTCTGCAGCGCCAGCTGTGGCGCGCTGGCAGAAACGAGCGGAGCTGCACCAAC	813				
Qy	41	ProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsnValGlnLysThrAlaCys	60				
Db	814	CCGGCGCCCTCTCAACGGGGCGCTTCTGTGAGGGGCGAGATGTCCAGAAACAGCCTGC	873				
Qy	61	AlaThrLeuCysProValAspGlySerTTPSerProTTPSerLysTTPSerAlaCysGly	80				
Db	874	GCCACCTGTGCCAGTGGACGGCAGCTGGAGCCGCTGGAGCAAGTGGTGGCTGTGGG	933				
Qy	81	LeuAspCysThrHisTTPArgSerArgGluCysSerAspProAlaProArgAsnGlyGly	100				
Db	934	CTGGACTGCACCCACTGGCGGAGCGCTGAGTGTCTTGACCCAGCACCCGCAACGGAGG	993				
Qy	101	GluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu	117				
Db	994	GAGGAGTGCAGGGCACTGACCTGGACACCCGCAACTGTACCACTGACCTC	1044				
RESULT 2							
LOCUS	AX449572	2752 bp	DNA	linear PAT 03-JUL-2002			
DEFINITION	Sequence 1 from Patent WO0210216.						
ACCESSION	AX449572						
VERSION	AX449572.1	GI:21698195					
KEYWORDS	Homo sapiens (human)						
SOURCE	Homo sapiens						
ORGANISM	Homo sapiens						
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
AUTHORS	Mammalia; Eutheria; Primates; Carnivora; Hominidae; Homo.						
TITLE	Padigaru, M., Mezes, P., Mishra, V., Burgess, C., Casman, S.,						
JOURNAL	Grosse, W.M., Alsbrook, J.P., Lepley, D.M., Gerlach, V.L.,						
	MacDougall, J.R. and Smithson, G.						
	Proteins and nucleic acids encoding same						
	Patent: WO 0210216-A 1 07-FEB-2002;						
	Curagen Corporation (US)						
FEATURES	Location/Qualifiers						
source	1..2752						
	/organism="Homo sapiens"						
	/mol_type="unassigned DNA"						
	/db_xref="taxon:9606"						
ORIGIN							
Alignment Scores:							
Pred. No.:	5.84e-36	Length:	2752				
Score:	682.00	Matches:	117				
Percent Similarity:	100.00%	Conservative:	0				
Best Local Similarity:	100.00%	Mismatches:	0				
Query Match:	100.00%	Indels:	0				
DB:	6	Gaps:	0				
US-10-624-932C-2_COPY_232_348 (1-117) x AX449572 (1-2752)							
Qy	1	SerAlaSerAlaAlaValIleValTyrValAsnGlyGlyTTPSerThrTTPThrGluTTP	20				
Db	739	AGCGCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGTGGTGCAGCTGACCGAGTGG	798				
Qy	21	SerValCysSerAlaSerCysGlyArgGlyTTPGlnLysArgSerArgSerCysThrAsn	40				
Db	799	TCCGTCTGCAGCGCCAGCTGTGGCGCGCTGGCAGAAACGAGCGGAGCTGCACCAAC	858				
Qy	41	ProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsnValGlnLysThrAlaCys	60				
RESULT 3							
LOCUS	MMU487852	3992 bp	mRNA	linear ROD 24-SEP-2002			
DEFINITION	Mus musculus mRNA for netrin receptor Unc5h1 (Unc5h1 gene).						
ACCESSION	AJ487852						
VERSION	AJ487852.1	GI:22035783					
KEYWORDS	netrin receptor Unc5h1; Unc5h1 gene.						
SOURCE	Mus musculus (house mouse)						
ORGANISM	Mus musculus						
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.						
TITLE	Engelkamp, D.						
JOURNAL	Cloning of three mouse Unc5 genes and their expression patterns at						
MEDLINE	mid-gestation						
PUBMED	Mech. Dev. 118 (1-2), 191-197 (2002)						
REFERENCE	2239710						
AUTHORS	12351186						
TITLE	2 (bases 1 to 3992)						
JOURNAL	Engelkamp, D.						
FEATURES	Submitted (15-MAY-2002) Neuroanatomy, Max Planck Institute for						
source	1..3992						
	Location/Qualifiers						
	/organism="Mus musculus"						
	/mol_type="mRNA"						
	/db_xref="taxon:10090"						
gene	1..3992						
	/gene="Unc5h1"						
CDS	232..2928						
	/gene="unc5h1"						
	/codon_start=1						
	/product="netrin receptor Unc5h1"						
	/protein_id="CAD32250.1"						
	/db_xref="GI:22035784"						
	/db_xref="GOA:Q8K1S4"						
	/db_xref="UniProt/TREMBL:Q8K1S4"						
	/translation="MAVRGLMALLGLVLTMLRGLSGAQSATVNPVPGANPDLLP						
	HFLVPEDEVDYIVKPKVLLVCKAVPATQIFKCNQEWVRVDHVIERSITDSSGLPTM						
	EVRINVSQVQVKEVGLVEYKVCVAMSSGTTKSKOAYIRIAYLRNFEQEPLEAVE						
	SLSQIIVLPCRPPEGIPPAEVEWLRNEDIVDPSLDPNVITREHSLVVRQAADTAN						
	YTCAKNIVARRRSASAVIYVNGSHSTWTSVCSACGRGQKRSRSTCAPLN						
	RGADLDTRNCTSDLCILHTSSGPEVALYIGLAVAVCLILLLLVLVLYCRKKGELS						
	DVADSSILTSGFQVSIKPSKADNPILLTIQPDLSITTTTYQGSICPRQDQSPKFLQ						
	SNGHLSPGSGRHTLHSSPTSEADVFSLRSTONYPRSLPRGTSNMYGTFNPLGG						
	RLMIPNTGISLIPDDAI PRGKIYIYLTLHKPEDVRLPLAGCOTLLSPVSCQPGV						
	LLTRPVILAMDHCGESPDSWSLRLKQSCGSEGWEDVHLGEESPSHYLYCOLBAGAC						
	YVTFQGRFALYGEALSVAATKRLLRLFPVACTSLSEYNIRVYLCHDTHDAKEVV						
	QLKQGLGQLIQEPRVLHFDSYHNRLSLTHDPSSLWKLKLLYSQEIPEYHWNGT						
	QVLYCHTFTLRVNASITDLACKVWVQVEGDSQSFNFNITKDTFAEMLALESEG						
	GGVALVGPSPAFKIPFLIRQKIITSLDPPCSRGDWRTLAOKLHDLHSLSPFASKPSP						
	AMILLWEARHFFPNGNLQGLAAAVAGLQPDAGLFTVSEAC"						
ORIGIN							
Alignment Scores:							
Pred. No.:	3.35e-35	Length:	3992				

gene

```
/db_xref="taxon:10118"
ORIGIN
Alignment Scores:
Pred. No.: 1.38e-34 Length: 2697
Score: 661.00 Matches: 113
Percent Similarity: 97.44% Conservative: 1
Best Local Similarity: 96.58% Mismatches: 3
Query Match: 96.92% Indels: 0
DB: 6 Gaps: 0
US-10-624-932C-2_COPY_232_348 (1-117) x AX268596 (1-2697)
Qy 1 SerAlaSerAlaAlaValIleValTyrValAsnGlyGlyTyrSerThrTyrThrGluTyr 20
Db 694 AGCACCTCTGACGGGTCATTGTTATGTGAACGGTGGTGGTGCAGCTGGAGCTGAGTGG 753
Qy 21 SerValCysSerAlaSerCysGlyArgGlyTyrGlnLysArgSerArgSerCysThrAsn 40
Db 754 TCCGCTCTGCAGCGCCAGCTGTGGCGTGGTGGAGTTCGTGGAGTAAGTGCAGCTGTGGG 933
Qy 81 LeuAspCysThrHisTyrArgSerArgGluCysSerAspProAlaProArgAsnGlyGly 100
Db 934 CTTGACTGCACCCACTGGCGAGCGCGAGTGTCTGACCCAGCAGCACCCTGAGTGGAGGT 993
Qy 101 GluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117
Db 994 GAGGAGTGTGGGGTGTCTGACCTGACGACCCGCACTGTACAGTGCACCTC 1044
RESULT 6
RN087305
LOCUS RN087305 2697 bp mRNA linear ROD 15-MAY-1997
DEFINITION Rattus norvegicus transmembrane receptor Unc5h1 mRNA, complete cds.
ACCESSION U87305
VERSION U87305.1 GI:2055391
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
REFERENCE 1 (bases 1 to 2697)
AUTHORS Leonardo,E.D., Hinck,L., Masu,M., Keino-Masu,K., Ackerman,S.L. and Tessier-Lavigne,M.
TITLE vertebrate homologues of C. elegans UNC-5 are candidate netrin receptors
JOURNAL Nature 386 (6627), 833-838 (1997)
MEDLINE 97271897
PUBMED 9126742
REFERENCE 2 (bases 1 to 2697)
AUTHORS Leonardo,E.D., Hinck,L., Masu,M., Keino-Masu,K. and Tessier-Lavigne,M.
TITLE Direct Submission
JOURNAL Submitted (28-JAN-1997) Anatomy, UCSF, 513 Parnassus, San Francisco, CA 94143-0452, USA
FEATURES
source
location/Qualifiers
1..2697
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/tissue_type="brain and ventral spinal cord"
/dev_stages="18 day embryo and 13 day embryo"
1..2697
/codon_start=1
/product="transmembrane receptor UNC5H1"
CDS
/protein_id="AAB57678.1"
/db_xref="GI:2055392"
/translation="MAVRPGLWPVLLGIVLAWLRGSGAQOQSAVTANVPVPGANPDLLP
HFLVEPEDVTVIRKKNPVLLVCKVAPATQIPFKCNGBWROVDHVIERTSSGSLPTM
EVRINVSQVQEVKVFGLSEYWCQCVAMSSGTTKSKQAYIRIAYLRKNFQEPPLAKEV
SLBQGIVLPCRPEGIPPAEVEWLRNEDVDSLDPNVYITREHSLVVRQARLADTAN
YTCVAKNIVARRRSTSAAVIVYVNGGWSWTWESVCSAGCRGWQKRSRCSCTNPAPLN
GGAFPCGNQVQKTACATLCEVDGSSMSWSKACGLDCTHWRRESCDPAPRNGREC
RGADLDRNCTSDLCHTASCPEADVALYIGLVAVAVCLFLLALLGLIYCKKEGLDS
DVADSSILTSGGFQVSIKPSKADNPDLHTIIPDLSTITTTTQGLSCSRQGPSPKPOL
SNGLHLSPLSGSFTHLHSSPTSEADVFVSRSTONYFRSLPRGTNMAVYTFNFLGG
RLMIPNTGISLIPDPAIPRGKIYEIYLTGHKPEDVRLPLAGCQTLISPVVSCGPGV
LLTRPVILAMDHCPEPSPDSLRLLKQSCGSEWEDVLHGESPSHLYYCOLEAGAC
VYFTEOLGEPALVGEALSVAATKRLRLLAPVACTSLEVINRVYCLQHDTHDAKEVV
QLSKQGGQLIQBPVILHFKDSTHNRSLSHDVPSLWKSLLVQSEIYFPYHWNGT
OQLHCTCTFLERINASTDLACKVWQVEGDCGSFNFINITKDRFAELLALESEG
GVPAIVGPSAFKIPFLIRQKIITIASLDPPCSRGDWRTLAQKLHDLHLSLFFASKPSPT
AMTILNLWEARHFPNGNLQLAAAAVAGLGPQDAGLFTVSEAC"
```

PI MARC TESSIER LAVIGNE, DAVID E LEONARDO, LINDSAY HINCK, MASAYUKI
PI MASU,
PI KAZUKO KEINO MASU
PC C07K1/00, C07K14/00, C07K17/00, C07H21/02, C07H21/04, G01N33/53 CC
Strandedness: Double;
CC topology: Linear;
FH Key Location/Qualifiers.

FEATURES
source
1. .3014
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Alignment Scores:
Pred. No.: 1.54e-34 Length: 3014
Score: 661.00 Matches: 113
Percent Similarity: 97.44% Conservative: 1
Best Local Similarity: 96.58% Mismatches: 3
Query Match: 96.92% Indels: 0
DB: 6 Gaps: 0

US-10-624-932C-2_COPY_232_348 (1-117) x BD057524 (1-3014)

Qy 1 SerAlaSerAlaAlaValIleValrValAenGlyGlyTrpSerThrTrpThrGluTrp 20
Db 694 AGCACCTCTGACGGGTCAATTGTTTATGTGAACGGTGGTGGTGCACGTGACCTGAGTGG 753
Qy 21 SerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArgSerArgSerCysThrAsn 40
Db 754 TCCGTCTGTACAGCGGCAGCTGTGGGGTGGCTGTGGCAGAAACGGAGCTGCACCAAC 813
Qy 41 ProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsnValGlnLysThrAlaCys 60
Db 814 CCGCACCTCTACAGGGGGGCCCTTCTGTGAGGGGAGATGTCCAGAAACAGCCTGC 873
Qy 61 AlaThrLeuCysProValAspGlySerTrpSerProTrpSerLysTrpSerAlaCysGly 80
Db 874 GCCACTCTGCCAGTGGATGGGAGCTGGAGTTCGTGGAGTAAGTGGTCAAGCTGTGGG 933
Qy 81 LeuAspCysThrHisTrpArgSerArgGluCysSerAspProAlaProArgAsnGlyGly 100
Db 934 CTTGACTGCACCCACTGGCGAGCGCGAGTGTCTGTACCCAGCACCCCGCAATGGAGGT 993
Qy 101 GluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117
Db 994 GAGGAGTGTGGGGTGTGACTGGACACCCGCACTGTACCACTGACCTC 1044

RESULT 8
CQ730306 2784 bp DNA linear PAT 03-FEB-2004
LOCUS
DEFINITION Sequence 16240 from Patent WO02068579.
ACCESSION CQ730306
VERSION CQ730306.1 GI:42303801
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 16240 06-SEP-2002;
PE Corporation (NY) (US)

FEATURES
source
1. .2784
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores:
Pred. No.: 2.42e-34 Length: 2784
Score: 657.50 Matches: 117
Percent Similarity: 80.14% Conservative: 0
Best Local Similarity: 80.14% Mismatches: 0
Query Match: 96.41% Indels: 29
DB: 6 Gaps: 1

US-10-624-932C-2_COPY_232_348 (1-117) x CQ730306 (1-2784)

Qy 1 SerAlaSerAlaAlaValIleValrValAenGlyGlyTrpSerThrTrpThrGluTrp 20
Db 694 AGCGCCTCGGCTGTGTATGTCTACGGTGGGCCCGGGGACTCCCTGGTGCACAGGGAGA 753
Qy 10 -----ValAsn 11
Db 754 GGCACCTGGGTGCCCCCTGGGCGAGTGACATGTGGGCTGTCTTCTGTGTCGGCCAGTGAAC 813
Qy 12 GlyGlyTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrp 31
Db 814 GGTGGGTGGTGCAGCTGCAGCCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGCGCGGCTGG 873
Qy 32 GlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGlu 51
Db 874 CAGAAACGAGCGCGAGCTGCACCAACCGCGGCTCTCAACGGGGGGCGCTTCTGTGAG 933
Qy 52 GlyGlnAsnValGlnLysThrAlaCysAlaThrLeuCysProValAspGlySerTrpSer 71
Db 934 GGGCAGATGTCCAGAAACAGACCTGCGCCACCTGTGCCCAGTGGAGCGGCGAGTGGAGC 993
Qy 72 ProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSerArgGluCys 91
Db 994 CCGTGGAGCAAGTGGTGGGCTGTGGGCTGTGAGTGCACCCACTGGCGGAGCCGTGAGTGC 1053
Qy 92 SerAspProAlaProArgAsnGlyGlyGluCysGlnGlyThrAspLeuAspThrArg 111
Db 1054 TCTGACCAGACACCCCGAAGGAGGAGTGGCCAGGCACTGACCTGGACACCCGC 1113
Qy 112 AsnCysThrSerAspLeu 117
Db 1114 AACTGTACCACTGACCTC 1131

RESULT 9
AX527916 2881 bp DNA linear PAT 21-NOV-2002
LOCUS
DEFINITION Sequence 1 from Patent WO0229038.
ACCESSION AX527916
VERSION AX527916.1 GI:25172359
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Herrmann, J.L., Rastelli, L. and Shimkets, R.A.
TITLE Novel proteins and nucleic acids encoding same and antibodies
directed against these proteins
JOURNAL Patent: WO 0229038-A 1 11-APR-2002;
Curagen Corporation (US)
FEATURES
source
1. .2881
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores:
Pred. No.: 5.01e-32 Length: 2881
Score: 622.50 Matches: 109
Percent Similarity: 94.07% Conservative: 2
Best Local Similarity: 92.37% Mismatches: 6
Query Match: 91.28% Indels: 1
DB: 6 Gaps: 1

US-10-624-932C-2_COPY_232_348 (1-117) x AX527916 (1-2881)

Qy 1 SerAlaSerAlaAlaValIleValTyrValAsnGlyGlyTrpSerThrTrpThrGluTrp 20
Db 780 AGCGCCCTCCGCTGCTGTCATCGTACGTGAACGGTGGTGGTGCAGCGACGAGTGG 839
Qy 21 SerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArgSerArgSerCysThrAsn 40
Db 840 TCCGTCCTGACGCCAGCTGTGGCGCGGCTGGCAGAAACGAGCCGAGCTGCACCAAC 899
Qy 41 ProAlaProLeuAsnGlyGlyValAlaPheCysGluGlyGlnAsnVal---GlnLysThrAla 59
Db 900 CCGCGGCTCTCAACGGGGGGCTTTCTGTGAGGGGAGATGTCATGACCGACCGCTC 959
Qy 60 CysAlaThrLeuCysProValAspGlySerTrpSerProTrpSerLysTrpSerAlaCys 79
Db 960 TCCTCTCTGCTGCTCTGTCGACGCGCAGCTGGAGCCGCTGGAGCAAGTGTGGCCTGT 1019
Qy 80 GlyLeuAspCysThrHisTrpArgSerArgGluCysSerAspProAlaProArgAsnGly 99
Db 1020 GGGCTGAGCTGACCCCACTGGCGAGCGGTGAGTGTCTGACCCAGCACCCCGCAACGGA 1079
Qy 100 GlyGluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117
Db 1080 GGGGAGGAGTGCCAGGCGCAGCTGACCTGGACACCCGCAACTGACAGTGACCTC 1133

RESULT 10
LOCUS BC0411156 2270 bp mRNA linear PRI 21-OCT-2003
DEFINITION Homo sapiens unc-5 homolog C (C. elegans), mRNA (cdna clone
MGC:48696 IMAGE:5208108), complete cds.

ACCESSION BC0411156
VERSION BC0411156.1 GI:27370704
KEYWORDS MGC.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2270)
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeebore,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Haieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Ustin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villaion,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywicki,M.I., Skalska,U., Smalios,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

MEDLINE 22388257

PUBMED 1247932

REFERENCE 2 (bases 1 to 2270)

Strauberg,R.

Direct Submission

Submitted (16-DEC-2002) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
contact: amadansystemsbiology.org
Anup Madan, Jessica Fahey, Brin Helton, Mark Kettman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 84 Row: d Column: 5
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 16933524.

FEATURES

source

1. .2270
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:48696 IMAGE:5208108"
/tissue_type="Lung, Spleen, fetal, pooled"
/clone_lib="NIH_MGC_122"
/lab_host="DH10B"
/notes="Vector: pCMV-SPORT6"

gene

1. .2270
/gene="UNC5C"
/note="synonym: UNC5H3"
/db_xref="LocusID:8633"
/db_xref="MIM:603610"
350. .2143
/gene="UNC5C"
/codon_start=1
/product="UNC5C protein"
/protein_id="AAH41156.1"
/db_xref="GI:27370705"
/db_xref="LocusID:8633"
/db_xref="MIM:603610"

CDS

translation="MRKGLRATAARCGILGGLYLLQMLVLPALALLSAGTGSAAQDDDD
FHELETPSPDPPEPLPHELEPERAYIVKNPNVLYCKASPATQIYFKCNSEWVHQ
KDHIVDERVDETSGLIVREVSIEISQOVELGPDYWCQCVAMWSAGTTKRKAVV
IADHNIIITKOARLSDTANYTCVAKNIIVARRKSTTATVIVYVNGWSTWTSVNSKC
WRRCRTAPAPKNGKDCGLQVSGKQVQIACITLCPVDGRWTPKWSKTCGTECH
SDVALLVGVIVIAIVCLAISSVVALFVYRKNRDPESDIIDSSALNGFQPVNKA
RQDLLAVPDLTSAAMYPGVALHDVSDKIPMTNSPILDLPLNLKIKYVNTSGAVT
PQDLSEFTSKLSFQMTQSLNEALSINKQSLARQTDPSCTAFGSPNSLGGHLIVEN
SGVSLIIPAGAIPOGRVYEMVYTVHRKTNR"

misc_feature

866. .1123
/gene="UNC5C"
/note="IG; Region: Immunoglobulin"
/db_xref="CDD:smart00409"

misc_feature

1136. .1291
/gene="UNC5C"
/note="TSPI; Region: Thrombospondin type 1 repeats"
/db_xref="CDD:smart00209"

misc_feature

1304. .1450
/gene="UNC5C"
/note="TSPI; Region: Thrombospondin type 1 repeats"
/db_xref="CDD:smart00209"

misc_feature

1988. .2140
/gene="UNC5C"
/note="ZU5; Region: Domain present in ZO-1 and Unc5-like
netrin receptors"
/db_xref="CDD:smart00218"

ORIGIN

Alignment Scores:

Pred. No.: 1,21e-26 Length: 2270
Score: 539.00 Matches: 86
Percent Similarity: 86.32% Conservative: 15
Best Local Similarity: 73.50% Mismatches: 16
Query Match: 79.03% Indels: 0


```
DB: 9 Gaps: 0
US-10-624-932C-2_COPY_232_348 (1-117) x BC041156 (1-2270)

QY 1 SerAlaSerAlaAlaValIleValTyrValAenGlyGlyTyrSerThrTyrThrGluTyrP 20
Db 1097 ACTACAACCTGCCACTGTCATAGTCTATGTCACCGGTGGCTGGTCCACCTGGACGGAGTGG 1156

QY 21 SerValCysSerAlaSerCysGlyArgGlyTyrGlnLysArgSerArgSerCysThrAen 40
Db 1157 TCTGTGTGTAAACAGCGCGTGTGGACGAGGGTATCAGAAACGTACAAAGACCTTGTTACCAAC 1216

QY 41 ProAlaProLeuAenGlyGlyAlaPheCysGluGlyGlnAenValGlnLysThrAlaCys 60
Db 1217 CCGGCACCACTCAATGGGGGTGCTTCTGTGAAGGCGCAGAGTGTGCAGAAATAGCCTGT 1276

QY 61 AlaThrLeuCysProValAspGlySerTyrSerProTyrSerTyrSerTyrSerAlaCysGly 80
Db 1277 ACTAGTGTATGCCAGTGGATGGCAGGTGGACGCCATGGAGCAAGTGTCTACTTGTGGA 1336

QY 81 LeuAspCysThrHisTyrArgSerArgGluCysSerAspProAlaProArgAenGlyGly 100
Db 1337 ACTGAGTGCACCACTGGCGCAGGAGGAGTGCACGGCCAGCCCCCAAGAAATGAGGC 1396

QY 101 GluGluCysGlnGlyThrAspLeuAspThrArgAenCysThrSerAspLeu 117
Db 1397 AAGGACTGCGAGCGCTCGTCTTGCAATCCAAAGACTGCACTGATGGGCTT 1447

RESULT 11
CQ881064
LOCUS CQ881064 2612 bp DNA linear PAT 11-OCT-2004
DEFINITION Sequence 13 from Patent WO2004083371.
ACCESSION CQ881064
VERSION CQ881064.1 GI:54034173
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Dahl, N.
TITLE Genes associated with obesity and methods for using the same
JOURNAL Patent: WO 2004083371-A 13 30-SEP-2004;
Astrazeneca AB (SE)

FEATURES
Location/Qualifiers
source 1..2612
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores: 1.4e-26 Length: 2612
Pred. No.: 539.00 Matches: 86
Score: 86.32% Conservative: 15
Percent Similarity: 73.50% Mismatches: 16
Best Local Similarity: 79.03% Indels: 0
Query Match: 6 Gaps: 0

US-10-624-932C-2_COPY_232_348 (1-117) x CQ881064 (1-2612)

QY 1 SerAlaSerAlaAlaValIleValTyrValAenGlyGlyTyrSerThrTyrThrGluTyrP 20
Db 748 AGTACAACCTGCCACTGTCATAGTCTATGTCACCGGTGGCTGGTCCACCTGGACGGAGTGG 807

QY 21 SerValCysSerAlaSerCysGlyArgGlyTyrGlnLysArgSerArgSerCysThrAen 40
Db 808 TCTGTGTGTAAACAGCGCGTGTGGACGAGGGTATCAGAAACGTACAAAGACCTTGTTACCAAC 867

QY 41 ProAlaProLeuAenGlyGlyAlaPheCysGluGlyGlnAenValGlnLysThrAlaCys 60
Db 868 CCGGCACCACTCAATGGGGGTGCTTCTGTGAAGGCGCAGAGTGTGCAGAAATAGCCTGT 927
```

```
QY 61 AlaThrLeuCysProValAspGlySerTyrSerProTyrSerTyrSerTyrSerAlaCysGly 80
Db 928 ACTAGTGTATGCCAGTGGATGGCAGGTGGACGCCATGGAGCAAGTGTCTACTTGTGGA 987

QY 81 LeuAspCysThrHisTyrArgSerArgGluCysSerAspProAlaProArgAenGlyGly 100
Db 988 ACTGAGTGCACCACTGGCGCAGGAGGAGTGCACGGCCAGCCCCCAAGAAATGAGGC 1047

QY 101 GluGluCysGlnGlyThrAspLeuAspThrArgAenCysThrSerAspLeu 117
Db 1048 AAGGACTGCGAGCGCTCGTCTTGCAATCCAAAGACTGCACTGATGGGCTT 1098

RESULT 12
CQ881054
LOCUS CQ881054 2780 bp DNA linear PAT 11-OCT-2004
DEFINITION Sequence 3 from Patent WO2004083371.
ACCESSION CQ881054
VERSION CQ881054.1 GI:54034167
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Dahl, N.
TITLE Genes associated with obesity and methods for using the same
JOURNAL Patent: WO 2004083371-A 3 30-SEP-2004;
Astrazeneca AB (SE)

FEATURES
Location/Qualifiers
source 1..2780
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores: 1.5e-26 Length: 2780
Pred. No.: 539.00 Matches: 86
Score: 86.32% Conservative: 15
Percent Similarity: 73.50% Mismatches: 16
Best Local Similarity: 79.03% Indels: 0
Query Match: 6 Gaps: 0

US-10-624-932C-2_COPY_232_348 (1-117) x CQ881054 (1-2780)

QY 1 SerAlaSerAlaAlaValIleValTyrValAenGlyGlyTyrSerThrTyrThrGluTyrP 20
Db 859 AGTACAACCTGCCACTGTCATAGTCTATGTCACCGGTGGCTGGTCCACCTGGACGGAGTGG 918

QY 21 SerValCysSerAlaSerCysGlyArgGlyTyrGlnLysArgSerArgSerCysThrAen 40
Db 919 TCTGTGTGTAAACAGCGCGTGTGGACGAGGGTATCAGAAACGTACAAAGACTTGTTACCAAC 978

QY 41 ProAlaProLeuAenGlyGlyAlaPheCysGluGlyGlnAenValGlnLysThrAlaCys 60
Db 979 CCGGCACCACTCAATGGGGGTGCTTCTGTGAAGGCGCAGAGTGTGCAGAAATAGCCTGT 1038

QY 61 AlaThrLeuCysProValAspGlySerTyrSerProTyrSerTyrSerTyrSerAlaCysGly 80
Db 1039 ACTAGTGTATGCCAGTGGATGGCAGGTGGACGCCATGGAGCAAGTGTCTACTTGTGGA 1098

QY 81 LeuAspCysThrHisTyrArgSerArgGluCysSerAspProAlaProArgAenGlyGly 100
Db 1099 ACTGAGTGCACCACTGGCGCAGGAGGAGTGCACGGCCAGCCCCCAAGAAATGAGGC 1158

QY 101 GluGluCysGlnGlyThrAspLeuAspThrArgAenCysThrSerAspLeu 117
Db 1159 AAGGACTGCGAGCGCTCGTCTTGCAATCCAAAGACTGCACTGATGGGCTT 1209

RESULT 13
CQ881052
LOCUS CQ881052 2986 bp DNA linear PAT 11-OCT-2004
DEFINITION Sequence 1 from Patent WO2004083371.
```

```
ACCESSION      CQ881052
VERSION         CQ881052.1  GI:54034166
KEYWORDS
SOURCE          Homo sapiens (human)
ORGANISM        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE       1
AUTHORS         Dahl, N.
TITLE           Genes associated with obesity and methods for using the same
JOURNAL         Patent: WO 2004083371-A 1 30-SEP-2004;
                AstraZeneca AB (SE)
FEATURES        Location/Qualifiers
                source
                1..2986
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.:      1.61e-26      Length:      2986
Score:          539.00      Matches:      86
Percent Similarity: 86.32%      Conservative: 15
Best Local Similarity: 73.50%      Mismatches:  16
Query Match:    79.03%      Indels:       0
DB:             6            Gaps:         0
US-10-624-932C-2_COPY_232_348 (1-117) x CQ881052 (1-2986)
Qy 1 SerAlaSerAlaAlaValIleValTyrValAsnGlyGlyTyrSerThrTrrThrGluTrrP 20
Db 859 AGTACAACCTGCCACTGTCATAGTCTATGTCAACGGTGGCTGGTCCACTGCAGCGAGTGG 918
Qy 21 SerValCysSerAlaSerCysGlyArgGlyTrrPTrpGlnLysArgSerArgSerCysThrAsn 40
Db 919 TCTGTGTGTAAACAGCCGCTGTGGACGAGGGTATCAGAAACGCTACAGGACTTGTACCAAC 978
Qy 41 ProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsnValGlnLysThrAlaCys 60
Db 979 CCGGCACCACCTCAATGGGGGTGCCTTCTGTGAAGGGCAGAGTGTGCAGAAATAGCCGTG 1038
Qy 61 AlaThrLeuCysProValAspGlySerTrrPTrpSerProTrrPTrpSerLysTrrPTrpSerAlaCysGly 80
Db 1039 ACTAGTTCATCCCGAGTGGATGGCAGGTGGACGCCATGGACCAAGTGGTCTACTTGTGGA 1098
Qy 81 LeuAspCysThrHisTrrPTrpArgSerArgGluCysSerAspProAlaProArgAsnGlyGly 100
Db 1099 ACTGAGTGCACCCACTGGCGCAGGAGGAGTGCACGGCGCCAGGCCCCCAAGATGGAGGC 1158
Qy 101 GluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117
Db 1159 AAGGACTCGCAGCGCCTCGTCTTGCAATCCAGAACTGCACTGATGGGCTT 1209
RESULT 14
LOCUS          CQ881060
DEFINITION     Sequence 9 from Patent WO2004083371.
ACCESSION      CQ881060
VERSION        CQ881060.1  GI:54034170
KEYWORDS
SOURCE          Homo sapiens (human)
ORGANISM        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE       1
AUTHORS         Dahl, N.
TITLE           Genes associated with obesity and methods for using the same
JOURNAL         Patent: WO 2004083371-A 9 30-SEP-2004;
                AstraZeneca AB (SE)
FEATURES        Location/Qualifiers
                source
                1..3646
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
```

```
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.:      1.98e-26      Length:      3646
Score:          539.00      Matches:      86
Percent Similarity: 86.32%      Conservative: 15
Best Local Similarity: 73.50%      Mismatches:  16
Query Match:    79.03%      Indels:       0
DB:             6            Gaps:         0
US-10-624-932C-2_COPY_232_348 (1-117) x CQ881060 (1-3646)
Qy 1 SerAlaSerAlaAlaValIleValTyrValAsnGlyGlyTrrPTrpSerThrTrrThrGluTrrP 20
Db 902 AGTACAACCTGCCACTGTCATAGTCTATGTCAACGGTGGCTGGTCCACTGCAGCGAGTGG 961
Qy 21 SerValCysSerAlaSerCysGlyArgGlyTrrPTrpGlnLysArgSerArgSerCysThrAsn 40
Db 962 TCTGTGTGTAAACAGCCGCTGTGGACGAGGGTATCAGAAACGCTACAGGACTTGTACCAAC 1021
Qy 41 ProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsnValGlnLysThrAlaCys 60
Db 1022 CCGGCACCACCTCAATGGGGGTGCCTTCTGTGAAGGGCAGAGTGTGCAGAAATAGCCGTG 1081
Qy 61 AlaThrLeuCysProValAspGlySerTrrPTrpSerProTrrPTrpSerLysTrrPTrpSerAlaCysGly 80
Db 1082 ACTACGTTATGCCAGTGGATGGCAGGTGGACGCCATGGAGCAAGTGGTCTACTTGTGGA 1141
Qy 81 LeuAspCysThrHisTrrPTrpArgSerArgGluCysSerAspProAlaProArgAsnGlyGly 100
Db 1142 ACTGAGTGCACCCACTGGCGCAGGAGGAGTGCACGGCGCCAGGCCCCCAAGATGGAGGC 1201
Qy 101 GluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117
Db 1202 AAGGACTCGCAGCGCCTCGTCTTGCAATCCAGAACTGCACTGATGGGCTT 1252
RESULT 15
LOCUS          AF055634
DEFINITION     Homo sapiens transmembrane receptor UNC5C (UNC5C) mRNA, complete cds.
ACCESSION      AF055634
VERSION        AF055634.1  GI:3789764
KEYWORDS
SOURCE          Homo sapiens (human)
ORGANISM        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE       1 (bases 1 to 3646)
AUTHORS         Ackerman, S.L. and Knowles, B.B.
TITLE           Cloning and mapping of the UNC5C gene to human chromosome 4q21-q23
JOURNAL         Genomics 52 (2), 205-208 (1998)
MEDLINE        99000841
PUBMED         9782087
REFERENCE       2 (bases 1 to 3646)
AUTHORS         Ackerman, S.L.
TITLE           Direct Submission
JOURNAL         Submitted (25-MAR-1998) The Jackson Laboratory, 600 Main St., Bar Harbor, ME 04609, USA
FEATURES        Location/Qualifiers
                source
                1..3646
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /chromosome="4"
                /map="4q21-q23"
                /tissue_type="brain"
                1..3646
                /gene="UNC5C"
                155..2950
                /gene="UNC5C"
                /codon_start=1
gene
CDS
```


THIS PAGE BLANK (08PT0)

THIS PAGE BLANK (08PT0)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 8, 2005, 20:54:46 ; Search time 605.088 Seconds
(without alignments)
1144.643 Million cell updates/sec

Title: US-10-624-932C-2_COPY_232_348

Perfect score: 682
Sequence: 1 SASAAVIVYNGWSTWET.....NGBECQGTDLDTNRCTSDL 117

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-O=/cgn2_1/USPRO.spool_h/US10624932/runat_08092005.161705.15766/app_query.fasta_1.1386
-DB=N_Geneseq -QFMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=BLOSUM62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10624932.qcgn 1 1 1052 @runat_08092005.161705.15766 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_16Dec04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001as:*
- 5: Geneseq2001bs:*
- 6: Geneseq2002as:*
- 7: Geneseq2002bs:*
- 8: Geneseq2003as:*
- 9: Geneseq2003bs:*
- 10: Geneseq2003cs:*
- 11: Geneseq2003ds:*
- 12: Geneseq2004as:*
- 13: Geneseq2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	682	100.0	1002	12 ADH71619	Adh71619 Human gen
2	682	100.0	1009	12 ADH71613	Adh71613 Human gen
3	682	100.0	2697	6 ABK52891	ABK52891 Human net
4	682	100.0	2752	6 ABK37922	ABK37922 cDNA enco
5	682	100.0	2752	12 ADH71617	Adh71617 Human gen

6	661	96.9	2697	6	AAS16843	Aas16843 Rat netri
7	661	96.9	3014	2	AAV52940	AAV52940 Rat UNC-5
8	657.5	96.4	2907	4	AAK52261	AAK52261 Human pol
9	622.5	91.3	993	12	ADH71611	Adh71611 Human gen
10	622.5	91.3	2880	12	ADH71633	Adh71633 Human gen
11	622.5	91.3	2881	6	ABK49422	ABK49422 DNA enco
12	622.5	91.3	2881	12	ADH71649	Adh71649 Human gen
13	622.5	91.3	2881	12	ADH71635	Adh71635 Human gen
14	622.5	91.3	2881	12	ADH71637	Adh71637 Human gen
15	622.5	91.3	2881	12	ADH71641	Adh71641 Human gen
16	622.5	91.3	2881	12	ADH71609	Adh71609 Human gen
17	622.5	91.3	2881	12	ADH71629	Adh71629 Human gen
18	622.5	91.3	2881	12	ADH71631	Adh71631 Human gen
19	622.5	91.3	2881	12	ADH71627	Adh71627 Human gen
20	622.5	91.3	2881	12	ADH71647	Adh71647 Human gen
21	622.5	91.3	2881	12	ADH71639	Adh71639 Human gen
22	622.5	91.3	2881	12	ADH71643	Adh71643 Human gen
23	622.5	91.3	2881	12	ADH71625	Adh71625 Human gen
24	622.5	91.3	2881	12	ADH71647	Adh71647 Human gen
25	617.5	90.5	2881	10	ADG42568	Novel hum
26	539	79.0	2612	13	ADR99261	Adr99261 Splice va
27	539	79.0	2780	13	ADR99251	Adr99251 Human sRO
28	539	79.0	2796	10	AAL56266	Aal56266 Human thr
29	539	79.0	2986	13	ADR99249	Adr99249 Human lRO
30	539	79.0	3646	5	AAS75738	Aas75738 DNA enco
31	539	79.0	3646	13	ADR99257	Adr99257 Human unc
32	523	76.7	2860	6	ABT06279	Abt06279 Human NOV
33	523	76.7	2860	6	ABT06280	Abt06280 Human NOV
34	523	76.7	2895	6	ABO93898	Abog93898 Human tra
35	523	76.7	2995	6	ABK92062	ABK92062 DNA enco
36	523	76.7	3501	11	ADN39805	Adn39805 Cancer/an
37	523	76.7	3884	4	AAS21316	Aas21316 Human cDN
38	523	76.7	3884	8	ACA03675	ACA03675 CDNA enco
39	523	76.7	3884	8	ABX89213	ABx89213 DNA enco
40	523	76.7	3884	8	ACD41867	ACd41867 Human sec
41	523	76.7	3884	8	ACA04096	ACA04096 Human cDN
42	523	76.7	3884	9	ADA45664	Ada45664 Novel hum
43	523	76.7	3884	9	ADA76095	Ada76095 Human PRO
44	523	76.7	3884	9	ADA18745	Ada18745 Human PRO
45	523	76.7	3884	9	ADA61368	Ada61368 Homo sapi

ALIGNMENTS

RESULT 1

ADH71619
ID ADH71619 standard; DNA; 1002 BP.

XX
AC ADH71619;

XX
DT 25-MAR-2004 (first entry)

XX
DE Human gene of the invention NOV21f SEQ ID NO:515.

XX
KW ds; gene; human; cytostatic; immunomodulator; neuroprotective; neurotropic;
KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.

XX
OS Homo sapiens.

XX
PN WO2003102155-A2.

XX
PD 11-DEC-2003.

XX
PF 03-JUN-2003; 2003WO-US017430.

XX
PR 03-JUN-2002; 2002US-0385120P.

PR 04-JUN-2002; 2002US-0385784P.

PR 05-JUN-2002; 2002US-0386041P.

PR 05-JUN-2002; 2002US-0386047P.

PR 06-JUN-2002; 2002US-0386376P.

ADH71613	13-AUG-2002; 2002US-0403448P.	PR
ID	ADH71613 standard; DNA; 1009 BP.	PR
XX	ADH71613;	PR
AC	ADH71613;	PR
DT	25-MAR-2004 (first entry)	PR
XX	Human gene of the invention NOV21c SEQ ID NO:509.	PR
DE	de; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;	PR
KW	anorectic; antidiabetic; antimicrobial; antilipaeamic; gene therapy;	PR
KW	vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;	PR
KW	obesity; diabetes; infectious disease; metabolic syndrome X;	PR
KW	dyslipidaemia.	PR
XX		PR
OS	Homo sapiens.	PR
XX		PR
PN	WO2003102155-A2.	PR
XX		PR
PD	11-DEC-2003.	PR
XX		PR
PF	03-JUN-2003; 2003WO-US017430.	PR
XX		PR
XX	03-JUN-2002; 2002US-0385120P.	PR
PR	04-JUN-2002; 2002US-0385784P.	PR
PR	05-JUN-2002; 2002US-0386041P.	PR
PR	05-JUN-2002; 2002US-0386047P.	PR
PR	06-JUN-2002; 2002US-0386376P.	PR
PR	06-JUN-2002; 2002US-0386453P.	PR
PR	06-JUN-2002; 2002US-0386864P.	PR
PR	06-JUN-2002; 2002US-0387016P.	PR
PR	07-JUN-2002; 2002US-0386796P.	PR
PR	07-JUN-2002; 2002US-0386816P.	PR
PR	07-JUN-2002; 2002US-0386931P.	PR
PR	07-JUN-2002; 2002US-0386942P.	PR
PR	07-JUN-2002; 2002US-0386971P.	PR
PR	07-JUN-2002; 2002US-0387262P.	PR
PR	08-JUN-2002; 2002US-0296960P.	PR
PR	10-JUN-2002; 2002US-0387400P.	PR
PR	11-JUN-2002; 2002US-0387535P.	PR
PR	11-JUN-2002; 2002US-0387610P.	PR
PR	11-JUN-2002; 2002US-0387625P.	PR
PR	11-JUN-2002; 2002US-0387634P.	PR
PR	11-JUN-2002; 2002US-0387668P.	PR
PR	11-JUN-2002; 2002US-0387696P.	PR
PR	11-JUN-2002; 2002US-0387702P.	PR
PR	11-JUN-2002; 2002US-0387836P.	PR
PR	11-JUN-2002; 2002US-0387859P.	PR
PR	12-JUN-2002; 2002US-0387933P.	PR
PR	12-JUN-2002; 2002US-0387934P.	PR
PR	12-JUN-2002; 2002US-0387960P.	PR
PR	12-JUN-2002; 2002US-0388022P.	PR
PR	12-JUN-2002; 2002US-0388096P.	PR
PR	13-JUN-2002; 2002US-0389123P.	PR
PR	14-JUN-2002; 2002US-0389118P.	PR
PR	14-JUN-2002; 2002US-0389120P.	PR
PR	14-JUN-2002; 2002US-0389144P.	PR
PR	14-JUN-2002; 2002US-0389146P.	PR
PR	17-JUN-2002; 2002US-0389729P.	PR
PR	17-JUN-2002; 2002US-0389742P.	PR
PR	18-JUN-2002; 2002US-0389884P.	PR
PR	19-JUN-2002; 2002US-0390006P.	PR
PR	19-JUN-2002; 2002US-0390209P.	PR
PR	21-JUN-2002; 2002US-0390763P.	PR
PR	17-JUL-2002; 2002US-0396706P.	PR
PR	06-AUG-2002; 2002US-0401628P.	PR
PR	09-AUG-2002; 2002US-0402156P.	PR
PR	09-AUG-2002; 2002US-0402256P.	PR
PR	09-AUG-2002; 2002US-0402389P.	PR
PR	12-AUG-2002; 2002US-0402786P.	PR
PR	12-AUG-2002; 2002US-0402816P.	PR
PR	12-AUG-2002; 2002US-0402821P.	PR
PR	12-AUG-2002; 2002US-0402832P.	PR
PR		PR
PI	Alsebrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;	PI
PI	Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;	PI
PI	Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;	PI
PI	Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;	PI
PI	MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;	PI
PI	Padigaru M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;	PI
PI	Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shinkets RA;	PI
PI	Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;	PI
XX	Zhong H;	XX
XX		XX
XX	WPI: 2004-081935/08.	XX
DR	P-PSDB; ADH71614.	DR
XX		XX
PT	New NOVX polypeptides and nucleic acid molecules useful for preventing or	PT
PT	treating NOVX-associated disorders, e.g. cancer, diabetes, infection or	PT
XX	obesity, and in chromosome mapping, tissue typing or pharmacogenomics.	XX
PS	Example 21; SEQ ID NO 509; 1880pp; English.	PS
XX		XX
CC	The invention relates to a novel isolated polypeptide (NOVX). A	CC
CC	polypeptide of the invention has cytostatic, immunomodulator,	CC
CC	neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and	CC
CC	antilipaeamic activity, and may have a use in gene therapy, and as a	CC
CC	vaccine. The polypeptides are encoded by NOVX polynucleotides comprising	CC
CC	any of the 303 fully defined nucleotide sequences given in the	CC
CC	specification. The polypeptide is useful in the manufacture of a	CC
CC	medicament for treating a syndrome associated with a human disease.	CC
CC		

PR	12-JUN-2002;	2002US-0387933P.	CC	The invention relates to a novel isolated polypeptide (NOVX). A
PR	12-JUN-2002;	2002US-0387934P.	CC	polypeptide of the invention has cytosstatic, immunomodulator,
PR	12-JUN-2002;	2002US-0387950P.	CC	neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
PR	12-JUN-2002;	2002US-0388022P.	CC	antilipaemic activity, and may have a use in gene therapy, and as a
PR	12-JUN-2002;	2002US-0388096P.	CC	vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
PR	13-JUN-2002;	2002US-0389123P.	CC	any of the 303 fully defined nucleotide sequences given in the
PR	14-JUN-2002;	2002US-0389118P.	CC	specification. The polypeptide is useful in the manufacture of a
PR	14-JUN-2002;	2002US-0389120P.	CC	medicament for treating a syndrome associated with a human disease. The
PR	14-JUN-2002;	2002US-0389144P.	CC	polypeptide, polynucleotide and antibody are useful in diagnosing,
PR	14-JUN-2002;	2002US-0389146P.	CC	treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
PR	17-JUN-2002;	2002US-0389729P.	CC	Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
PR	17-JUN-2002;	2002US-0389742P.	CC	diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
PR	18-JUN-2002;	2002US-0389884P.	CC	further used as hybridisation probes, in chromosome mapping, tissue
PR	19-JUN-2002;	2002US-0390006P.	CC	typing, preventive medicine, and pharmacogenomics. The present sequence
PR	19-JUN-2002;	2002US-0390209P.	CC	encodes a NOVX polypeptide of the invention.
PR	21-JUN-2002;	2002US-0390763P.	XX	
PR	17-JUL-2002;	2002US-0396706P.	SQ	Sequence 2752 BP; 505 A; 937 C; 829 G; 481 T; 0 U; 0 Other;
PR	06-AUG-2002;	2002US-0401628P.		
PR	09-AUG-2002;	2002US-0402156P.	Alignment Scores:	
PR	09-AUG-2002;	2002US-0402256P.	Pred. No.:	8.45e-39
PR	09-AUG-2002;	2002US-0402389P.	Score:	682.00
PR	12-AUG-2002;	2002US-0402786P.	Percent Similarity:	100.00%
PR	12-AUG-2002;	2002US-0402816P.	Best Local Similarity:	100.00%
PR	12-AUG-2002;	2002US-0402821P.	Query Match:	100.00%
PR	12-AUG-2002;	2002US-0402832P.	Indels:	0
PR	13-AUG-2002;	2002US-0403448P.	Gaps:	12
PR	13-AUG-2002;	2002US-0403459P.		
PR	13-AUG-2002;	2002US-0403531P.	US-10-624-932C-2_COPY_232_348 (1-117) x ADH71617 (1-2752)	
PR	13-AUG-2002;	2002US-0403532P.	Qy	1 SerAlaSerAlaAlaValIleValTyrValAsnGlyGlyTyrSerThrTrrThrGluTrrp 20
PR	13-AUG-2002;	2002US-0403563P.	Db	739 AGCGCCTCGCTGTCATCGTACGTGAACGGTGGTGGTGGACCGAGTGG 798
PR	15-AUG-2002;	2002US-0406317P.	Qy	21 SerValCysSerAlaSerCysGlyArgGlyTrrpGlnLysArgSerArgSerCysThrAsn 40
PR	26-AUG-2002;	2002US-0406182P.	Db	799 TCCGTCTGCAGCGCCAGCTGTGGCGCGCTGGCAGAAACGGAGCGGAGCTGCACCAAC 858
PR	27-AUG-2002;	2002US-0406240P.	Qy	41 ProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsnValGlnLysThrAlaCys 60
PR	20-SEP-2002;	2002US-0412528P.	Db	859 CCGCGCGCTCTCAACGGGGGCGCTTCTGTGAGGGGCGAGTGTCCAGAAACAGCTGC 918
PR	23-SEP-2002;	2002US-0412731P.	Qy	61 AlaThrLeuCysProValAspGlySerTrrpSerTrrpSerProTrrpSerLysTrrpSerAlaCysGly 80
PR	30-SEP-2002;	2002US-0414801P.	Db	919 GCCACCCGTGTGCCAGTAGACGCGCAGCTGGAGCCGCTGGAGCAAGTGGTGGCTGTGGG 978
PR	30-SEP-2002;	2002US-0414839P.	Qy	81 LeuAspCysThrHisTrrpArgSerArgGluCysSerAspProAlaProArgAsnGlyGly 100
PR	30-SEP-2002;	2002US-0414840P.	Db	979 CTGGACTGCACCCACCTGGCGGAGCCGCTGAGTGTCTTGACCCAGCACCCCGGAGGGG 1038
PR	09-OCT-2002;	2002US-0417186P.	Qy	101 GluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117
PR	23-OCT-2002;	2002US-0420639P.	Db	1039 GAGGAGTGCCAGGGCAGCTGACCTGGACACCCCGCACTGTACCACTGACCTC 1089
PR	28-OCT-2002;	2002US-0421156P.	RESULT 6	
PR	31-OCT-2002;	2002US-0422690P.	AAS16843	
PR	01-NOV-2002;	2002US-0423130P.	ID	AAS16843 standard; cDNA; 2697 BP.
PR	05-NOV-2002;	2002US-00423798.	XX	XX
PR	05-NOV-2002;	2002US-0423798P.	XX	XX
PR	12-NOV-2002;	2002US-0425453P.	XX	XX
PA	(CURA-) CURAGEN CORP.		XX	XX
PI	Alsbrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;		XX	XX
PI	Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;		XX	XX
PI	Etenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;		XX	XX
PI	Gusev Vi, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;		XX	XX
PI	Maciachian T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;		XX	XX
PI	Padigar M, Patturajan M, Pena CE, Peyman JA, Raha D, Rastelli L;		XX	XX
PI	Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shinkets RA;		XX	XX
PI	Smithson G, Spytek KA, Stone DJ, Vernet CM, Voss EZ, Zhong M;		XX	XX
PI	Zhong H;		XX	XX
XX			XX	XX
DR	WPI; 2004-081935/08.		XX	XX
DR	P-PSDB; ADH71618.		XX	XX
XX			XX	XX
PT	New NOVX polypeptides and nucleic acid molecules useful for preventing or		XX	XX
PT	treating NOVX-associated disorders, e.g. cancer, diabetes, infection or		XX	XX
PT	obesity, and in chromosome mapping, tissue typing or pharmacogenomics.		XX	XX
XX			XX	XX
PS	Example 21; SEQ ID NO 513; 1880pp; English.		XX	XX

CC The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytosstatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.
XX
SQ Sequence 2752 BP; 505 A; 937 C; 829 G; 481 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.45e-39 Length: 2752
Score: 682.00 Matches: 117
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-10-624-932C-2_COPY_232_348 (1-117) x ADH71617 (1-2752)

Qy 1 SerAlaSerAlaAlaValIleValTyrValAsnGlyGlyTyrSerThrTrrThrGluTrrp 20
Db 739 AGCGCCTCGCTGTCATCGTACGTGAACGGTGGTGGTGGACCGAGTGG 798

Qy 21 SerValCysSerAlaSerCysGlyArgGlyTrrpGlnLysArgSerArgSerCysThrAsn 40
Db 799 TCCGTCTGCAGCGCCAGCTGTGGCGCGCTGGCAGAAACGGAGCGGAGCTGCACCAAC 858

Qy 41 ProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsnValGlnLysThrAlaCys 60
Db 859 CCGCGCGCTCTCAACGGGGGCGCTTCTGTGAGGGGCGAGTGTCCAGAAACAGCTGC 918

Qy 61 AlaThrLeuCysProValAspGlySerTrrpSerTrrpSerProTrrpSerLysTrrpSerAlaCysGly 80
Db 919 GCCACCCGTGTGCCAGTAGACGCGCAGCTGGAGCCGCTGGAGCAAGTGGTGGCTGTGGG 978

Qy 81 LeuAspCysThrHisTrrpArgSerArgGluCysSerAspProAlaProArgAsnGlyGly 100
Db 979 CTGGACTGCACCCACCTGGCGGAGCCGCTGAGTGTCTTGACCCAGCACCCCGGAGGGG 1038

Qy 101 GluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117
Db 1039 GAGGAGTGCCAGGGCAGCTGACCTGGACACCCCGCACTGTACCACTGACCTC 1089

RESULT 6
AAS16843
ID AAS16843 standard; cDNA; 2697 BP.
XX
XX
AC AAS16843;
XX
DT 14-FEB-2002 (first entry)
XX
DE Rat netrin receptor UNC5H1 (YSG7) cDNA.
XX
XX YSG; YSG7; schizophrenia; chronic animal model; LCGU; netrin receptor;
XX local cerebral glucose utilisation; phosphodiesterase 1-alpha; UNC5H1;
XX calcium-independent alpha-latrotoxin receptor; CIRL; trkE; synapsin 1A;
XX epithelial discoidin domain receptor 1; synapsin 1B; neuroleptic; ss;
XX tumour necrosis factor alpha; TNF-alpha; rat.
OS Rattus sp.
XX
XX Key Location/Qualifiers
FH CDS 1..2697
PT CDS /*tag= a
FT

/product= "Rat netrin receptor UNC5H1"

FT WO200175440-A2.
XX
XX
XX PD 11-OCT-2001.
XX PF 02-APR-2001; 2001WO-GB001486.
XX PR 31-MAR-2000; 2000GB-00007880.
XX PR 26-MAY-2000; 2000GB-00012768.
XX PA (WELF-) WELFIDE CORP.
XX
XX Cochran S, Paterson G, Ohashi Y, Morris B, Pratt J;
XX WPI; 2002-010813/01.
XX DR P-PSDB; AAU10543.
XX
XX Novel chronic animal model of schizophrenia, useful for identifying anti-
XX psychotic drugs and genes that are associated with schizophrenia.
XX
XX Claim 1; Fig 8a; 79pp; English.
XX
XX The invention relates to YSG polynucleotide fragments for use in
XX diagnosing and/or developing treatments for schizophrenia using chronic
XX animal models. The polynucleotides and their encoded polypeptides are
XX used for identification of compounds which modulate the expression of YSG
XX molecules, leading to the manufacture of schizophrenia medicaments. The
XX sequences can also be used for testing candidate compounds for any effect
XX on the polypeptides. Anti-schizophrenic effects of a compound can be
XX determined by measuring local cerebral glucose utilisation (LCGU) or
XX comparing its expression level with that of a control group. The
XX sequences are useful in the identification of genes associated with
XX schizophrenic states and in the development of an antibody. The sequences
XX of the invention include phosphodiesterase 1-alpha, calcium-independent
XX alpha-latrotoxin receptors (CIRL)-1,2&3, epithelial discoidin domain
XX receptor 1 (lrke), netrin receptor (UNC5H1), synapsins IA and AB and
XX tumour necrosis factor (TNF) alpha. This sequence represents rat netrin
XX receptor UNC5H1 (YSG7) DNA
XX
XX Sequence 2697 BP; 541 A; 864 C; 766 G; 526 T; 0 U; 0 Other;
XX
XX
XX Alignment Scores:
XX Pred. NO.: 2.48e-37 Length: 2697
XX Score: 661.00 Matches: 113
XX Percent Similarity: 97.44% Conservative: 1
XX Best Local Similarity: 96.58% Mismatches: 3
XX Query Match: 96.92% Indels: 0
XX DB: 6 Gaps: 0
XX
XX US-10-624-932C-2_COPY_232_348 (1-117) x AAS16843 (1-2697)
XX
XX Qy 1 SerAlaSerAlaAlaValIleValIyTyrValAnGlyGlyTyrSerThrTyrThrGluTyr 20
XX Db 694 AGCACTCTGACGGCGGTCAATTGTATTGTGAACCGTGGTGGTGCACGTGACGTGAGTGG 753
XX
XX Qy 21 SerValCysSerAlaSerCysGlyArgGlyTyrGlnLysArgSerArgSerCysThrAsn 40
XX Db 754 TCCGTCTGCAGCGCCAGCTGTGGGCGTGTGGCAGAAACGGAGCCGAGGTGCACCCAC 813
XX
XX Qy 41 ProAlaProLeuAnGlyGlyAlaPheCysGluGlyGlnAnValGlnLysThrAlaCys 60
XX Db 814 CCGGCACCTCTCAACGGGGGCGCCCTCTGTGAGGGGCGAGATGTCCAGAAACAGCCTGC 873
XX
XX Qy 61 AlaThrLeuCysProValAspGlySerTyrProTyrSerTyrSerTyrSerAlaCysGly 80
XX Db 874 GCCACTCTGTGCCAGTGGATGGGAGCTGGAGTTCGTGGAGTAAGTGTACGCTGTGGG 933
XX
XX Qy 81 LeuAspCysThrHisTyrArgSerArgGluCysSerAspProAlaProArgAsnGlyGly 100
XX Db 934 CTTGACTGCACCCACTGGCGGAGCGCGAGTGTCTGTACCCAGCACCCCGCAATGGAGGT 993
XX
XX Qy 101 GluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117

Db 994 GAGGAGTGTGGGTGCTGACCTGGACACCGCACTGTACCACTGACGACCTC 1044
XX
XX RESULT 7
XX AAV52940
XX ID AAV52940 standard; cDNA; 3014 BP.
XX AC AAV52940;
XX XX 25-MAR-2003 (revised)
XX DT 21-DEC-1998 (first entry)
XX DE Rat UNC-5 homologue unc5h-1 cDNA.
XX KW UNC5H-1; rat; netrin receptor; cell migration; axon guidance;
XX KW diagnosis; therapy; ds.
XX OS Rattus sp.
XX FH Key Location/Qualifiers
XX FT CDS 1..2697
XX FT /*tag= a
XX
XX WO9837085-A1.
XX PD 27-AUG-1998.
XX PF 19-FEB-1998; 98WO-US003143.
XX PR 19-FEB-1997; 97US-00808982.
XX PA (REGC) UNIV CALIFORNIA.
XX PI Tessier-Lavigne M, Leonardo ED, Hinck L, Masu M, Keinomasu K;
XX DR WPI; 1998-495364/42.
XX DR P-PSDB; AAW78898.
XX XX Netrin-binding, vertebrate proteins - useful for diagnosis, therapy and
XX the biopharmaceutical industry.
XX PS Claim 7; Page 15-17; 32pp; English.
XX
XX This cDNA, termed unc5h-1, comprises a rat homologue of Caenorhabditis
XX elegans unc-5. Rat unc5h-1 and unc5h-2 (see AAV52942) cDNAs were isolated
XX from an E18 brain cDNA library. The predicted proteins (see AAW78898 and
XX AAW78900) show similarity with UNC-5. They are predicted to be involved
XX in cell migration and axon guidance, and are characterised as receptor
XX proteins for netrins. Gene expression is observed in regions where
XX differentiating neurons are undergoing axogenesis. Human unc5h-1 (see
XX AAV52941) and unc5h-2 (see AAV52943) cDNAs are also claimed. Vertebrate
XX UNC-5 proteins may be produced recombinantly from transfected host cells
XX by utilising these vertebrate UNC-5 nucleic acids. The invention also
XX provides unc-5 hybridisation probes and primers, vertebrate UNC-5-
XX specific binding agents such as specific antibodies, and methods of
XX making and using the subject compositions in diagnosis (e.g. genetic
XX hybridisation screens for vertebrate unc-5 transcripts), therapy (e.g.
XX gene therapy to modulate vertebrate unc-5 gene expression) and in the
XX biopharmaceutical industry (e.g. as immunogens, reagents for modulating
XX cell guidance, reagents for screening chemical libraries for lead
XX pharmacological agents, etc.). (Updated on 25-MAR-2003 to correct PI
XX field.)
XX SQ Sequence 3014 BP; 596 A; 977 C; 849 G; 592 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 2.79e-37 Length: 3014
XX Score: 661.00 Matches: 113
XX Percent Similarity: 97.44% Conservative: 1
XX Best Local Similarity: 96.58% Mismatches: 3
XX Query Match: 96.92% Indels: 0
XX DB: 2 Gaps: 0

```
US-10-624-932C-2_COPY_232_348 (1-117) x AAV52940 (1-3014)
Qy 1 SerAlaSerAlaAlaValIleValTyrValAsnGlyGlyTrpSerThrTrpThrGluTrp 20
Db 694 AGCACCTCTGCAGCGGTCAATTGTTATGTGAACGGTGGTGGTCCAGCTGAGTGG 753
Qy 21 SerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArgSerArgSerCysThrAsn 40
Db 754 TCCGCTCTGCAGCGGTCAATTGTTATGTGAACGGTGGTGGTCCAGCTGAGTGG 813
Qy 41 ProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsnValGlnLysThrAlaCys 60
Db 814 CCGGCACCTCTCAACGGGGGGCGCTTCTGTGAGGGGCGAATGTCAGAAACAGCCTGC 873
Qy 61 AlaThrLeuCysProValAspGlySerTrpSerProTrpSerProTrpSerAlaCysGly 80
Db 874 GCCACTCTGTGCCAGTGGATGGAGCTGGAGTTCGTGGAGTAAAGTGGTGCAGCCTGTGGG 933
Qy 81 LeuAspCysThrHisTrpArgSerArgGluCysSerAspProAlaProArgAsnGlyGly 100
Db 934 CTTGACTGCACCCACTGGCGAGCGCGAGTCTCTGACCCAGCACCCTCCGCAATGGAGGT 993
Qy 101 GluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117
Db 994 GAGGAGTGTGGGGTGTGCTGACCTGGACACCCGCAACTGTACCACTGACCTC 1044
RESULT 8
AAK52261
ID AAK52261 standard; cDNA; 2907 BP.
XX
AC AAK52261;
XX
DE 06-NOV-2001 (first entry)
XX
XX Human polynucleotide SEQ ID NO 806.
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX tissue growth factor; immunomodulatory; cancer; leukaemia;
XX nervous system disorder; arthritis; inflammation; ss.
XX
OS Homo sapiens.
XX
XX WO200157190-A2.
XX
XX 09-AUG-2001.
XX
XX 05-FEB-2001; 2001WO-US004098.
XX
XX 03-FEB-2000; 2000US-00496914.
XX
XX 27-APR-2000; 2000US-00560875.
XX
XX 20-JUN-2000; 2000US-00598075.
XX
XX 19-JUL-2000; 2000US-00620325.
XX
XX 01-SEP-2000; 2000US-00654936.
XX
XX 15-SEP-2000; 2000US-00663561.
XX
XX 20-OCT-2000; 2000US-00693325.
XX
XX 30-NOV-2000; 2000US-00728422.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
XX Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
XX Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
XX WPI; 2001-476283/51.
XX
XX P-PSDB; AAM79128.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
XX in diagnosis and gene therapy.
XX
XX Claim 1; Page 2691-2694; 6221pp; English.
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
XX
```

```
CC encoded polypeptides (AAM78323-AAK80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication
XX
SQ Sequence 2907 BP; 552 A; 966 C; 881 G; 508 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4,74e-37 Length: 2907
Score: 657,50 Matches: 117
Percent Similarity: 80.14% Conservative: 0
Best Local Similarity: 80.14% Mismatches: 0
Query Match: 96.41% Indels: 29
DB: 4 Gaps: 1

US-10-624-932C-2_COPY_232_348 (1-117) x AAK52261 (1-2907)
Qy 1 SerAlaSerAlaAlaValIleValTyr----- 9
Db 817 AGCGCTCTCCGCTGCTGTCTACGCTGCGGCGGCGGACTCCCTGGTCACAGGGAGA 876
Qy 10 -----Valasn 11
Db 877 GGCACTGCGGTGCCCCCTGGGCGAGTGACATGGGTGTCTCTCTGTCGCGCCAGTGAAC 936
Qy 12 GlyGlyTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrp 31
Db 937 GGTGGGTGGTGCAGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGG 996
Qy 32 GlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGlu 51
Db 997 CAGAACGGAGCGGAGCTGCACACCCGCGCTCTCAACGGGGCGCTTCTGTGTGAG 1056
Qy 52 GlyGlnAsnValGlnLysThrAlaCysAlaThrLeuCysProValAspGlySerTrpSer 71
Db 1057 GGGCAGAAATGTCCAGAAACAGAGCTGCGCCACCTGTGCCAGTGGAGCGGCGAGTGGAGC 1116
Qy 72 ProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSerArgGluCys 91
Db 1117 CCGTGGAGCAAGTGGTCCGCTGTGGCTGGACTGCAACCCAGTGGAGCGGAGCCGCGAGTGC 1176
Qy 92 SerAspProAlaProArgAsnGlyGlyGluGluCysGlnGlyThrAspLeuAspThrArg 111
Db 1177 TCTGACCCAGACACCCCGCAACGGAGGGGAGAGTGGCCAGGGGCACTGACCTGGACACCCGC 1236
Qy 112 AsnCysThrSerAspLeu 117
Db 1237 AACTGTACCAGTGACCTC 1254

RESULT 9
ADH71611
ID ADH71611 standard; DNA; 993 BP.
XX
XX AC ADH71611;
XX
XX 25-MAR-2004 (first entry)
XX
XX Human gene of the invention NOV21b SEQ ID NO:507.
XX
XX ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
XX anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;
XX vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
XX obesity; diabetes; infectious disease; metabolic syndrome X;
XX dyslipidaemia.
XX
```



```
Qy      60  CysAlaThrLeuCysProValAspGlySerTrpSerProTrpSerLysTrpSerAlaCys 79
Db      :::
799  TCCTCTCTGCTTGTCTCTGTGGACGGCAGCTGGAGCCCGCTGGACCAAGTGTGCGCCTGT 858

Qy      80  GlyLeuAspCysThrHisTrpArgSerArgGluCysSerAspProAlaProArgAsnGly 99
Db      |||||
859  GGGCTGAGCTGACCCACTGGCGGAGCGGTGAGTGTCTGTGACCCAGCACCCCGCAACGGA 918

Qy      100 GlyGluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117
Db      |||||
919  GGGGAGGAGTGCCAGGGCAGCTGACCTGGACACCGCAACTGTACCACTGACCTC 972

RESULT 10
ADH71633
ID  ADH71633 standard; DNA; 2880 BP.
XX
AC  ADH71633;
XX
XX
DT  25-MAR-2004 (first entry)
XX
DE  Human gene of the invention NOV21m SEQ ID NO:529.
XX
KW  ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW  anorectic; antidiabetic; antimicrobial; antilipaeamic; gene therapy;
KW  vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW  obesity; diabetes; infectious disease; metabolic syndrome X;
KW  dyslipidaemia.
XX
OS  Homo sapiens.
XX
PN  WO2003102155-A2.
XX
PD  11-DEC-2003.
XX
PF  03-JUN-2003; 2003WO-US017430.
XX
PR  03-JUN-2002; 2002US-0385120P.
PR  04-JUN-2002; 2002US-0385784P.
PR  05-JUN-2002; 2002US-0386041P.
PR  05-JUN-2002; 2002US-0386047P.
PR  06-JUN-2002; 2002US-0386376P.
PR  06-JUN-2002; 2002US-0386453P.
PR  06-JUN-2002; 2002US-0386864P.
PR  06-JUN-2002; 2002US-0387016P.
PR  07-JUN-2002; 2002US-0386796P.
PR  07-JUN-2002; 2002US-0386816P.
PR  07-JUN-2002; 2002US-0386931P.
PR  07-JUN-2002; 2002US-0386942P.
PR  07-JUN-2002; 2002US-0386971P.
PR  07-JUN-2002; 2002US-0387262P.
PR  08-JUN-2002; 2002US-0296960P.
PR  10-JUN-2002; 2002US-0387400P.
PR  10-JUN-2002; 2002US-0387535P.
PR  11-JUN-2002; 2002US-0387610P.
PR  11-JUN-2002; 2002US-0387625P.
PR  11-JUN-2002; 2002US-0387634P.
PR  11-JUN-2002; 2002US-0387668P.
PR  11-JUN-2002; 2002US-0387696P.
PR  11-JUN-2002; 2002US-0387702P.
PR  11-JUN-2002; 2002US-0387836P.
PR  11-JUN-2002; 2002US-0387859P.
PR  12-JUN-2002; 2002US-0387933P.
PR  12-JUN-2002; 2002US-0387934P.
PR  12-JUN-2002; 2002US-0388022P.
PR  12-JUN-2002; 2002US-0388096P.
PR  13-JUN-2002; 2002US-0389123P.
PR  14-JUN-2002; 2002US-0389118P.
PR  14-JUN-2002; 2002US-0389120P.
PR  14-JUN-2002; 2002US-0389144P.
PR  14-JUN-2002; 2002US-0389146P.
PR  17-JUN-2002; 2002US-0389729P.
PR  17-JUN-2002; 2002US-0389742P.

18-JUN-2002; 2002US-0389884P.
19-JUN-2002; 2002US-0390006P.
19-JUN-2002; 2002US-0390209P.
21-JUN-2002; 2002US-0390763P.
17-JUL-2002; 2002US-0396706P.
06-AUG-2002; 2002US-0401628P.
09-AUG-2002; 2002US-0402156P.
09-AUG-2002; 2002US-0402356P.
09-AUG-2002; 2002US-0402389P.
12-AUG-2002; 2002US-0402786P.
12-AUG-2002; 2002US-0402816P.
12-AUG-2002; 2002US-0402821P.
12-AUG-2002; 2002US-0402832P.
13-AUG-2002; 2002US-0403448P.
13-AUG-2002; 2002US-0403459P.
13-AUG-2002; 2002US-0403531P.
13-AUG-2002; 2002US-0403532P.
13-AUG-2002; 2002US-0403563P.
15-AUG-2002; 2002US-0406317P.
15-AUG-2002; 2002US-0403617P.
26-AUG-2002; 2002US-0406182P.
26-AUG-2002; 2002US-0406355P.
27-AUG-2002; 2002US-0406240P.
12-SEP-2002; 2002US-0410084P.
20-SEP-2002; 2002US-0412528P.
21-SEP-2002; 2002US-0412731P.
30-SEP-2002; 2002US-0414801P.
30-SEP-2002; 2002US-0414839P.
30-SEP-2002; 2002US-0414840P.
09-OCT-2002; 2002US-0417186P.
09-OCT-2002; 2002US-0417406P.
23-OCT-2002; 2002US-0420639P.
31-OCT-2002; 2002US-0421156P.
28-OCT-2002; 2002US-0422690P.
01-NOV-2002; 2002US-0423130P.
05-NOV-2002; 2002US-00423798.
05-NOV-2002; 2002US-0423798P.
12-NOV-2002; 2002US-0425453P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
XX Catterton E, Chapeval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
XX Eitenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
XX Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
XX Maciachlan T, Malyankar UM, Mezick AU, Millet I, Mishra VS;
XX Padigaru M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
XX Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
XX Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
XX Zhong H;
XX
XX WPI; 2004-081935/08.
XX P-PSDB; ADH71634.
XX
XX New NOVX polypeptides and nucleic acid molecules useful for preventing or
XX treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
XX obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
XX Example 21; SEQ ID NO 529; 1980pp; English.
XX
XX The invention relates to a novel isolated polypeptide (NOVX). A
XX polypeptide of the invention has cytostatic, immunomodulator,
XX neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
XX antilipaeamic activity, and may have a use in gene therapy, and as a
XX vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
XX any of the 303 fully defined nucleotide sequences given in the
XX specification. The polypeptide is useful in the manufacture of a
XX medicament for treating a syndrome associated with a human disease. The
XX polypeptide, polynucleotide and antibody are useful in diagnosing.
XX treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
XX Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
XX diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
```

CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.

SQ Sequence 2880 BP; 527 A; 984 C; 867 G; 502 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.36e-34 Length: 2880
Score: 622.50 Matches: 109
Percent Similarity: 94.07% Conservative: 2
Best Local Similarity: 92.37% Mismatches: 6
Query Match: 91.28% Indels: 1
Gaps: 12

US-10-624-932C-2_COPY_232_348 (1-117) x ADH71633 (1-2880)

Qy 1 SerAlaSerAlaAlaValIleValTyrValaenGlyGlyTyrSerThrTrpThrGluTrp 20
Db 779 AGCGCTCCGCTGCTGCTACGTGAAACGGTGGTGTGACGTGGACCGAGTGG 838
Qy 21 SerValCysSerAlaSerCysGlyArgGlyTyrGlnLysArgSerArgSerCysThrAsn 40
Db 839 TCCGCTCTCAGCGCCAGCTGTGGCGCGCTGGCAGAAACGGAGCCGAGCTGCACCAAC 898
Qy 41 ProAlaProLeuAenGlyGlyAlaPheCysGluGlyGlnAenVal---GlnLysThrAla 59
Db 899 CCGCGCTCTCAACGGGGCGCTTCTGTGAGGGGCGAGATGTCCATGACCGCACCGTC 958
Qy 60 CysAlaThrLeuCysProValAspGlySerTrpSerProTrpSerLysTrpSerAlaCys 79
Db 959 TCCTCTCTGCTGTCTGTGAGCGAGCTGGAGCCCGTGGAGCAAGTGTGGCCCTGT 1018
Qy 80 GlyLeuAspCysThrHisTrpArgSerArgGluCysSerAspProAlaProArgAsnGly 99
Db 1019 GGGCTGGACTGACCCACTGGCGGAGCGTGTGAGTCTCTGACCCAGCACCCGCAACGGA 1078
Qy 100 GlyGluGluCysGlnGlyThrAspLeuAspThrArgAenCysThrSerAspLeu 117
Db 1079 GGGGAGGAGTGCCAGGGCACTGACCTGGACACCCCGCAACTGTACCAGTGCCTC 1132

RESULT 11

ABK49422
ID ABK49422 standard; DNA; 2881 BP.

XX AC ABK49422;

XX DT 15-JUL-2002 (first entry)

XX DE DNA encoding human UNC5-like protein NOV1.

XX KW Human; NOVX polypeptide; cardiomyopathy; atherosclerosis; cancer;
KW cell signal processing; metabolic pathway modulation; cancerous tissue;
KW antibody; diabetes; transgenic animal; UNC5-like protein; NOV1;
KW chromosome 13; gene; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX CDS 87..2786

XX FT /tag= a

XX FT /product= "Human UNC5-like protein NOV1"

XX FN WO200229038-A2.

XX PD 11-APR-2002.

XX XX 04-OCT-2001; 2001WO-US031377.

XX XX 04-OCT-2000; 2000US-0237862P.

XX XX (CURA-) CURAGEN CORP.

XX XX Herrmann JL, Rastelli L, Shimkets RA;

XX DR WPI; 2002-340104/37.

XX DR P-PSDB; AAU79939.

XX PT Novel isolated NOVX polypeptide, and encoded polynucleotide, useful for
XX FT treating cardiomyopathy, atherosclerosis, and cancer.

XX PS Claim 8; Page 7-8; 180pp; English.

XX CC The present invention relates to a new NOVX polypeptide having a 900
XX CC (NOV1), 4349 (NOV2), 940 (NOV3), 798 (NOV4), 865 (NOV5), or 331 (NOV6)
XX CC residue amino acid sequence, as given in the specification. The novel
XX CC polypeptide, and its encoding polynucleotide, are used to treat
XX CC cardiomyopathy, atherosclerosis, cancer or a disease related to cell
XX CC signal processing and metabolic pathway modulation, in a human. Detecting
XX CC the polypeptide or polynucleotide is useful for identifying cancerous
XX CC tissue. The antibody can be used to treat diabetes or cancer. The host
XX CC cells can be used to produce non-human transgenic animals useful in drug
XX CC screening. The present nucleic acid sequence is that of the human UNC5-
XX CC like NOV1 gene located on chromosome 13. This sequence encodes the human
XX CC UNC5-like protein NOV1 of the invention

SQ Sequence 2881 BP; 526 A; 985 C; 868 G; 502 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.36e-34 Length: 2881
Score: 622.50 Matches: 109
Percent Similarity: 94.07% Conservative: 2
Best Local Similarity: 92.37% Mismatches: 6
Query Match: 91.28% Indels: 1
Gaps: 12

US-10-624-932C-2_COPY_232_348 (1-117) x ABK49422 (1-2881)

Qy 1 SerAlaSerAlaAlaValIleValTyrValaenGlyGlyTyrSerThrTrpThrGluTrp 20

Db 780 AGCGCTCCGCTGCTGCTACGTGAAACGGTGGTGTGACGTGGACCGAGTGG 839

Qy 21 SerValCysSerAlaSerCysGlyArgGlyTyrGlnLysArgSerArgSerCysThrAsn 40

Db 840 TCCGCTCTCAGCGCCAGCTGTGGCGCGCTGGCAGAAACGGAGCCGAGCTGCACCAAC 899

Qy 41 ProAlaProLeuAenGlyGlyAlaPheCysGluGlyGlnAenVal---GlnLysThrAla 59

Db 900 CCGCGCTCTCAACGGGGCGCTTCTGTGAGGGGCGAGATGTCCATGACCGCACCGTC 959

Qy 60 CysAlaThrLeuCysProValAspGlySerTrpSerProTrpSerLysTrpSerAlaCys 79

Db 960 TCCTCTCTGCTGTCTGTGAGCGAGCTGGAGCCCGTGGAGCAAGTGTGGCCCTGT 1019

Qy 80 GlyLeuAspCysThrHisTrpArgSerArgGluCysSerAspProAlaProArgAsnGly 99

Db 1020 GGGCTGGACTGACCCACTGGCGGAGCGTGTGAGTCTCTGACCCAGCACCCGCAACGGA 1079

Qy 100 GlyGluGluCysGlnGlyThrAspLeuAspThrArgAenCysThrSerAspLeu 117

Db 1080 GGGGAGGAGTGCCAGGGCACTGACCTGGACACCCCGCAACTGTACCAGTGCCTC 1133

RESULT 12

ADH71649

ID ADH71649 standard; DNA; 2881 BP.

XX AC ADH71649;

XX XX 25-MAR-2004 (first entry)

XX DE Human gene of the invention NOV21u SEQ ID NO:545.

XX KW ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antileptemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.

```
XX OS Homo sapiens.
XX PN WO2003102155-A2.
XX PD 11-DEC-2003.
XX PF 03-JUN-2003; 2003WO-US017430.
XX 03-JUN-2002; 2002US-03851120P.
XX 04-JUN-2002; 2002US-0385784P.
XX 05-JUN-2002; 2002US-0386041P.
XX 06-JUN-2002; 2002US-0386047P.
XX 06-JUN-2002; 2002US-0386376P.
XX 06-JUN-2002; 2002US-0386453P.
XX 06-JUN-2002; 2002US-0386864P.
XX 06-JUN-2002; 2002US-0387016P.
XX 07-JUN-2002; 2002US-0386796P.
XX 07-JUN-2002; 2002US-0386816P.
XX 07-JUN-2002; 2002US-0386931P.
XX 07-JUN-2002; 2002US-0386942P.
XX 07-JUN-2002; 2002US-0386971P.
XX 07-JUN-2002; 2002US-0387262P.
XX 08-JUN-2002; 2002US-0296960P.
XX 10-JUN-2002; 2002US-0387400P.
XX 10-JUN-2002; 2002US-0387535P.
XX 11-JUN-2002; 2002US-0387610P.
XX 11-JUN-2002; 2002US-0387625P.
XX 11-JUN-2002; 2002US-0387634P.
XX 11-JUN-2002; 2002US-0387668P.
XX 11-JUN-2002; 2002US-0387696P.
XX 11-JUN-2002; 2002US-0387702P.
XX 11-JUN-2002; 2002US-0387836P.
XX 11-JUN-2002; 2002US-0387859P.
XX 12-JUN-2002; 2002US-0387933P.
XX 12-JUN-2002; 2002US-0387934P.
XX 12-JUN-2002; 2002US-0387960P.
XX 12-JUN-2002; 2002US-0388032P.
XX 12-JUN-2002; 2002US-0388096P.
XX 13-JUN-2002; 2002US-03891123P.
XX 14-JUN-2002; 2002US-0389118P.
XX 14-JUN-2002; 2002US-0389144P.
XX 14-JUN-2002; 2002US-0389146P.
XX 17-JUN-2002; 2002US-0389729P.
XX 17-JUN-2002; 2002US-0389742P.
XX 18-JUN-2002; 2002US-0389884P.
XX 19-JUN-2002; 2002US-0390006P.
XX 19-JUN-2002; 2002US-0390209P.
XX 21-JUN-2002; 2002US-0390763P.
XX 17-JUN-2002; 2002US-0396706P.
XX 06-AUG-2002; 2002US-0401628P.
XX 09-AUG-2002; 2002US-0402156P.
XX 09-AUG-2002; 2002US-0402256P.
XX 09-AUG-2002; 2002US-0402389P.
XX 12-AUG-2002; 2002US-0402786P.
XX 12-AUG-2002; 2002US-0402816P.
XX 12-AUG-2002; 2002US-0402821P.
XX 12-AUG-2002; 2002US-0402832P.
XX 13-AUG-2002; 2002US-0403448P.
XX 13-AUG-2002; 2002US-0403459P.
XX 13-AUG-2002; 2002US-0403531P.
XX 13-AUG-2002; 2002US-0403532P.
XX 13-AUG-2002; 2002US-0403563P.
XX 13-AUG-2002; 2002US-0406317P.
XX 15-AUG-2002; 2002US-0403617P.
XX 26-AUG-2002; 2002US-0406182P.
XX 26-AUG-2002; 2002US-0406355P.
XX 27-AUG-2002; 2002US-0406240P.
XX 12-SEP-2002; 2002US-0410084P.
XX 20-SEP-2002; 2002US-0412528P.
XX 23-SEP-2002; 2002US-0412731P.
XX 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 23-OCT-2002; 2002US-0417406P.
PR 28-OCT-2002; 2002US-0420639P.
PR 31-OCT-2002; 2002US-0421156P.
PR 01-NOV-2002; 2002US-0422690P.
PR 05-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
XX (CURA-) CURAGEN CORP.
XX Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ertterberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigaru M, Patturajan M, Pena CE, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CM, Voss EZ, Zhong M;
PI Zhong H;
XX WPI; 2004-081935/08.
XX P-PSDB; ADH71650.
XX New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX Example 21; SEQ ID NO 545; 1880pp; English.
XX The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antitumorigenic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.
XX SQ Sequence 2881 BP; 526 A; 986 C; 868 G; 501 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1.36e-34 Length: 2881
Score: 622.50 Matches: 109
Percent Similarity: 94.07% Conservative: 2
Best Local Similarity: 92.37% Mismatches: 6
Query Match: 91.28% Indels: 1
DB: 12
US-10-624-932C-2_COPY_232_348 (1-117) x ADH71649 (1-2881)
Qy 1 SerAlaSerAlaValIleValTyrValAsnGlyGlyTrpSerThrTrpGluTrp 20
Db 780 AGCGCCTCCCGTGTGTCATCGTACGTGAACGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 839
Qy 21 SerValCysSerAlaSerCysGlyArgGlyTrpGlnIlyArgSerArgSerCysThrAsn 40
Db 840 TCCGTCTGCAGCGCCACGTGTGGCGCGGTGGCGAGAACGGAGCGGAGCTGCACCAAC 899
Qy 41 ProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsnVal---GlnIlyThrAla 59
Db 900 CCGCGCGCTCTCAACGCGGGGGCGCTTTTCTGTGAGGGGCGAGATGTCCATGATGCCGCCGTC 959
```



```
QY      60  CysAlaThrLeuCyProValAspGlySerTrpSerProTrpSerLysTrpSerAlaCys 79
      :::
Db      960  TCCTCTCTGCTGTCTGTGGACGGCAGCTGGAGCCCGTGGAGCAAGTGGTGGCCCTGT 1019

QY      80  GlyLeuAspCysThrHisTrpArgSerArgGluCysSerAspProAlaProArgAnGly 99
      |||||
Db      1020  GGGCTGGACTCACCCACTGGCGGAGCGGTGAGTGCTCTGACCCAGCACCCCGCAACGGA 1079

QY      100  GlyGluGluCysGlnGlyThrAspLeuAspThrArgAsnCyThrSerAspLeu 117
      |||||
Db      1080  GGGGAGGAGTCCAGGGGCACTGACCTGGACCCCGCAACTGTACCACTGACCTC 1133

RESULT 13
ADH71635
ID      ADH71635 standard; DNA; 2881 BP.
XX
AC      ADH71635;
XX
DT      25-MAR-2004 (first entry)
XX
DB      Human gene of the invention NOV21n SEQ ID NO:531.
XX
KW      ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW      anorectic; antidiabetic; antimicrobial; antilipaeamic; gene therapy;
KW      vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW      obesity; diabetes; infectious disease; metabolic syndrome X;
KW      dyslipidaemia.
XX
OS      Homo sapiens.
XX
FN      WO2003102155-A2.
XX
PD      11-DEC-2003.
XX
PP      03-JUN-2003; 2003WO-US017430.
XX
PR      03-JUN-2002; 2002US-0385120P.
PR      04-JUN-2002; 2002US-0385784P.
PR      05-JUN-2002; 2002US-0386041P.
PR      05-JUN-2002; 2002US-0386047P.
PR      06-JUN-2002; 2002US-0386376P.
PR      06-JUN-2002; 2002US-0386453P.
PR      06-JUN-2002; 2002US-0386864P.
PR      06-JUN-2002; 2002US-0387016P.
PR      07-JUN-2002; 2002US-0386796P.
PR      07-JUN-2002; 2002US-0386816P.
PR      07-JUN-2002; 2002US-0386931P.
PR      07-JUN-2002; 2002US-0386942P.
PR      07-JUN-2002; 2002US-0386971P.
PR      07-JUN-2002; 2002US-0387262P.
PR      08-JUN-2002; 2002US-0296960P.
PR      10-JUN-2002; 2002US-0387400P.
PR      10-JUN-2002; 2002US-0387535P.
PR      11-JUN-2002; 2002US-0387610P.
PR      11-JUN-2002; 2002US-0387625P.
PR      11-JUN-2002; 2002US-0387634P.
PR      11-JUN-2002; 2002US-0387666P.
PR      11-JUN-2002; 2002US-0387696P.
PR      11-JUN-2002; 2002US-0387702P.
PR      11-JUN-2002; 2002US-0387836P.
PR      11-JUN-2002; 2002US-0387859P.
PR      12-JUN-2002; 2002US-0387933P.
PR      12-JUN-2002; 2002US-0387934P.
PR      12-JUN-2002; 2002US-0388022P.
PR      12-JUN-2002; 2002US-0388096P.
PR      13-JUN-2002; 2002US-0389123P.
PR      14-JUN-2002; 2002US-0389118P.
PR      14-JUN-2002; 2002US-0389120P.
PR      14-JUN-2002; 2002US-0389144P.
PR      14-JUN-2002; 2002US-0389146P.
PR      17-JUN-2002; 2002US-0389729P.
```

```
PR      17-JUN-2002; 2002US-0389742P.
PR      18-JUN-2002; 2002US-0389884P.
PR      19-JUN-2002; 2002US-0390066P.
PR      19-JUN-2002; 2002US-0390209P.
PR      21-JUN-2002; 2002US-0390763P.
PR      17-JUL-2002; 2002US-0396706P.
PR      06-AUG-2002; 2002US-0401628P.
PR      09-AUG-2002; 2002US-0402156P.
PR      09-AUG-2002; 2002US-0402256P.
PR      09-AUG-2002; 2002US-0402389P.
PR      12-AUG-2002; 2002US-0402786P.
PR      12-AUG-2002; 2002US-0402816P.
PR      12-AUG-2002; 2002US-0402821P.
PR      12-AUG-2002; 2002US-0402832P.
PR      13-AUG-2002; 2002US-0403448P.
PR      13-AUG-2002; 2002US-0403459P.
PR      13-AUG-2002; 2002US-0403531P.
PR      13-AUG-2002; 2002US-0403532P.
PR      13-AUG-2002; 2002US-0403563P.
PR      15-AUG-2002; 2002US-0403617P.
PR      15-AUG-2002; 2002US-0403617P.
PR      26-AUG-2002; 2002US-0406182P.
PR      26-AUG-2002; 2002US-0406355P.
PR      27-AUG-2002; 2002US-0406240P.
PR      12-SEP-2002; 2002US-0410084P.
PR      20-SEP-2002; 2002US-0412528P.
PR      23-SEP-2002; 2002US-0412731P.
PR      30-SEP-2002; 2002US-0414801P.
PR      30-SEP-2002; 2002US-0414839P.
PR      30-SEP-2002; 2002US-0414840P.
PR      30-SEP-2002; 2002US-0414954P.
PR      09-OCT-2002; 2002US-0417186P.
PR      09-OCT-2002; 2002US-0417406P.
PR      23-OCT-2002; 2002US-0420639P.
PR      28-OCT-2002; 2002US-0421156P.
PR      31-OCT-2002; 2002US-0422650P.
PR      01-NOV-2002; 2002US-0423130P.
PR      05-NOV-2002; 2002US-0423798P.
PR      05-NOV-2002; 2002US-0423798P.
PR      12-NOV-2002; 2002US-0425453P.
XX
XX      (CURA-) CURAGEN CORP.
XX
PI      Alsobrook JP, Alvarez E, Anderson DW, Boldog PL, Casman SJ;
PI      Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI      Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI      Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI      MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI      Padigaru M, Patturajan M, Pena CE, Peyman JA, Raha D, Rastelli L;
PI      Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI      Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI      Zhong H;
XX
XX      WPI; 2004-081935/08.
DR      P-PSDB; ADH71636.
XX
XX      New NOVX polypeptides and nucleic acid molecules useful for preventing or
XX      treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
XX      obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
XX      Example 21; SEQ ID NO 531; 1880pp; English.
XX
XX      The invention relates to a novel isolated polypeptide (NOVX). A
XX      polypeptide of the invention has cytostatic, immunomodulator,
XX      neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
XX      antilipaeamic activity, and may have a use in gene therapy, and as a
XX      vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
XX      any of the 303 fully defined nucleotide sequences given in the
XX      specification. The polypeptide is useful in the manufacture of a
XX      medicament for treating a syndrome associated with a human disease. The
XX      polypeptide, polynucleotide and antibody are useful in diagnosing,
XX      treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
XX      Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
```

CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.

XX
SQ Sequence 2881 BP; 527 A; 985 C; 867 G; 502 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.36e-34 Length: 2881
Score: 622.50 Matches: 109
Percent Similarity: 94.07% Conservative: 2
Best Local Similarity: 92.37% Mismatches: 6
Query Match: 91.28% Indels: 1
DB: 12 Gaps: 1

US-10-624-932C-2_COPY_232_348 (1-117) x ADH71635 (1-2881)

Qy 1 SerAlaSerAlaAlaValIleValTyrValAsnGlyGlyTyrSerThrTrpThrGluTyr 20
Db 780 AGCGCTCCGCTGCTGTCATCGTCTACGTGACGGTGGTGGTGCACGACGACTGG 839
Qy 21 SerValCysSerAlaSerCysGlyArgGlyTyrGlnLysArgSerArgSerCysThrAsn 40
Db 840 TCCGCTCTGCAGCGCCAGCTGTGGCGCGGCTGTGGCAGAAACGGAGCCGAGTGACCAAC 899
Qy 41 ProAlaProLeuAnGlyGlyAlaPheCysGluGlyGlnAnVal---GlnLysThrAla 59
Db 900 CCGCGCGCTCTCAACGGGGCGCTTCTGTGAGGGGAGATGTCATGACCGCACCGTC 959
Qy 60 CysAlaThrLeuCysProValAspGlySerTyrProTyrSerTyrSerLysTyrSerAlaCys 79
Db 960 TCCTCTGCTTGTCTCTGTGGACGGCAGCTGGAGCCGCTGGAGCAAGTGGTGGCTGT 1019
Qy 80 GlyLeuAspCysThrHisTyrArgSerArgGluCysSerAspProAlaProArgAsnGly 99
Db 1020 GGGCTGGACTGCACCCACTGGCGAGCGCTGAGTGTCTGTACCCAGCACCCCGCAACGGA 1079
Qy 100 GlyGluGluCysGlnGlyThrAspLeuAspThrArgAnCysThrSerAspLeu 117
Db 1080 GGGGAGGAGTGCACGGGCACTGACCTGACACCCGCACTGTACAGTGACCTC 1133

RESULT 14

ADH71637
ID ADH71637 standard; DNA; 2881 BP.
XX
XX
AC ADH71637;
XX
XX 25-MAR-2004 (first entry)
XX
XX Human gene of the invention NOV210 SEQ ID NO:533.
XX
XX ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
XX anorectic; antidiabetic; antimicrobial; antipapemic; gene therapy;
XX vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
XX obesity; diabetes; infectious disease; metabolic syndrome X;
XX dyslipidaemia.
XX
XX Homo sapiens.
OS
PN WO2003102155-A2.
XX
XX 11-DEC-2003.
XX
XX 03-JUN-2003; 2003WO-US017430.
XX
XX 03-JUN-2002; 2002US-0385120P.
XX 04-JUN-2002; 2002US-0385784P.
XX 05-JUN-2002; 2002US-0386041P.
XX 05-JUN-2002; 2002US-0386047P.
XX 06-JUN-2002; 2002US-0386376P.
XX 06-JUN-2002; 2002US-0386453P.
XX 06-JUN-2002; 2002US-0386864P.
XX 06-JUN-2002; 2002US-0387016P.

PR 07-JUN-2002; 2002US-0386796P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0403617P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-0423798P.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.

(CURA-) CURAGEN CORP.

XX Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;

PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI MacLachlan T, Malvankar UM, Mexick AJ, Millet I, Mishra VS;
PI Padigaru M, Patturajan M, Pena CE, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shinkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;
XX WPI; 2004-081935/08.
DR P-PSDB; ADH71638.

XX New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

XX Example 21; SEQ ID NO 533; 1880pp; English.

XX The invention relates to a novel isolated polypeptide (NOVX). A

CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.

XX SQ Sequence 2881 BP; 527 A; 985 C; 867 G; 502 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.36e-34 Length: 2881
Score: 622.50 Matches: 109
Percent Similarity: 94.07% Conservative: 2
Best Local Similarity: 92.37% Mismatches: 6
Query Match: 91.28% Indels: 1
DB: 12 Gaps: 1

US-10-624-932c-2_copy_232_348 (1-117) x ADH71637 (1-2881)

Qy 1 SerAlaSerAlaValIleValTyrValAenGlyGlyTrpSerThrTrpThrGluTrp 20
Db 780 AGCCCTCCGCTGCTGTCATCTCTACGTGAACGGTGGTGGTGCAGCGTGGACCGAGTGG 839
Qy 21 SerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArgSerArgSerCysThrAsn 40
Db 840 TCCGCTCTGCAGCGCCAGCTGTGGCGCGCTGGCAGAAACGAGCGGAGCTGCACCAAC 899
Qy 41 ProAlaProLeuAenGlyGlyAlaPheCysGluGlyGlnAenVal---GlnLysThrAla 59
Db 900 CCGCGCGCTCTCAACGGGGGGCGCTTCTGTGAGGGGCGAGATGTCCATGACCGCCACCGTC 959
Qy 60 CysAlaThrLeuCysProValAspGlySerTrpSerProTrpSerLysTrpSerAlaCys 79
Db 960 TCCTCTCTGCTTGTCTGTGTGGAGCGGACGTGGAGCCCGTGGAGCAAGTGTGCGCTGT 1019
Qy 80 GlyLeuAspCysThrHisTrpArgSerArgGluCysSerAspProAlaProArgAsnGly 99
Db 1020 GGGCTGGACTGCACCCACTGCGGAGCGCTGAGTGTCTGTGACCCAGCACCCCGCAACCGA 1079
Qy 100 GlyGluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117
Db 1080 GGGGAGGAGTCCAGGGGCACTGACCTGGACACCCCGCAACCTGTACAGTGACCTC 1133

RESULT 15

ADH71641

ID ADH71641 standard; DNA; 2881 BP.

XX

AC ADH71641;
XX 25-MAR-2004 (first entry)
XX Human gene of the invention NOV21q SEQ ID NO:537.
DE ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX Homo sapiens.
OS WO2003102155-A2.
XX 11-DEC-2003.
XX 03-JUN-2003; 2003WO-US017430.
XX 03-JUN-2002; 2002US-0385120P.
XX 04-JUN-2002; 2002US-0385784P.
XX 05-JUN-2002; 2002US-0386041P.
XX 05-JUN-2002; 2002US-0386047P.
XX 06-JUN-2002; 2002US-0386376P.
XX 06-JUN-2002; 2002US-0386453P.
XX 06-JUN-2002; 2002US-0386864P.
XX 06-JUN-2002; 2002US-0387016P.
XX 07-JUN-2002; 2002US-0386796P.
XX 07-JUN-2002; 2002US-0386816P.
XX 07-JUN-2002; 2002US-0386931P.
XX 07-JUN-2002; 2002US-0386942P.
XX 07-JUN-2002; 2002US-0386971P.
XX 07-JUN-2002; 2002US-0387262P.
XX 08-JUN-2002; 2002US-0296960P.
XX 10-JUN-2002; 2002US-0387400P.
XX 10-JUN-2002; 2002US-0387535P.
XX 11-JUN-2002; 2002US-0387610P.
XX 11-JUN-2002; 2002US-0387625P.
XX 11-JUN-2002; 2002US-0387634P.
XX 11-JUN-2002; 2002US-0387668P.
XX 11-JUN-2002; 2002US-0387696P.
XX 11-JUN-2002; 2002US-0387702P.
XX 11-JUN-2002; 2002US-0387836P.
XX 11-JUN-2002; 2002US-0387859P.
XX 12-JUN-2002; 2002US-0387933P.
XX 12-JUN-2002; 2002US-0387934P.
XX 12-JUN-2002; 2002US-0387950P.
XX 12-JUN-2002; 2002US-0388022P.
XX 12-JUN-2002; 2002US-0388096P.
XX 13-JUN-2002; 2002US-0389123P.
XX 14-JUN-2002; 2002US-0389118P.
XX 14-JUN-2002; 2002US-0389120P.
XX 14-JUN-2002; 2002US-0389144P.
XX 14-JUN-2002; 2002US-0389146P.
XX 17-JUN-2002; 2002US-0389729P.
XX 17-JUN-2002; 2002US-0389742P.
XX 18-JUN-2002; 2002US-0389884P.
XX 19-JUN-2002; 2002US-0390006P.
XX 19-JUN-2002; 2002US-0390209P.
XX 21-JUN-2002; 2002US-0390763P.
XX 17-JUL-2002; 2002US-0396706P.
XX 06-AUG-2002; 2002US-0401628P.
XX 09-AUG-2002; 2002US-0402156P.
XX 09-AUG-2002; 2002US-0402256P.
XX 09-AUG-2002; 2002US-0402389P.
XX 12-AUG-2002; 2002US-0402786P.
XX 12-AUG-2002; 2002US-0402816P.
XX 12-AUG-2002; 2002US-0402821P.
XX 12-AUG-2002; 2002US-0402832P.
XX 13-AUG-2002; 2002US-0403448P.
XX 13-AUG-2002; 2002US-0403459P.
XX 13-AUG-2002; 2002US-0403531P.

PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0403617P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-0423798P.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
XX
XX

PA (CURA-) CURAGEN CORP.

XX Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Eitenberg S, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI MacLachlan T, Malvankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigaru M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shinkets RA;
PI Smithson G, Spytek KA, Stone DU, Vernet CM, Voss EZ, Zhong M;
PI Zhong H;
XX

XX WPI: 2004-081935/08.
DR P-PSDB; ADH71642.
DR

XX New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX

XX Example 21; SEQ ID NO 537; 1880pp; English.

XX The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.

XX Sequence 2881 BP; 526 A; 986 C; 867 G; 502 T; 0 U; 0 Other;

XX Alignment Scores:

Pred. No.:	1.36e-34	Length:	2881
Score:	622.50	Matches:	109
Percent Similarity:	94.07%	Conservative:	2
Best Local Similarity:	92.37%	Mismatches:	6
Query Match:	91.28%	Indels:	1
DB:	12	Gaps:	1

XX US-10-624-932C-2_COPY_232_348 (1-117) x ADH71641 (1-2881)

Qy 1 SerAlaSerAlaAlaValIleValTyrValAsnGlyGlyTyrSerThrTyrThrGluTyr 20
Db |||||
780 AGCGCCTCCCGCTGCTGTCATCTGCTAGTGAACGGTGGTGGTGGACGAGTGG 839
Qy 21 SerValCysSerAlaSerCysGlyArgGlyTyrGlnLysArgSerArgSerCysThrAsn 40
Db |||||
840 TCCGCTCTGCAGCGCCAGCTGTGGCGCGGTGGCAGAAACGGAGCGGAGCTGCACCAAC 899
Qy 41 ProAlaProLeuAsnGlyGlyAlaPheCysGlyGlnAsnVal---GlnLysThrAla 59
Db |||||
900 CCGCGCGCTCTCAACCGGGCGCTTTCTGTGAGGGGCGAGATGTCCATGATGACCGCACCGTC 959
Qy 60 CysAlaThrLeuCysProValAspGlySerTyrSerProTyrSerLysTyrSerAlaCys 79
Db |||||
960 TCCTCTCTGCTTGTCTCTGTGGACGGCAGCTGGAGCCCGTGGAGCAAGTGTGGCCCTGT 1019
Qy 80 GlyLeuAspCysThrHisTyrArgSerArgGlyCysSerAspProAlaProArgAsnGly 99
Db |||||
1020 GGGCTGGACTGCACCCCACTGGCGGAGCGGTAGTGTCTCTGACCCAGCACCCCGCACCGGA 1079
Qy 100 GlyGluGlyCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117
Db |||||
1080 GGGGAGGAGTGCACGGGCACTGACCTGGACACCCCGCAACTGTACCACTGACCTC 1133

Search completed: September 9, 2005, 00:42:46

Job time : 612.088 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 8, 2005, 23:51:22 ; Search time 186.494 Seconds
(without alignments)
1026.543 Million cell updates/sec

Title: US-10-624-932C-2_COPY_232_348

Perfect score: 682

Sequence: 1 SASAAIVYVNGSWTTEW.....NGBECQGTDLTRNCTSDL 117

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/h/US10624932/runat_08092005.161706.15822/app_query.fasta_1.1386
-DB=Issued Patents NA -QWMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=Dlosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10624932 @CGN 1.1 187 @runat_08092005.161706.15822 -NCPU=6 -ICPU=3
-NO.MWAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	661	96.9	3014	2	US-08-808-982-1
2	661	96.9	3014	3	US-09-306-902A-1
3	539	79.0	3008	4	US-09-949-016-4794
4	522	76.5	2831	2	US-08-808-982-3
5	522	76.5	2831	3	US-09-306-902A-3
6	290	42.5	114139	4	US-09-949-016-16536
7	286	41.9	349	4	US-09-471-276-345
8	268	39.3	5749	4	US-09-262-537-48
9	266	39.0	5784	4	US-09-949-016-462
10	262	38.4	5722	4	US-09-657-472-1
11	261.5	38.3	2820	4	US-09-854-845-15
12	261.5	38.3	2865	4	US-09-854-845-13

13	261.5	38.3	3105	4	US-09-854-845-5	Sequence 5, Appli
14	261.5	38.3	3150	4	US-09-854-845-1	Sequence 1, Appli
15	261.5	38.3	3237	4	US-09-854-845-7	Sequence 7, Appli
16	261.5	38.3	3282	4	US-09-854-845-3	Sequence 3, Appli
17	261.5	38.3	3411	4	US-09-854-845-11	Sequence 11, Appli
18	261.5	38.3	3456	4	US-09-854-845-9	Sequence 9, Appli
19	261.5	38.3	4074	4	US-09-854-845-17	Sequence 17, Appli
20	258	37.8	7231	4	US-09-919-172-64	Sequence 64, Appli
21	243	35.6	1701	4	US-09-949-016-3827	Sequence 3827, Ap
c	240.5	35.3	457	4	US-09-270-767-1598	Sequence 31598, A
c	240.5	35.3	2006	4	US-09-270-767-15258	Sequence 15258, A
23	240.5	34.7	657	3	US-08-985-526-2	Sequence 2, Appli
24	236.5	34.7	1326	3	US-08-985-526-4	Sequence 4, Appli
25	236.5	34.1	5178	4	US-09-949-016-5241	Sequence 5241, Ap
26	232.5	34.1	5178	4	US-09-949-016-15569	Sequence 15569, A
27	211	30.9	10082	4	US-09-949-016-12204	Sequence 12204, A
28	186.5	27.3	41737	4	US-09-949-016-16983	Sequence 16983, A
29	186.5	27.3	41741	4	US-09-969-532-7	Sequence 7, Appli
30	182	26.7	1659	4	US-09-969-532-5	Sequence 5, Appli
31	182	26.7	1692	4	US-09-969-532-3	Sequence 3, Appli
32	182	26.7	1701	4	US-09-969-532-1	Sequence 1, Appli
33	182	26.7	1734	4	US-09-969-532-15	Sequence 15, Appli
34	182	26.7	2661	4	US-09-969-532-13	Sequence 13, Appli
35	182	26.7	2694	4	US-09-969-532-11	Sequence 11, Appli
36	182	26.7	2703	4	US-09-969-532-9	Sequence 9, Appli
37	182	26.7	2736	4	US-09-969-532-23	Sequence 23, Appli
38	182	26.7	3411	4	US-09-969-532-33	Sequence 33, Appli
39	177	26.0	966	4	US-09-969-532-21	Sequence 21, Appli
40	177	26.0	999	4	US-09-969-532-19	Sequence 19, Appli
41	177	26.0	1008	4	US-09-969-532-17	Sequence 17, Appli
42	177	26.0	1041	4	US-09-969-532-31	Sequence 31, Appli
43	177	26.0	1968	4	US-09-969-532-29	Sequence 29, Appli
44	177	26.0	2001	4	US-09-969-532-27	Sequence 27, Appli
45	177	26.0	2010	4	US-09-969-532-27	Sequence 27, Appli

ALIGNMENTS

RESULT 1

US-08-808-982-1
; Sequence 1, Application US/080808982
; Patent No. 5939271
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; APPLICANT: Leonardo, E. David
; APPLICANT: Hink, Lindsey
; APPLICANT: Masu, Masayuki
; APPLICANT: Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,982
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:

```
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 3014 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
US-08-808-982-1

Alignment Scores:      2.54e-47      Length:      3014
Pred. No.:            661.00      Matches:      113
Score:                97.44%      Conservative: 1
Best Local Similarity: 96.58%      Mismatches:  3
Query Match:          96.92%      Indels:      0
DB:                    2          Gaps:          0

US-10-624-932C-2_COPY_232_348 (1-117) x US-08-808-982-1 (1-3014)

Qy  1 SerAlaSerAlaValIleValTyrValAsnGlyGlyTTPSerThrTTPThrGluTTP 20
Db  694 AGCACTCTGCAGCGGTCATTTATGTGAACGGTGGTGGTGCAGCTGAGCTGAGTGG 753

Qy  21 SerValCysSerAlaSerCysGlyArgGlyTTPGlnLysArgSerArgSerCysThrAsn 40
Db  754 TCCGTCTGCAGCGGTCAGTGTGGCGTGGTGGCGAGAAACGGAGCGGAGCTGCACCAAC 813

Qy  41 ProAlaProLeuAnGlyGlyAlaPheCysGluGlyGlnAsnValGlnLysThrAlaCys 60
Db  814 CCGGCACCTCTCAACGGGGCGCCCTCTGTGAGGGCGAGATGTCCAGAAACAGCCTGC 873

Qy  61 AlaThrLeuCysProValAspGlySerTTPSerProTTPSerLysTTPSerAlaCysGly 80
Db  874 GCCACTCTGCCAGTGGATGGAGCTGGAGTTCTGTGGAGTAAGTGTGAGCTGTGGG 933

Qy  81 LeuAspCysThrHisTTPArgSerArgGluCysSerAspProAlaProArgAsnGlyGly 100
Db  934 CTTGACTGCACCCACTGCGGGTGTGACCTGGACACCCGCGAGTGTACCAATGGAGGT 993

Qy  101 GluLysCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117
Db  994 GAGGAGTGTGGGGTGTGCTGACCTGGACACCCGCGCAACTGTACCACTGACCTC 1044

RESULT 2
US-09-306-902A-1
; Sequence 1, Application US/09306902A
; Patent No. 627585
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindsey
; Masu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/306,902A
; FILING DATE: 07-May-1999
; CLASSIFICATION: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
```

```
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 3014 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-306-902A-1

Alignment Scores:      2.54e-47      Length:      3014
Pred. No.:            661.00      Matches:      113
Score:                97.44%      Conservative: 1
Best Local Similarity: 96.58%      Mismatches:  3
Query Match:          96.92%      Indels:      0
DB:                    3          Gaps:          0

US-10-624-932C-2_COPY_232_348 (1-117) x US-09-306-902A-1 (1-3014)

Qy  1 SerAlaSerAlaValIleValTyrValAsnGlyGlyTTPSerThrTTPThrGluTTP 20
Db  694 AGCACTCTGCAGCGGTCATTTATGTGAACGGTGGTGGTGCAGCTGAGCTGAGTGG 753

Qy  21 SerValCysSerAlaSerCysGlyArgGlyTTPGlnLysArgSerArgSerCysThrAsn 40
Db  754 TCCGTCTGCAGCGGTCAGTGTGGCGTGGTGGCGAGAAACGGAGCGGAGCTGCACCAAC 813

Qy  41 ProAlaProLeuAnGlyGlyAlaPheCysGluGlyGlnAsnValGlnLysThrAlaCys 60
Db  814 CCGGCACCTCTCAACGGGGCGCCCTCTGTGAGGGCGAGATGTCCAGAAACAGCCTGC 873

Qy  61 AlaThrLeuCysProValAspGlySerTTPSerProTTPSerLysTTPSerAlaCysGly 80
Db  874 GCCACTCTGCCAGTGGATGGAGCTGGAGTTCTGTGGAGTAAGTGTGAGCTGTGGG 933

Qy  81 LeuAspCysThrHisTTPArgSerArgGluCysSerAspProAlaProArgAsnGlyGly 100
Db  934 CTTGACTGCACCCACTGCGGGTGTGACCTGGACACCCGCGAGTGTCTGACCCAGCAGCCGCAATGGAGGT 993

Qy  101 GluLysCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117
Db  994 GAGGAGTGTGGGGTGTGCTGACCTGGACACCCGCGCAACTGTACCACTGACCTC 1044

RESULT 3
US-09-949-016-4794
; Sequence 4794, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4794
; LENGTH: 3008
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4794
```

Alignment Scores:
Pred. No.: 7.22e-37 Length: 3008
Score: 539.00 Matches: 86
Percent Similarity: 86.32% Conservative: 15
Best Local Similarity: 73.50% Mismatches: 16
Query Match: 79.03% Indels: 0
DB: 4 Gaps: 0

US-10-624-932C-2_COPY_232_348 (1-117) x US-09-949-016-4794 (1-3008)

Qy 1 SerAlaSerAlaAlaValIleValTrValAenGlyGlyTrpSerThrTrpThrGluTrp 20
Db 264 ACTACACTGCCACTGTCTATGTCTATGTCAACGGTGGCTGCTCCACTGGACGGAGTGG 323

Qy 21 SerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArgSerArgSerCysThrAsn 40
Db 324 TCTGTGTACAGCCGCTGTGGACGAGGTATCAGAAACGTACAAAGACTGTATCAAC 383

Qy 41 ProAlaProLeuAenGlyGlyAlaPheCysGluGlyGlnAenValGlnLysThrAlaCys 60
Db 384 CCGCACCACTCAATGGGGTGCCTTCTGTGAAGGCGCAGAGTGTGCAGAAATAGCCTGT 443

Qy 61 AlaThrLeuCysProValAspGlySerTrpSerProTrpSerLysTrpSerAlaCysGly 80
Db 444 ACTAGTTATGCCAGTGGATGGCAGGTGGAGCCCATGGAGCAAGTGTCTACTTGTGGA 503

Qy 81 LeuAspCysThrHisTrpArgSerArgGluCysSerAspProAlaProArgAsnGlyGly 100
Db 504 ACTGAGTGACCCACTGTGGCGCAGGAGGAGTGCACGGCGCCAGCCCCCAAGATGGAGGC 563

Qy 101 GluGluCysGlnGlyThrAspLeuAspThrArgAenCysThrSerAspLeu 117
Db 564 AAGGACTCGCAGCGGCTCGTCTTCAATCCAGAACTGCACCTGATGGGCTT 614

RESULT 4
US-08-808-982-3
; Sequence 3, Application US/08808982
; Patent No. 5939271
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; APPLICANT: Leonardo, E. David
; APPLICANT: Hink, Lindsey
; APPLICANT: Masu, Masayuki
; APPLICANT: Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,982
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2831 base pairs
; TYPE: nucleic acid

STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-808-982-3
Alignment Scores:
Pred. No.: 1.92e-35 Length: 2831
Score: 522.00 Matches: 84
Percent Similarity: 82.05% Conservative: 12
Best Local Similarity: 71.79% Mismatches: 21
Query Match: 76.54% Indels: 0
DB: 2 Gaps: 0

US-10-624-932C-2_COPY_232_348 (1-117) x US-08-808-982-3 (1-2831)

Qy 1 SerAlaSerAlaAlaValIleValTrValAenGlyGlyTrpSerThrTrpThrGluTrp 20
Db 700 AGCAGCGCGCCAGTCTATGTGAACGGAGTTGGTCCAGTGGCAGATGG 759

Qy 21 SerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArgSerArgSerCysThrAsn 40
Db 760 TCACCTGTCTAACCGCTGCGCGGAGTTGGCAGAAACGTACTAGGACCTGCACCAAC 819

Qy 41 ProAlaProLeuAenGlyGlyAlaPheCysGluGlyGlnAenValGlnLysThrAlaCys 60
Db 820 CCAGCCCACTCAATGGAGTGCCTTCTGCGAGGACAGAGTGTCCAGAACGCGCTTGC 879

Qy 61 AlaThrLeuCysProValAspGlySerTrpSerProTrpSerLysTrpSerAlaCysGly 80
Db 880 ACCACGTTGTGCCAGTGGATGGAGCGTGGAGTGTGAGTGAGCAAGTGTTCGCTTCGAC 939

Qy 81 LeuAspCysThrHisTrpArgSerArgGluCysSerAspProAlaProArgAsnGlyGly 100
Db 940 ACAGAGTGTGGCACTGGCGCAGCGGAGTGTGATGGAGCAAGTGTTCGCTTCGACGAGGC 999

Qy 101 GluGluCysGlnGlyThrAspLeuAspThrArgAenCysThrSerAspLeu 117
Db 1000 CGTGACTGCAGCGGAGCGCTACTTACTCCAGAACTGCACCGATGGGCTG 1050

RESULT 5
US-09-306-902A-3
; Sequence 3, Application US/09306902A
; Patent No. 6277585
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; APPLICANT: Leonardo, E. David
; APPLICANT: Hink, Lindsey
; APPLICANT: Masu, Masayuki
; APPLICANT: Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/306,902A
; FILING DATE: 07-May-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341

```
;
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 2831 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-306-902A-3

Alignment Scores:
Pred. No.: 1.92e-35 Length: 2831
Score: 522.00 Matches: 84
Percent Similarity: 82.05% Conservative: 12
Best Local Similarity: 71.79% Mismatches: 21
Query Match: 76.54% Indels: 0
DB: 3 Gaps: 0

US-10-624-932C-2_COPY_232_348 (1-117) x US-09-306-902A-3 (1-2831)
Qy 1 SerAlaSerAlaValIleValTyrValAsnGlyGlyTrpSerThrTrpThrGluTrp 20
Db 700 AGCAGCGGCGGCACAGTCATCGTCTATGTGAACGAGGTTGGTCCAGCTGGGCAGAAATGG 759

Qy 21 SerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArgSerArgSerCysThrAsn 40
Db 760 TCACCCCTGCTTAACCGCTGCGGGCGAGGTTGGCAGAAACGTACTAGGACCTGCACCAAC 819

Qy 41 ProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsnValGlnLysThrAlaCys 60
Db 820 CCAGCCCACTCATGNGGTCCTTCTGCGAGGACAGGCTTCCAGAGACGGCTTGC 879

Qy 61 AlaThrLeuCysProValAspGlySerTrpSerProTrpSerLysTrpSerAlaCysGly 80
Db 880 ACCACCGGTGCCAGGTGGATGGAGCGTGGACTCAGTGGAGCAAGTGTCCGCTGCAGC 939

Qy 81 LeuAspCysThrHisTrpArgSerArgGluCysSerAspProAlaProArgAsnGlyGly 100
Db 940 ACAGAGTGTGCGCACTGGCGGCGCGGAGTGCATGGCACC CGCCGCCCAAGACGGAGGC 999

Qy 101 GluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117
Db 1000 CGTGACTGCAGCGGACGCTACTTGGACTCCCAAGAACTGCACCGATGGGCTG 1050

RESULT 6
US-09-949-016-16536
; Sequence 16536, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16536
; LENGTH: 114139
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(114139)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16536

;
; Alignment Scores:
; Pred. No.: 1.45e-13 Length: 114139
; Score: 290.00 Matches: 47
; Percent Similarity: 93.22% Conservative: 8
; Best Local Similarity: 79.66% Mismatches: 4
; Query Match: 42.52% Indels: 0
; DB: 4 Gaps: 0

US-10-624-932C-2_COPY_232_348 (1-117) x US-09-949-016-16536 (1-114139)
Qy 7 IleValTyrValAsnGlyGlyTrpSerThrTrpThrGluTrpSerValCysSerAlaSer 26
Db 35216 CTCCTTTCAGTCAACGGTGGCTGGTCCACTGGACGGAGTGGTCTGTGTGTAAAGCGCGC 35275

Qy 27 CysGlyArgGlyTrpGlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGly 46
Db 35276 TGTGGACGAGGCTATCAGAAACGTACAGGACTTGTACCAACCGCGCACCACTCAATGGG 35335

Qy 47 GlyAlaPheCysGluGlyGlnAsnValGlnLysThrAlaCysAlaThrLeuCysPro 65
Db 35336 GGTGCGCTTCTGTGAAGGCGAGAGTGTGCAGAAATAGCTGTACTACGTTATGCCCA 35392

RESULT 7
US-09-471-276-345
; Sequence 345, Application US/09471276
; Patent No. 6822072
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6822072
; FILE REFERENCE: GENSET.025CP1
; CURRENT APPLICATION NUMBER: US/09/471,276
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 09/057,719
; EARLIER FILING DATE: 1998-04-09
; EARLIER APPLICATION NUMBER: 09/069,047
; EARLIER FILING DATE: 1998-04-28
; EARLIER APPLICATION NUMBER: PCT/IB99/00712
; EARLIER FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1622
; SOFTWARE: Patent.pm
; SEQ ID NO 345
; LENGTH: 349
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 207..347
; NAME/KEY: sig_peptide
; LOCATION: 207..278
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 5.40000009536743
; OTHER INFORMATION: seq SCCCLSSSSFIAG/RR
US-09-471-276-345

Alignment Scores:
Pred. No.: 2.36e-16 Length: 349
Score: 286.00 Matches: 51
Percent Similarity: 98.08% Conservative: 0
Best Local Similarity: 98.08% Mismatches: 1
Query Match: 41.94% Indels: 1
; DB: 4 Gaps: 0

US-10-624-932C-2_COPY_232_348 (1-117) x US-09-471-276-345 (1-349)
Qy 66 ValAspGlySerTrpSerProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHis 85
Db 12 GTGGACGCGAGCTGGAGCCCGGTGAGCAAGTGTGCGCCCTGTGGGCTGGAGCTGCCACCCAC 71

Qy 86 TrpArgSerArgGluCysSerAspProAlaProArgAsnGlyGlyGluCysGlnGly 105
```



```

Db      72 TGGCGGAC-CGTGAGTGTCTGACCCAGCAGCCGCCCAACGAGGGAGGAGTGCAGGGC 130
Qy      106 ThrAspLeuAspThrArgAsnCysThrSerAspLeu 117
Db      131 ACTGACCTGGACACCCCGCACTGTACCACTGACCTGACCTC 166

RESULT 8
US-09-262-537-48
; Sequence 48, Application US/09262537
; Patent No. 6479256
; GENERAL INFORMATION:
; APPLICANT: Haylick, Joel
; TITLE OF INVENTION: Lectomedin Materials and Methods
; FILE REFERENCE: 27866/35307
; CURRENT APPLICATION NUMBER: US/09/262,537
; PRIOR FILING DATE: 1999-03-04
; EARLIER APPLICATION NUMBER: 60/076,782
; EARLIER FILING DATE: 1998-03-04
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 48
; LENGTH: 5749
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-262-537-48

Alignment Scores:
Pred. No.:      2,7e-13      Length:      5749
Score:          268.00      Matches:      50
Percent Similarity: 58.33%      Conservative: 13
Best Local Similarity: 46.30%      Mismatches: 37
Query Match:    39.30%      Indels:      8
DB:             4          Gaps:      4

US-10-624-932c-2_COPY_232_348 (1-117) x US-09-262-537-48 (1-5749)
Qy      10 ValAsnGlyGlyTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArg 29
Db      1759 GTACAGCGAGTATGGGAGGAATGGTCACCATGGAGTTTATGTTTATTACATGTTGTCGA 1818
Qy      30 GlyTrpGlnLysArgSerArgSerCysThrSerAsnProAlaProLeuAsnGlyGlyAlaPhe 49
Db      1819 GGCACAAAGCAACAAAGAACAGTATGTCACA-----CCTCCTCAGTATGGAGGAGGCCG 1872
Qy      50 CysGluGlyGlnAsnValGlnLysThrAlaCys---AlaThrLeuCysProValAspGly 68
Db      1873 TGTGAGGACCTGAAACACATCATAGCCTTGTATATATTGCTCTTTGCCAGTTGATGGA 1932
Qy      69 SerTrpSerProTrpSerLysThrSerAlaCysGlyLeuAspCys-----ThrHis 85
Db      1933 CAGTGGCAAGAGTGGAGTTGCTGGAGCCAGTGTCTCAGTAACGTGCTCGAATGGGACTCAG 1992
Qy      86 TrpArgSerArgGluCysSerAspProAlaProArgAsnGlyGlyGluCysGlnGly 105
Db      1993 CAGAGAACCCGCGCAGTGCAC-----GCAGTCCCATGGAGGCTCCGAATGCAGAGGG 2046
Qy      106 ThrAspLeuAspThrArgAsnCys 113
Db      2047 CCATGGGCAGAAAGCAGAGAGTGC 2070

RESULT 9
US-09-949-016-462
; Sequence 462, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
```

```

; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 462
; LENGTH: 5784
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-462

Alignment Scores:
Pred. No.:      4.04e-13      Length:      5784
Score:          266.00      Matches:      47
Percent Similarity: 57.01%      Conservative: 14
Best Local Similarity: 43.93%      Mismatches: 42
Query Match:    39.00%      Indels:      4
DB:             4          Gaps:      2

US-10-624-932c-2_COPY_232_348 (1-117) x US-09-949-016-462 (1-5784)
Qy      11 AsnGlyGlyTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGly 30
Db      1548 GACGCGCGCTGGAGCCACTGGTGCACCTTGGTCTTTCATGCTCTGTGACCTGTGGAGTTGC 1607
Qy      31 TrpGlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCys 50
Db      1608 AATATCACACGATCCGCTCTGCACTGCCAGTGCCCGAGATGGGGGCAAGAAATTC 1667
Qy      51 GluGlyGlnAsnValGlnLysThrAlaCys---AlaThrLeuCysProValAspGlySer 69
Db      1668 AAGGGAGTGGCGGGAGACCAAGCCTGCAGGGCGCCCATGATCGATCGATGCCCGC 1727
Qy      70 TrpSerProTrpSerLysThrSerAlaCysGlyLeuAspCysThr-----HisTrp 86
Db      1728 TGGAGCCCTGTGCTCCCGTGGTGGCTGCACTGTGACCTGTGCGGTTGGGATCCGGGAG 1787
Qy      87 ArgSerArgGluCysSerAspProAlaProArgAsnGlyGlyGluGluCysGlnGlyThr 106
Db      1788 GCGACCCGGGTCTGCACAGCCCTGAGCCTCAGTACGAGGAGGAGGCTCGCTGGGGGAT 1847
Qy      107 AspLeuAspThrArgAsnCys 113
Db      1848 GTGCAGGAGCGTCAGATGTC 1868

RESULT 10
US-09-657-472-1
; Sequence 1, Application US/09657472
; Patent No. 6727063
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Bolk, Stacey
; APPLICANT: Daley, George Q.
; APPLICANT: McCarthy, Jeanette J.
; TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
; FILE REFERENCE: 2825.1027-001
; CURRENT APPLICATION NUMBER: US/09/657,472
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/153,357
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 60/220,947
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: US 60/225,724
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2551
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 5722
; TYPE: DNA
```

```
; ORGANISM: Homo sapiens
US-09-657-472-1

Alignment Scores:
Pred. No.:      8.77e-13      Length:      5722
Score:          262.00      Matches:      45
Percent Similarity: 57.94%      Conservative: 17
Best Local Similarity: 42.06%      Mismatches:  41
Query Match:     38.42%      Indels:      4
DB:              4          Gaps:      2

US-10-624-932C-2_COPY_232_348 (1-117) x US-09-657-472-1 (1-5722)

Qy  11 AsnGlyGlyTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGly 30
    :::::::::::::::::::::
Db  1414 GATGGTGGCTGGAGCCACTGTGTCGCCGGTGGTCATCTTGTTCGTGACATGGGTGGT 1473
    :::::::::::::::::::::

Qy  31 TrpGlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCys 50
    :::::::::::::::::::::
Db  1474 GTGATCAACAGGATCCGGCTCTGCACTCTCCAGCCCCCAGATGAATGGGAACCTGT 1533
    :::::::::::::::::::::

Qy  51 GluGlyGlnAsnValGlnLysThrAlaCys---AlaThrLeuCysProValAspGlySer 69
    :::::::::::::::::::::
Db  1534 GAAGCGAAGCGCGGAGACCAAGACCTGCAAGAAAGACGCTGCCCCCATCAATGGAGGC 1593
    :::::::::::::::::::::

Qy  70 TrpSerProTrpSerLysTrpSerAlaCysGlyLeuAspCys-----ThrHisTrp 86
    :::::::::::::::::::::
Db  1594 TGGGGTCTTGGTCACCATGGAGCATCTGTCTGTCACTGTGGAGGAGGGGTACAGAAA 1653
    :::::::::::::::::::::

Qy  87 ArgSerArgGluCysSerAspProAlaProArgAsnGlyGlyGluGluCysGlnGlyThr 106
    :::::::::::::::::::::
Db  1654 CGTAGTCGTCTGCAACAACCCCGCACCCAGTTTGGAGGCAAGGACTGGTTGGTGCAT 1713
    :::::::::::::::::::::

Qy  107 AspLeuAspThrArgAsnCys 113
    :::::::::::::::::::::
Db  1714 GTAACAGAAACACAGATCTGC 1734

RESULT 11
US-09-854-845-15
; Sequence 15, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encod
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 2820
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-854-845-15

Alignment Scores:
Pred. No.:      4.01e-13      Length:      2820
Score:          261.50      Matches:      50
Percent Similarity: 56.19%      Conservative:  9
Best Local Similarity: 47.62%      Mismatches:  41
Query Match:     38.34%      Indels:      5
DB:              4          Gaps:      3

US-10-624-932C-2_COPY_232_348 (1-117) x US-09-854-845-15 (1-2820)

Qy  10 ValAsnGlyGlyTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArg 29
    :::::::::::::::::::::
Db  2134 GTTCGGGTGCTTGGTCTCTGCTGACCTCATGCTCTCCATGCTCAGCTTCTCTGTGGTGG 2193
    :::::::::::::::::::::

Qy  30 GlyTrpGlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPhe 49
    :::::::::::::::::::::
Db  2194 GGTCACTATCAACGACACCCGTTCTGTGACACGACCCCGACCTCCCGNGGTGAGACATC 2253
    :::::::::::::::::::::

Qy  50 CysGluGlyGlnAsnValGlnLysThrAlaCysAlaThr---LeuCysProValAspGly 68
    :::::::::::::::::::::
Db  2254 TGTCTCGGGCTGCACACGAGGAGGCATATGTGCCACACAGGCTGCCCA-----GAA 2307
    :::::::::::::::::::::

Qy  69 SerTrpSerProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSer 88
    :::::::::::::::::::::
Db  2308 GGCTGGTGGCTGGTCTGCTGAGTGGAGTAACTGACGACGAGCCGAGCGGAGC 2367
    :::::::::::::::::::::

Qy  89 ArgGluCysSerAspProAlaProArgAsnGlyGlyGluGluCysGlnGlyThrAspLeu 108
    :::::::::::::::::::::
Db  2368 CGGCACCTGTGAGGAGCTCTCCCA-----GGGTCCAGCGCTGTGTGGAACAGCAGC 2421
    :::::::::::::::::::::

Qy  109 AspThrArgAsnCys 113
    :::::::::::::::::::::
Db  2422 CAGAGCGCGCCCTGC 2436

RESULT 12
US-09-854-845-13
; Sequence 13, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encod
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 2865
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-854-845-13

Alignment Scores:
Pred. No.:      4.09e-13      Length:      2865
Score:          261.50      Matches:      50
Percent Similarity: 56.19%      Conservative:  9
Best Local Similarity: 47.62%      Mismatches:  41
Query Match:     38.34%      Indels:      5
DB:              4          Gaps:      3

US-10-624-932C-2_COPY_232_348 (1-117) x US-09-854-845-13 (1-2865)

Qy  10 ValAsnGlyGlyTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArg 29
    :::::::::::::::::::::
Db  2134 GTTCGGGTGCTTGGTCTCTGCTGACCTCATGCTCTCCATGCTCAGCTTCTCTGTGGTGG 2193
    :::::::::::::::::::::

Qy  30 GlyTrpGlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPhe 49
    :::::::::::::::::::::
Db  2194 GGTCACTATCAACGACACCCGTTCTGTGACACGACCCCGACCTCCCGNGGTGAGACATC 2253
    :::::::::::::::::::::

Qy  50 CysGluGlyGlnAsnValGlnLysThrAlaCysAlaThr---LeuCysProValAspGly 68
    :::::::::::::::::::::
Db  2254 TGTCTCGGGCTGCACACGAGGAGGCATATGTGCCACACAGGCTGCCCA-----GAA 2307
    :::::::::::::::::::::

Qy  69 SerTrpSerProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSer 88
    :::::::::::::::::::::
Db  2308 GGCTGGTGGCTGGTCTGCTGAGTGGAGTAACTGACGACGAGCCGAGCGGAGC 2367
    :::::::::::::::::::::
```

```

; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: NO. 6750054e1 Human Semaphorin Homologs and Polynucleotides Encod
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3150
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-854-845-1

Alignment Scores:
Pred. No.: 4,6e-13 Length: 3150
Score: 261.50 Matches: 50
Percent Similarity: 56.19% Conservative: 9
Best Local Similarity: 47.62% Mismatches: 41
Query Match: 38.34% Indels: 5
DB: 4 Gaps: 3

US-10-624-932C-2_COPY_232_348 (1-117) x US-09-854-845-1 (1-3150)

Qy 10 valaenglyGlytrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArg 29
Db 2419 GTTCGGGGTGTCTGGTCTCTGCTGGACCTCATGGTCTCCATGCTCAGCTTCCTGTGGTGG 2478
Qy 30 GlyTrpGlnLysArgSerArgSerCysThrAsnProAlaProLeuAenGlyGlyAlaPhe 49
Db 2479 GGTCACTATCAACGACGACCGGTCTCTGCACCACGCCCGCCGCCCTCCAGGAGGACATC 2538
Qy 50 CysGluGlyGlnAenValGlnLysThrAlaCysAlaThr---LeuCysProValAspGly 68
Db 2539 TGTCTGGGCTGCACACGAGGAGGAGGACACTATGTGCCACACAGGCGCTGCCCA-----GAA 2592
Qy 69 SerTrpSerProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSer 88
Db 2593 GGCTGTGTCGCCCTGGTCTCTGAGTGGAGTAGTGCACCTGACGACGAGGCCAGCGCGAAGC 2652
Qy 89 ArgGluCysSerAspProAlaProAlaProArgaenGlyGlyGluGluCysGlnGlyThrAspLeu 108
Db 2653 CGGCACTGTGAGAGAGCTCCTCCCA-----GGGTCCAGGCGCTGTGCTGGAACACAGCAGC 2706
Qy 109 AspThrArgAenCys 113
Db 2707 CAGAGCGCGCCCTGC 2721

RESULT 15
US-09-854-845-7
; Sequence 7, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: NO. 6750054e1 Human Semaphorin Homologs and Polynucleotides Encod
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0

```

; SEQ ID NO 7
; LENGTH: 3237
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-854-845-7

Alignment Scores:
Pred. NO.: 4 76e-13 Length: 3237
Score: 261.50 Matches: 50
Percent Similarity: 56.19% Conservative: 9
Best Local Similarity: 47.62% Mismatches: 41
Query Match: 38.34% Indels: 5
DB: 4 Gaps: 3

US-10-624-932C-2_COPY_232_348 (1-117) x US-09-854-845-7 (1-3237)

```
Qy 10 ValAsnGlyGlyTrpSerThrTrpGluTrpSerValCysSerAlaSerCysGlyArg 29
Db 2551 GTTCGGGTGCTTGGTCTCTGGACCTCATGGTCTCCATGCTCAGCTTCCTGTGGTGG 2610

Qy 30 GlyTrpGlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPhe 49
Db 2611 GGTCACTATCAACGACCCGTTCTTGCCACCCCGCCCTCCCGAGGTGAGGACATC 2670

Qy 50 CysGluGlyGlnAsnValGlnLysThrAlaCysAlaThr---LeuCysProValAspGly 68
Db 2671 TGTCTCGGGCTGCACACGGAGGAGGACTATGTGCCACACAGGCTGCCCA-----GAA 2724

Qy 69 SerTrpSerProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSer 88
Db 2725 GGCTGGTCCGCCCTGGTCTGAGTGGAGTAAGTGCACTGACGACGGAGCCAGAGCCGAAGC 2784

Qy 89 ArgGluCysSerAspProAlaProArgAsnGlyGlyGluGluCysGlnGlyThrAspLeu 108
Db 2785 CGGCACTGTGAGGAGCTCTCCCA-----GGGTCCAGCCCTGTGTGGAAACAGCAGC 2838

Qy 109 AspThrArgAsnCys 113
Db 2839 CAGAGCCGCCCTGC 2853
```

Search completed: September 9, 2005, 09:51:14
Job time : 208.494 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 9, 2005, 04:41:16 ; Search time 1167.56 Seconds
(without alignments)
658.098 Million cell updates/sec

Title: US-10-624-932C-2_COPY_232_348

Perfect score: 682

Sequence: 1 SASAAVIVYVNGWSTWET.....NGEBCQGTDLDRNCTSDL 117

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 731250 seqs, 3283620254 residues

Total number of hits satisfying chosen parameters: 14702500

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n model -DEV=xlh
-Q=/cgn2_1/USPTO_spool_h/US10624932/runat_08092005_161709_15882/app_query.fasta_1.1386
-DB=Published Applications NA -QWITS=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFWT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10624932 @CGN 1 1 989 @runat_08092005_161709_15882
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOC=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
-YGAPEXT=6 -YGAPEXT=7 -YGAPEXT=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*
- 20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
- 21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
- 22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
- 24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	682	100.0	2752	10	US-09-918-779-1	Sequence 1, Appli
2	682	100.0	2752	18	US-10-624-932-1	Sequence 1, Appli
3	661	96.9	2697	16	US-10-240-154-15	Sequence 15, Appl
4	661	96.9	3014	10	US-09-933-461-1	Sequence 1, Appli
5	661	96.9	3014	14	US-10-256-702-1	Sequence 1, Appli
6	622.5	91.3	2881	10	US-09-970-944-1	Sequence 1, Appli
7	523	76.7	2860	17	US-10-087-684-1	Sequence 1, Appli
8	523	76.7	2860	17	US-10-087-684-3	Sequence 3, Appli
9	523	76.7	2860	17	US-10-218-779-1	Sequence 1, Appli
10	523	76.7	2860	17	US-10-218-779-3	Sequence 3, Appli
11	523	76.7	2895	18	US-10-037-417-37	Sequence 37, Appl
12	523	76.7	2995	11	US-09-972-211-55	Sequence 55, Appl
13	523	76.7	2995	18	US-10-096-625-55	Sequence 55, Appl
14	523	76.7	3485	9	US-09-816-828-18	Sequence 18, Appl
15	523	76.7	3501	17	US-10-295-027-1123	Sequence 1123, Ap
16	523	76.7	3884	14	US-10-028-072-145	Sequence 145, App
17	523	76.7	3884	14	US-10-140-808-145	Sequence 145, App
18	523	76.7	3884	14	US-10-121-049-145	Sequence 145, App
19	523	76.7	3884	14	US-10-123-904-145	Sequence 145, App
20	523	76.7	3884	14	US-10-140-470-145	Sequence 145, App
21	523	76.7	3884	14	US-10-175-746-145	Sequence 145, App
22	523	76.7	3884	14	US-10-176-518-145	Sequence 145, App
23	523	76.7	3884	14	US-10-137-865-145	Sequence 145, App
24	523	76.7	3884	14	US-10-140-474-145	Sequence 145, App
25	523	76.7	3884	14	US-10-142-431-145	Sequence 145, App
26	523	76.7	3884	14	US-10-143-114-145	Sequence 145, App
27	523	76.7	3884	14	US-10-142-419-145	Sequence 145, App
28	523	76.7	3884	14	US-10-123-262-145	Sequence 145, App
29	523	76.7	3884	14	US-10-142-423-145	Sequence 145, App
30	523	76.7	3884	14	US-10-121-050-145	Sequence 145, App
31	523	76.7	3884	14	US-10-141-755-145	Sequence 145, App
32	523	76.7	3884	14	US-10-143-032-145	Sequence 145, App
33	523	76.7	3884	14	US-10-123-108-145	Sequence 145, App
34	523	76.7	3884	14	US-10-123-236-145	Sequence 145, App
35	523	76.7	3884	14	US-10-123-261-145	Sequence 145, App
36	523	76.7	3884	14	US-10-140-921-145	Sequence 145, App
37	523	76.7	3884	14	US-10-140-928-145	Sequence 145, App
38	523	76.7	3884	14	US-10-121-045-145	Sequence 145, App
39	523	76.7	3884	14	US-10-123-292-145	Sequence 145, App
40	523	76.7	3884	14	US-10-123-903-145	Sequence 145, App
41	523	76.7	3884	14	US-10-124-819-145	Sequence 145, App
42	523	76.7	3884	14	US-10-124-822-145	Sequence 145, App
43	523	76.7	3884	14	US-10-140-925-145	Sequence 145, App
44	523	76.7	3884	14	US-10-160-498-145	Sequence 145, App
45	523	76.7	3884	14	US-10-160-498-145	Sequence 145, App

ALIGNMENTS

RESULT 1
US-09-918-779-1
; Sequence 1, Application US/09918779
; Publication No. US20030064369A1
; GENERAL INFORMATION:
; APPLICANT: Taupier, Raymond
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Rastelli, Luca
; APPLICANT: Spaderna, Steven
; APPLICANT: Shinkets, Richard
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Spytek, Kimberly
; APPLICANT: Shenoy, Sureeh
; APPLICANT: Li, Li
; APPLICANT: Gusev, Vladimir
; APPLICANT: Grosse, William

; APPLICANT: Alsobrook, John
; APPLICANT: Lepley, Denise
; APPLICANT: Burgess, Catherine
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Smithson, Glennda
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-074 US
; CURRENT APPLICATION NUMBER: US/09/918,779
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/221,409
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/222,840
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,752
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,762
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,770
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,769
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/225,146
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/225,392
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/225,470
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/225,697
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: 60/263,662
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/281,645
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2752
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-779-1

Alignment Scores:
Pred. No.: 5,62e-60 Length: 2752
Score: 682.00 Matches: 117
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-624-932c-2_COPY_232_348 (1-117) x US-09-918-779-1 (1-2752)

Qy 1 SerAlaSerAlaValIleValTyrValAsnGlyGlyTrpSerThrTrpThrGluTrp 20
Db 739 AGCGCTCCGTGCTGTCTATGCTACGTGAACGGTGGGTGCTGACGTGACCGAGTGG 798

Qy 21 SerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArgSerArgSerCysThrAsn 40
Db 799 TCCGTCTCAGCGCCAGCTGTGGGCGCGCTGGCAGAAACGGAGCGGAGCTGCACCAAC 858

Qy 41 ProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsnValGlnLysThrAlaCys 60
Db 859 CCGCGCGCTCTCAACGGGGGGCGCTTCTGTGAGGGGCGAGAATGTCAGAAACAGCCCTGC 918

Qy 61 AlaThrLeuCysProValAspGlySerTrpSerProTrpSerLysTrpSerAlaCysGly 80
Db 919 GCCACCTGTGCCAGTAGACGGCAGCTGGAGCCGCTGAGCAAGTGTCCGCTGTGGG 978

Qy 81 LeuAspCysThrHisTrpArgSerArgGluCysSerAspProAlaProArgAsnGlyGly 100
Db 979 CTGGACTGCACCCACTGCGCGAGCGGTGAGTGTCTGACCCAGCACCCCGCAACGGAGGG 1038

Qy 101 GluCluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117
Db 1039 GAGGAGTGCCAGGGCACTGACCTGGACACCGCAACTGTACCACTGACCTC 1089

RESULT 2
US-10-624-932-1
; Sequence 1, Application US/10624932
; Publication No. US20040096877A1
; GENERAL INFORMATION:
; APPLICANT: Taupier, Raymond
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Rastelli, Luca
; APPLICANT: Spaderna, Steven
; APPLICANT: Shimkets, Richard
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Spytek, Kimberly
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Gusev, Vladimir
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook, John
; APPLICANT: Lepley, Denise
; APPLICANT: Burgess, Catherine
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Smithson, Glennda
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-074 US
; CURRENT APPLICATION NUMBER: US/10/624,932
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: 09/918,779
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/221,409
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/222,840
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,752
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,762
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,770
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,769
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/225,146
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/225,392
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/225,470
; PRIOR FILING DATE: 2000-08-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2752
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-624-932-1

Alignment Scores:
Pred. No.: 5,62e-60 Length: 2752
Score: 682.00 Matches: 117
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-10-624-932c-2_COPY_232_348 (1-117) x US-10-624-932-1 (1-2752)

Qy 1 SerAlaSerAlaValIleValTyrValAsnGlyGlyTrpSerThrTrpThrGluTrp 20

```

Db      934  CTTGACTGCACCCACTGGCGAGCGCGAGTGTCTTGACCCACACCCCGCAATGGAGT 993
QY      101  GluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117
Db      994  GAGGAGTGTGGGGTGTGCTGACCTGGACACCCCGCACTGTACCAGTACCTC 1044

RESULT 4
US-09-933-261-1
; Sequence 1, Application US/09933261
; Publication No. US20030040046A1
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindsay
; Masu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/933,261
; FILING DATE: 20-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/808,982
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3014 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-933-261-1

Alignment Scores:
Pred. No.:      8.77e-58      Length:      3014
Score:          661.00      Matches:     113
Percent Similarity: 97.44%      Conservative: 1
Best Local Similarity: 96.58%      Mismatches:  3
Query Match:      96.92%      Indels:      0
DB:              10      Gaps:        0

US-10-624-932C-2_COPY_232_348 (1-117) x US-09-933-261-1 (1-3014)

QY      1  SerAlaSerAlaAlaValIleValTyrValAsnGlyTyrSerThrTrpThrGluTrp 20
Db      694  AGCACCCTCTGCAGCGCGTCAVTTGTTTATGTGAACGGTGGTGGTGCAGCGTGAAGTGG 753
QY      21  SerValCysSerAlaSerCysGlyArgGlyTrpGlnIleArgSerArgSerCysThrAsn 40
Db      754  TCCGCTCTGCAGCGCAGCTGTGGCGGTGGTGGCGAAGACGGAGCCGGAGCTGCACCAAC 813

```

```
Qy 41 ProAlaProLeuAasnGlyGlyAlaPheCysGluGlyGlnAasnValGlnLysThrAlaCys 60
Db 814 CCGGACCTCTCAACGGGGGGCCCTTCTGTAGGGGGCAGAAATGTCAGAAAACAGCCTGC 873
Qy 61 AlaThrLeuCysProValAspGlySerTrpSerProTrpSerLysTrpSerAlaCysGly 80
Db 874 GCCACTCTGTGCCAGTGGATGGAGCTGGAGTTCGTGGAGTAAGTGGTCAGCCTGTGGG 933
Qy 81 LeuAspCysThrHisTrpArgSerArgGluCysSerAspProAlaProArgAasnGlyGly 100
Db 934 CTTGACTGCACCCACTGGCGAGCGCGAGTGTCTGACCCAGCACCCCGCAATGGAGGT 993
Qy 101 GluGluCysGlnGlyThrAspLeuAspThrArgAasnCysThrSerAspLeu 117
Db 994 GAGGAGTGTGGGGTGTGACCTGGACACCCGCAACTGTACCACTGACCTC 1044

RESULT 5
US-10-256-702-1
; Sequence 1, Application US/10256702
; Publication No. US20030059859A1
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindsey
; Maeu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/256,702
; FILING DATE: 27-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/933,261
; FILING DATE: 20-Aug-2001
; APPLICATION NUMBER: 08/808,982
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3014 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-256-702-1
Alignment Scores:
Pred. No.: 8.77e-58 Length: 3014
Score: 661.00 Matches: 113
Percent Similarity: 97.44% Conservative: 1
Best Local Similarity: 96.58% Mismatches: 3
Query Match: 96.92% Indels: 0
DB: 14 Gaps: 0
```

```
US-10-624-932c-2_COPY_232_348 (1-117) x US-10-256-702-1 (1-3014)
Qy 1 SerAlaSerAlaAlaValIleValTyrValAasnGlyGlyTrpSerThrTrpThrGluTrp 20
Db 694 AGCACCTCTCGACGGGTCAATTGTTATGTGAACGGTGGTGGTGCACGTCGACTGAGTGG 753
Qy 21 SerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArgSerArgSerCysThrAsn 40
Db 754 TCCGTCTGACGCCACAGCTGTGGCGGTGGTGGCAGAAAACGGAGCCGAGCTGCACCAAC 813
Qy 41 ProAlaProLeuAasnGlyGlyAlaPheCysGluGlyGlnAasnValGlnLysThrAlaCys 60
Db 814 CCGGACCTCTCAACGGGGGGCGCTTCTGTGAGGGGCAGAAATGTCAGAAAACAGCCTGC 873
Qy 61 AlaThrLeuCysProValAspGlySerTrpSerProTrpSerLysTrpSerAlaCysGly 80
Db 874 GCCACTCTGTGCCAGTGGATGGAGCTGGAGTTCGTGGAGTAAGTGGTCAGCCTGTGGG 933
Qy 81 LeuAspCysThrHisTrpArgSerArgGluCysSerAspProAlaProArgAasnGlyGly 100
Db 934 CTTGACTGCACCCACTGGCGAGCGCGAGTGTCTGACCCAGCACCCCGCAATGGAGGT 993
Qy 101 GluGluCysGlnGlyThrAspLeuAspThrArgAasnCysThrSerAspLeu 117
Db 994 GAGGAGTGTGGGGTGTGACCTGGACACCCGCAACTGTACCACTGACCTC 1044

RESULT 6
US-09-970-944-1
; Sequence 1, Application US/09970944
; Publication No. US20030204052A1
; GENERAL INFORMATION:
; APPLICANT: Herrman, John L
; APPLICANT: Rastelli, Luca
; APPLICANT: Shimkets, Richard A
; TITLE OF INVENTION: No. US20030204052A1e1 Antibodies Directed Against these Proteins
; FILE REFERENCE: 21402-138
; CURRENT APPLICATION NUMBER: US/09/970,944
; CURRENT FILING DATE: 2002-05-02
; PRIOR FILING DATE: 60/237,862
; APPLICATION NUMBER: 2000-10-04
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2881
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-970-944-1
Alignment Scores:
Pred. No.: 7.38e-54 Length: 2881
Score: 622.50 Matches: 109
Percent Similarity: 94.07% Conservative: 2
Best Local Similarity: 92.37% Mismatches: 6
Query Match: 91.28% Indels: 1
DB: 10 Gaps: 1

US-10-624-932c-2_COPY_232_348 (1-117) x US-09-970-944-1 (1-2881)
Qy 1 SerAlaSerAlaAlaValIleValTyrValAasnGlyGlyTrpSerThrTrpThrGluTrp 20
Db 780 AGCGCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGTGGTGGTGCAGCTGACCGAGTGG 839
Qy 21 SerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArgSerArgSerCysThrAsn 40
Db 840 TCCGTCTGACGCCACAGCTGTGGCGCGGTGGCAGAAAACGGAGCCGAGCTGCACCAAC 899
Qy 41 ProAlaProLeuAasnGlyGlyAlaPheCysGluGlyGlnAasnVal---GlnLysThrAla 59
Db 900 CCGGCGCTCTCAACGGGGGGCGCTTCTGTGAGGGGCAGAAATGTCATGACCGCAGCGTC 959
Qy 60 CysAlaThrLeuCysProValAspGlySerTrpSerProTrpSerLysTrpSerAlaCys 79
```


Db 960 TCCTCTGCTGTGTTCTGTGGAGCGCAGCTGGAGCCGCTGGAGCAAGTGGTCGGCCTGT 1019
Qy 80 GlyLeuAspCysThrHisTrpArgSerArgGluCysSerAspProAlaProArgAsnGly 99
Db 1020 GGGCTGGACTGACCCACTGGCGAGCCGCTGAGTGCTCTGACCCAGCACCCCGCAACGGA 1079
Qy 100 GlyGluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117
Db 1080 GGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACTGTACCAAGTGACCTC 1133

RESULT 7

US-10-087-684-1
; Sequence 1, Application US/10087684
; Publication No. US20040029116A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: MacDougall, John R.
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David J.
; APPLICANT: Grosse, William M.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie, J.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Rastelli, Luca
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Zernusen, Bryan D.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Miller, Charles E.
; APPLICANT: Gangolli, Esha A.
; TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-214 CIP
; CURRENT FILING DATE: 2003-03-10
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/253,834
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,926
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/264,180
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/274,194
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/313,656
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/327,456
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 1
; LENGTH: 2860
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (59)..(2857)
US-10-087-684-1

Alignment Scores:
Pred. No.: 1.15e-43 Length: 2860
Score: 523.00 Matches: 84
Percent Similarity: 82.05% Conservative: 12
Best Local Similarity: 71.79% Mismatches: 21
Query Match: 76.69% Indels: 0

DB: 17 Gaps: 0
US-10-624-932C-2_COPY_232_348 (1-117) x US-10-087-684-1 (1-2860)
Qy 1 SerAlaSerAlaAlaValIleValTyrValAsnGlyGlyTrpSerThrTrpThrGluTrp 20
Db 764 AGCACCACTGCCACCGTCATCGTCTACGTGAATGGCGCTGGTCCAGCTGGCGACAGTGG 823
Qy 21 SerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArgSerArgSerCysThrAsn 40
Db 824 TCACCTGCTCCAACCGCTGTGGCCGAGGCTGGCAGAAGCGCACCCGACCTGCACCAAC 883
Qy 41 ProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsnValGlnLysThrAlaCys 60
Db 884 CCCGCTCACTCAACGGAGGGCGCTTCTGCGAGGGCCAGGCATTTCCAGAAACCGCGCTGC 943
Qy 61 AlaThrLeuCysProValAspGlySerTrpSerProTrpSerLysTrpSerAlaCysGly 80
Db 944 ACCACCATCTGCCCGAGTCGATGGGGCGTGGACGAGTGGAGCAAGTGTCAAGCTGCAGC 1003
Qy 81 LeuAspCysThrHisTrpArgSerArgGluCysSerAspProAlaProArgAsnGlyGly 100
Db 1004 ACTGAGTGTGCCCACTGGCGTAGCGCGAGTGCATGGCGCCCCCACCACCCAGACGGAGGC 1063
Qy 101 GluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117
Db 1064 CGTGAAGTGCAGCGGGACGCTGCTCGACTCTAAGAACTGCACAGATGGGCTG 1114

RESULT 8

US-10-087-684-3
; Sequence 3, Application US/10087684
; Publication No. US20040029116A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: MacDougall, John R.
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David J.
; APPLICANT: Grosse, William M.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie, J.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Rastelli, Luca
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Zernusen, Bryan D.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Miller, Charles E.
; APPLICANT: Gangolli, Esha A.
; TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-214 CIP
; CURRENT FILING DATE: 2003-03-10
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/253,834
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,926
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/264,180
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/274,194
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/313,656
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/327,456
; PRIOR FILING DATE: 2001-10-05

```
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 3
; LENGTH: 2860
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (59)..(2857)
US-10-087-684-3

Alignment Scores:
Pred. No.: 1,15e-43 Length: 2860
Score: 523.00 Matches: 84
Percent Similarity: 82.05% Conservatives: 12
Best Local Similarity: 71.79% Mismatches: 21
Query Match: 76.69% Indels: 0
DB: 17 Gaps: 0

US-10-624-932c-2_COPY_232_348 (1-117) x US-10-087-684-3 (1-2860)
Qy 1 SerAlaSerAlaAlaValIleValTyrValAsnGlyGlyTrpSerThrTrpThrGluTrp 20
Db 764 AGCACCACTGCCACCGTCATCGTCTACGTGAATGGCGGCTGGTCCAGCTGGGCAGAGTGG 823
Qy 21 SerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArgSerArgSerCysThrAsn 40
Db 824 TCACCCCTGCTCCAAACCGCTGTGGCCGAGGCTGGCAGAGCGCACCCCGACCTGCACCAAC 883
Qy 41 ProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsnValGlnLysThrAlaCys 60
Db 884 CCCGCTCCACTCAACGAGGGGCGCTTCTGCAGGGCCAGGCATTCCAGAGACCGCCTGC 943
Qy 61 AlaThrLeuCysProValAspGlySerTrpSerProTrpSerLysTrpSerAlaCysGly 80
Db 944 ACCACCATCTGCCAGTCGATGGGCGTGGACGAGTGGAGCAAGTGGTCAGCCTGCAGC 1003
Qy 81 LeuAspCysThrHisTrpArgSerArgGluCysSerAspProAlaProArgAsnGlyGly 100
Db 1004 ACTGAGTGTGCCCACTGGCGTAGCCGAGTGCATGGCGCCCGCCCGCCCGCCCGAGGCG 1063
Qy 101 GluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117
Db 1064 CGTGACTGCAGCGGACGCTCTCGACTCTAAGAACTGCACAGATGGGCTG 1114

RESULT 9
US-10-218-779-1
; Sequence 1, Application US/10218779
; Publication No. US20040029222A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit
; APPLICANT: MacDougall, John
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David
; APPLICANT: Gerlach, Valerie
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook II, John
; APPLICANT: Lepley, Denise
; APPLICANT: Rieger, Daniel
; APPLICANT: Burgess, Catherine
; APPLICANT: Caaman, Stacie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Patturajan, Meera
; APPLICANT: Shenoy, Suresh
; APPLICANT: Rastelli, Luca
; APPLICANT: Tchernev, Velizar
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan

; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 3
; LENGTH: 2860
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (59)..(2857)
US-10-087-684-3

Alignment Scores:
Pred. No.: 1,15e-43 Length: 2860
Score: 523.00 Matches: 84
Percent Similarity: 82.05% Conservatives: 12
Best Local Similarity: 71.79% Mismatches: 21
Query Match: 76.69% Indels: 0
DB: 17 Gaps: 0

US-10-624-932c-2_COPY_232_348 (1-117) x US-10-087-684-3 (1-2860)
Qy 1 SerAlaSerAlaAlaValIleValTyrValAsnGlyGlyTrpSerThrTrpThrGluTrp 20
Db 764 AGCACCACTGCCACCGTCATCGTCTACGTGAATGGCGGCTGGTCCAGCTGGGCAGAGTGG 823
Qy 21 SerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArgSerArgSerCysThrAsn 40
Db 824 TCACCCCTGCTCCAAACCGCTGTGGCCGAGGCTGGCAGAGCGCACCCCGACCTGCACCAAC 883
Qy 41 ProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsnValGlnLysThrAlaCys 60
Db 884 CCCGCTCCACTCAACGAGGGGCGCTTCTGCAGGGCCAGGCATTCCAGAGACCGCCTGC 943
Qy 61 AlaThrLeuCysProValAspGlySerTrpSerProTrpSerLysTrpSerAlaCysGly 80
Db 944 ACCACCATCTGCCAGTCGATGGGCGTGGACGAGTGGAGCAAGTGGTCAGCCTGCAGC 1003
Qy 81 LeuAspCysThrHisTrpArgSerArgGluCysSerAspProAlaProArgAsnGlyGly 100
Db 1004 ACTGAGTGTGCCCACTGGCGTAGCCGAGTGCATGGCGCCCGCCCGCCCGAGGCG 1063
Qy 101 GluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117
Db 1064 CGTGACTGCAGCGGACGCTCTCGACTCTAAGAACTGCACAGATGGGCTG 1114

RESULT 10
US-10-218-779-3
; Sequence 3, Application US/10218779
; Publication No. US20040029222A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit
; APPLICANT: MacDougall, John
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David
; APPLICANT: Gerlach, Valerie
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook II, John
```


Db 829 CCGCTCCACTCAACGGAGGGCCCTCTGCGAGGGCCAGGCATTCCAGAACGCCCTGC 888
Qy 61 AlaThrLeuCysProValAspGlySerTrpSerProTrpSerLysTrpSerAlaCysGly 80
Db 889 ACCACCATCTCCCGACTCGATGGGCGGTGGACGAGTGGAGCAAGTGTCAAGCTGCAGC 948
Qy 81 LeuAspCysThrHisTrpArgGlyCysSerAspProAlaProArgAsnGlyGly 100
Db 949 ACTGAGTGTGCCACTGCGTAGCGCGAGTGCATGGGCCCCCACCACCCAGAACGGAGGC 1008
Qy 101 GluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117
Db 1009 CGTGACTGCAGCGGACGCTGCTCGACTCTTAAGAACTGCACAGATGGGCTG 1059

RESULT 15

US-10-295-027-1123
; Sequence 1123, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1123
; LENGTH: 3501
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-295-027-1123

Alignment Scores:

Pred. No.:	1.42e-43	Length:	3501
Score:	523.00	Matches:	84
Percent Similarity:	82.05%	Conservative:	12
Best Local Similarity:	71.79%	Mismatches:	21
Query Match:	76.69%	Indels:	0
DB:	17	Gaps:	0

US-10-624-932C-2_COPY_232_348 (1-117) x US-10-295-027-1123 (1-3501)

Qy 1 SerAlaSerAlaAlaValIleValTyrValAsnGlyGlyTrpSerThrTrpThrGluTrp 20
Db 721 AGCACCACTGCCACCGTCATCGTCTAGTGAATGGCGGCTGGTCCAGCTGGGCAGAGTGG 780
Qy 21 SerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArgSerArgSerCysThrAsn 40
Db 781 TCACCTGTCTCCAACCGCTGTGGCCGAGGCTGGCAGAAGCGCACCCCGACCTGCACCAAC 840
Qy 41 ProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsnValGlnLysThrAlaCys 60
Db 841 CCGCTCCACTCAACGGAGGGGCTTCTGCGAGGGCCAGGCATTCCAGAAAGACCGCCTGC 900
Qy 61 AlaThrLeuCysProValAspGlySerTrpSerProTrpSerLysTrpSerAlaCysGly 80
Db 901 ACCACCATCTGCCAGTCTCGATGGGGCTGGACGGAGTGGAGCAAGTGTTCAGCTGCAGC 960
Qy 81 LeuAspCysThrHisTrpArgSerArgGluCysSerAspProAlaProArgAsnGlyGly 100
Db 961 ACTGAGTGTGCCACTGGCGTAGCCGCGAGTGCATGGCGGCCCCACCCAGAACGGAGGC 1020
Qy 101 GluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117
Db 1021 CGTGACTGCAGCGGAGCGCTGCTCGACTCTTAAGAACTGCACAGATGGGCTG 1071

Search completed: September 9, 2005, 18:52:13

Job time : 1175.56 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 8, 2005, 22:38:37 ; Search time 3850.68 Seconds
(without alignments)
1156.553 Million cell updates/sec

Title: US-10-624-932C-2_COPY_232_348

Perfect score: 682
Sequence: 1 SASAAVIVYVNGWSTWTEW.....NGBECQGTDLDRNCTSDL 117

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool_h/US10624932/runat_08092005_161706_15792/app_query.fasta_1.1386
-DB=EST -QFMT=fastap -SUFFIX=first -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10624932 @CNC 1 1 8180 @runat_08092005_161706_15792 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_hcc: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gest1: *
9: gb_gest2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query %	ID	Description
1	594	87.1	548	5	BX452510 BX452510
2	539	79.0	2802	9	AY406491 Homo sapi
3	539	79.0	2802	9	AY406492 Pan trogl
4	531	77.9	875	7	CO807001 AGENCOURT
5	531	77.9	2791	3	AY406493 Mus muscu
6	531	77.9	3790	3	AK031655 Mus muscu
7	529	77.6	709	1	AJ729963 AJ729963
8	523	76.7	2532	9	AY411747 Homo sapi
9	522	76.5	693	6	CB246544 UI-M-F10

10	522	76.5	2532	9	AY411749	Mus muscu
11	522	76.5	3866	3	AK018177	Mus muscu
12	520	76.2	594	6	CA711550	io72f10.Y
13	508	74.5	856	7	CN164143	994266 MA
14	505	74.0	678	2	BF098738	601750874
15	502	73.6	746	5	BX872585	EX872585
16	502	73.6	751	5	BX871388	EX871388
17	502	73.6	761	5	EX878537	EX878537
18	498	73.0	577	7	CO670344	CG33-5803
19	496	72.7	487	5	BQ037844	ppn1c.pko
20	492	72.1	354	4	BM257107	520613.WA
21	492	72.1	720	1	AI959236	td25810.Y
22	485	71.1	681	2	BF313643	601900292
23	485	71.1	733	5	EX920046	EX920046
24	485	71.1	2775	9	AY401469	Homo sapi
25	484	71.0	801	7	CV110922	AGENCOURT
26	484	71.0	2775	9	AY401471	Mus muscu
27	466	68.3	774	5	BUS65958	603785840
28	439	64.4	679	7	CO045001	UI-M-G10-
29	433	63.5	632	2	BE314077	601146259
30	430.5	63.1	1175	9	CL642218	CH213-26B
31	429	62.9	2532	9	AY411748	Pan trogl
32	399	58.5	969	2	BF206813	601870209
33	388	56.9	605	5	EX913103	EX913103
34	359	52.6	608	4	BM487397	pgm2h.pko
35	357	52.3	604	5	BP005582	BP005582
36	357	52.3	607	5	BM349971	BM349971
37	357	52.3	676	5	BM353356	BM353356
38	357	52.3	737	5	BM309289	BM309289
39	355	52.1	564	2	AV959198	AV959198
40	344	50.4	386	6	CBS06444	AMGNNUC.N
41	343	50.3	1054	9	CNS02H8B	AL197300
42	340	49.9	1034	4	BI758231	603029876
43	337	49.4	361	7	CR477550	CR477550
44	330	48.4	500	8	BZ921959	BZ921959
45	327.5	48.0	1532	3	BC033727	Homo sapi

ALIGNMENTS

RESULT 1
BX452510
LOCUS CS0DN001YE16 5-PRIME, mRNA sequence.
DEFINITION BX452510 Homo sapiens ADULT BRAIN Homo sapiens CDNA clone
ACCESSION BX452510
VERSION BX452510.2 GI:47063451
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 548)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 22, 2003 this sequence version replaced gi:31026396.
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, Cp 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five cloned
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 3529.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?e=CS0BAG0692F06_CS06574_1&c=3529.f

FEATURES
source
1..548
/organism="Homo sapiens"

/mol_type="mrna"
 /db_xref="taxon:9606"
 /clone="CSODN001YE16"
 /tissue_type="ADULT BRAIN"
 /dev_stage="adult"
 /clone_lib="Homo sapiens ADULT BRAIN"
 /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN

Alignment Scores:
 Pred. No.: 4.48e-39 Length: 548
 Score: 594.00 Matches: 102
 Percent Similarity: 92.11% Conservative: 3
 Best Local Similarity: 89.47% Mismatches: 9
 Query Match: 87.10% Indels: 0
 DB: 5 Gaps: 0

US-10-624-932C-2_COPY_232_348 (1-117) x BX452510 (1-548)

Qy 1 SerAlaSerAlaAlaValIleValTyrValAsnGlyGlyTTPSerThrTTPThrGluTTP 20
 |||||
 Db 188 AGCGCTCCGCTGCTGTCATCGTACGTGAACGGTGGTGGTGCACCGAGTGG 247
 |||||
 Qy 21 SerValCysSerAlaSerCysGlyArgGlyTTPGlnLysArgSerArgSerCysThrAsn 40
 |||||
 Db 248 TCCGTCTCAGCGCCAGCTGTGGCGCGGTGGCAGAAACGAGCGCGAGCTGCACCAAC 307
 |||||
 Qy 41 ProAlaProLeuAenGlyGlyAlaPheCysGluGlyGlnAenValGlnLysThrAlaCys 60
 |||||
 Db 308 CGCGCGCTGTCAACGGGGCGCTTCTGTGAGGGGAGAGTGTTCAGAAACAGCCCTGC 367
 |||||
 Qy 61 AlaThrLeuCysProValAspGlySerTTPSerProTTPSerLysTTPSerAlaCysGly 80
 |||||
 Db 368 GCCACCTGTGCCCGAGTGGAGTGGAGCCGCTGGAGCAAGTGGTGGTGGG 427
 |||||
 Qy 81 LeuAspCysThrHisTTPArgSerArgGluCysSerAspProAlaProArgAsnGlyGly 100
 |||||
 Db 428 CTGGACTGCACCCACTGGCGGAGCGTGGAGTGTCTGACCCAGTACCCCGCAACGGAGGG 487
 |||||
 Qy 101 GluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThr 114
 |||||
 Db 488 GTGAGTGTGAGTTTCTGTCTGTACCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 529
 |||||

RESULT 2

LOCUS AY406491 2802 bp DNA linear GSS 15-DEC-2003
 DEFINITION Homo sapiens UNC5C gene, VIRTUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.
 ACCESSION AY406491
 VERSION AY406491.1 GI:39762465
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 2802)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 2802)

Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.

TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering
 them based on alignment.

FEATURES

source 1..2802
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 <1..>2802
 /gene="UNC5C"
 /locus_tag="HCM2575"

ORIGIN

Alignment Scores:
 Pred. No.: 1.23e-33 Length: 2802
 Score: 539.00 Matches: 86
 Percent Similarity: 86.32% Conservative: 15
 Best Local Similarity: 73.50% Mismatches: 16
 Query Match: 79.03% Indels: 0
 DB: 9 Gaps: 0

US-10-624-932C-2_COPY_232_348 (1-117) x AY406491 (1-2802)

Qy 1 SerAlaSerAlaAlaValIleValTyrValAsnGlyGlyTTPSerThrTTPThrGluTTP 20
 |||||
 Db 754 AGTCAACACTGCACCTGTCATAGTCTATGTCAACGGTGGTGGTGCACCTGACCGAGTGG 813
 |||||
 Qy 21 SerValCysSerAlaSerCysGlyArgGlyTTPGlnLysArgSerArgSerCysThrAsn 40
 |||||
 Db 814 TCTGTGTAAACACCCCTGTGGACGAGGTATCAGAAACGTACAGGACTTGTACCAAC 873
 |||||
 Qy 41 ProAlaProLeuAenGlyGlyAlaPheCysGluGlyGlnAenValGlnLysThrAlaCys 60
 |||||
 Db 874 CCGGACACCTCAATGGGGTGCCTTCTGTGAGGGCAGAGTGTGCGAATAATAGCCTGT 933
 |||||
 Qy 61 AlaThrLeuCysProValAspGlySerTTPSerProTTPSerLysTTPSerAlaCysGly 80
 |||||
 Db 934 ACTAGTTATGCCAGTGGATGGCAGGTGGACGCCATGGAGCAAGTGGTCTACTTGTGGA 993
 |||||
 Qy 81 LeuAspCysThrHisTTPArgSerArgGluCysSerAspProAlaProArgAsnGlyGly 100
 |||||
 Db 994 ACTGAGTGCACCCACTGGCGCAGGAGGTGTCACGGCGCCAGCCCAAGATGTGAGGC 1053
 |||||
 Qy 101 GluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117
 |||||
 Db 1054 AAGGACTGCGACGGCTCTTGTCAATCCAGAACTGCACCTGATGGGCTT 1104
 |||||

RESULT 3

LOCUS AY406492 2802 bp DNA linear GSS 15-DEC-2003
 DEFINITION Pan troglodytes UNC5C gene, VIRTUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.
 ACCESSION AY406492
 VERSION AY406492.1 GI:39762466
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM Pan troglodytes

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 1 (bases 1 to 2802)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 2802)

Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Adams,M.D. and Cargill,M.

Perriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES

source
1..2802
Location/Qualifiers
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..>2802
/gene="UNC5C"
/locus_tag="HCW2575"

ORIGIN

Alignment Scores:
Pred. No.: 1.23e-33 Length: 2802
Score: 539.00 Matches: 86
Percent Similarity: 86.32% Conservative: 15
Best Local Similarity: 73.50% Mismatches: 16
Query Match: 79.03% Indels: 0
DB: 9 Gaps: 0

US-10-624-932C-2_COPY_232_348 (1-117) x AY406492 (1-2802)

Qy 1 SerAlaSerAlaAlaValIleValTyrValAsnGlyGlyTyrSerThrThrThrGluTrp 20
Db 754 AGTCAACTGCACCTGCTATAGTCTATGTCACAGTGGCTGTCACCTGACGAGTGG 813
Qy 21 SerValCysSerAlaSerCysGlyArgGlyTyrGlnLysArgSerArgSerCysThrAsn 40
Db 814 TCTGTGTGTACAGCGCGCTGTGGACGAGGATCAGAAACGTACAGGACTGTGTACCAAC 873
Qy 41 ProAlaProLeuAasnGlyGlyAlaPheCysGluGlyGlnAasnValGlnLysThrAlaCys 60
Db 874 CCGGACCACCTCAATGGGGGTGCCTTCTGTGAAGGGCAGAGTGTGCAGAAATAGCCGTG 933
Qy 61 AlaThrLeuCysProValAspGlySerTyrSerProTyrSerLysThrSerAlaCysGly 80
Db 934 ACTAGTTATGCCAGTGGATGGAGGTGGAGGCCATGGACAGTGTCTACTTTGGGA 993
Qy 81 LeuAspCysThrHisTyrArgSerArgGluCysSerAspProAlaProArgAasnGlyGly 100
Db 994 ACTGAGTGCACCCACTGCGCAGGAGGGAGTGCACGGCGCCAGCCCCCAAGATGGAGGC 1053
Qy 101 GluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117
Db 1054 AAGGACTGCGATGGCCTCGCTTGTCAATCCAAAGAACTGCACTGATGGGCTT 1104

RESULT 4

CO807001
LOCUS
DEFINITION
AGNCOURT 30255333 NIH_MGC 257 Mus musculus cDNA clone
IMAGE:30932367 5', mRNA sequence.

CO807001

CO807001.1 GI:51022265

EST.

Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 875)

NIH-MGC <http://mgs.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Kathleen Horner, Stanford University

cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: NDAMI181 row: i column: 16

High quality sequence stop: 671.

FEATURES

Location/Qualifiers
1..875

source

/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:30932367"
/lab_host="DH10B Tona"
/clone_lib="NIH_MGC_257"
/note="Organ: oocyte; Vector: pExpress-1; Site: 1: EcorV;
Site 2: NotI; cDNA was primed using oligo-dT primer:
5'-pGACTAGTTCTAGATCGAGCGGCCCTT-3' and cloned into
the EcorV/NotI sites of pExpress-1. Size-selection >0.5 kb
resulted in an average insert size of 1.0kb. This is a
normalized library (primary library is NIH_MGC_256) and
was constructed by Express Genomics (Frederick, MD). Note:
this is a NIH_MGC library"

ORIGIN

Alignment Scores:
Pred. No.: 1.23e-33 Length: 875
Score: 531.00 Matches: 85
Percent Similarity: 85.47% Conservative: 15
Best Local Similarity: 72.65% Mismatches: 17
Query Match: 77.86% Indels: 0
DB: 7 Gaps: 0

US-10-624-932C-2_COPY_232_348 (1-117) x CO807001 (1-875)

Qy 1 SerAlaSerAlaAlaValIleValTyrValAsnGlyGlyTyrSerThrThrThrGluTrp 20
Db 139 AGCACCCAGCCACTGTCATCGTGTATGTTAATGGTGGCTGTCACCTGGACAGATGG 198
Qy 21 SerValCysSerAlaSerCysGlyArgGlyTyrGlnLysArgSerArgSerCysThrAsn 40
Db 199 TCTGTGTGTACAGCGCGCTGTGGGAGGATCAGAAACGTACAGGAACTGTGCACCAAC 258
Qy 41 ProAlaProLeuAasnGlyGlyAlaPheCysGluGlyGlnAasnValGlnLysThrAlaCys 60
Db 259 CCACCCCACTCANTGTGGGCTTCTGTGAGGGCAGAGTGTGCAGAAATAGCATGC 318
Qy 61 AlaThrLeuCysProValAspGlySerTyrSerProTyrSerLysThrSerAlaCysGly 80
Db 319 ACTAGTTATGCCAGTGGATGGTGGAGCTTCATGGAGCAATGTCAACCTGTGGG 378
Qy 81 LeuAspCysThrHisTyrArgSerArgGluCysSerAspProAlaProArgAasnGlyGly 100
Db 379 ACTGAATGCACCCACTGCGCAGGAGGGAGTGTACAGCACCAGCCCCCAAGACGGGGT 438
Qy 101 GluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117
Db 439 AAGGACTGTGATGGCCTCGCTTCCAATCCAAAGAACTGCACTGATGGGCTG 489

RESULT 5

AY406493

LOCUS

DEFINITION

Mus musculus UNC5C gene, VIRTUAL TRANSCRIPT, partial sequence,

genomic survey sequence.

AY406493

AY406493.1 GI:39762467

GSS.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 2791)

REFERENCE

1 (bases 1 to 2791)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 2791)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers

source 1..2791

gene /organism="Mus musculus"
/db_xref="taxon:10090"
<1..>2791
/gene="UNC5C"
/locus_tag="HCN2575"

ORIGIN

Alignment Scores: 5.56e-33 Length: 2791

Pred. No.: 531.00 Matches: 85

Score: 85.47% Conservative: 15

Percent Similarity: 72.65% Mismatches: 17

Best Local Similarity: 77.86% Indels: 0

Query Match: 9 Gaps: 0

DB:

US-10-624-932C-2_COPY_232_348 (1-117) x AV406493 (1-2791)

Qy 1 SerAlaSerAlaAlaValIleValTy-rValAnGlyGlyTrpSerThrTrpThrGluTrp 20
||| :|||

Db 743 AGCACCCACAGCCACTGCATCGTGTATGTTAATGTGGTGTCCACCTGGACAGATGG 802
||| :|||

Qy 21 SerValCysSerHisTrpArgGlyTrpGlnLysArgSerArgSerCysThrAsn 40
||| :|||

Db 803 TCTGTGTACACGCCCTGTGGCGGAGATATCAGAAACCCACAGAACCTGCACCCAC 862
||| :|||

Qy 41 ProAlaProLeuAnGlyGlyAlaPheCysGluGlyGlnAnValGlnLysThrAlaCys 60
||| :|||

Db 863 CCAGCCCCACTCAATGGTGGGCCCTTCTGTGAGGGCGAGAGTGTGCAGAAAATAGCATGC 922
||| :|||

Qy 61 AlaThrLeuCysProValAspGlySerTrpSerProTrpSerLysTrpSerAlaCysGly 80
||| :|||

Db 923 ACTACGTTATGTCAGTGGATGGTGGTGGACTTCATGGAGCAAAATGGTCAACCTGTGGG 982
||| :|||

Qy 81 LeuAspCysThrHisTrpArgSerArgGluCysSerAspProAlaProArgAsnGlyGly 100
||| :|||

Db 983 ACTGAATGACCCCACTGGCGCAGAGGAGGTGTACAGCACCCAGCCCCCAAGACGGGGGT 1042
||| :|||

Qy 101 GluGluCysGlnGlyThrAspLeuAspThrArgAnCysThrSerAspLeu 117
||| :|||

Db 1043 AAGGACTGTGATGGCTGCTCCATCCAAAGAACTGCATGTATGGGCTG 1093
||| :|||

RESULT 6

AK031655

LOCUS AK031655 3790 bp mRNA linear HTC 03-APR-2004

DEFINITION Mus musculus 13 days embryo male testis cDNA, RIKEN full-length enriched library, clone:6030473H24 product:unc5 homolog (C. elegans) 3, full insert sequence.

ACCESSION AK031655

VERSION AK031655.1 GI:26327502

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

PUBMED 99279253

REFERENCE 2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

PUBMED 20499374

REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsuunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kiza,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

PUBMED 20530913

REFERENCE 4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

PUBMED 11076861

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

PUBMED 12405330

REFERENCE 6 (bases 1 to 3790)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,P., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

FEATURES Location/Qualifiers

source 1..3790

organism "Mus musculus"

mol_type "mRNA"

Qy 81 LeuAspCysThrHisTrpArgSerArgGluCysSerAspProAlaProArgAsnGly 100
:::|||||
Db 640 ACAGTGTGGCAGTGGCGAGCGAGTGCATGGCACCGCCACCCAGAACGGAGGC 699

Qy 101 GluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117
:::|||||
Db 700 CGTGAAGTGGAGCGGAGCGTACTTGAAGTCCAGAACTGCACATGGGCTG 750

RESULT 11
AKO18177
LOCUS
DEFINITION
Mus musculus adult male medulla oblongata cDNA, RIKEN full-length
enriched library, clone:630415E02 product:TRANSMEMBRANE RECEPTOR
UNC5H2 homolog [Rattus norvegicus], full insert sequence.
ACCESSION
AKO18177
VERSION
KEYWORDS
SOURCE
ORGANISM
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE
2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE
3 Shikama, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujitake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, S., Watanabe, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE
4 The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 695-699 (2001)
REFERENCE
5 The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE
6 (bases 1 to 3866)
ADACHI, J., AIZAWA, K., AKAHARA, S., AKIMURA, T., ARAI, A., AONO, H.,
ARAKAWA, T., BONO, H., CARNINCI, P., FUKUDA, S., FUKUNISHI, Y.,
FURUNO, M., HANAGAKI, T., HARA, A., HAYATSU, N., HIRAMOTO, K.,
HIROAKA, T., HORI, F., IMOTANI, K., ISHII, Y., ITOH, M., IZAWA, M.,
KASUKAWA, T., KATO, H., KAWAI, J., KOJIMA, Y., KONNO, H., KODA, M.,
KOYA, S., KURIHARA, C., MATSUMOTO, T., MIYAZAKI, A., NISHI, K.,
NOMURA, K., NUMAZAKI, R., OHNO, M., OKAZAKI, Y., OKIDO, T., OWA, C.,
SAITO, H., SAITO, R., SAKAI, C., SAKAI, K., SANO, H., SASAKI, D.,
SHIBATA, K., SHIBATA, Y., SHINAGAWA, A., SHIRAKI, T., SOGABE, Y.,
SUZUKI, H., TAGAMI, M., TAGAWA, A., TAKAHASHI, F., TANAKA, T.,
TEJIMA, Y., TOYA, T., YAMAMURA, T., YASUNISHI, A., YOSHIDA, K.,
YOSHINO, M., YURAMATSU, M. and HAYASHIZAKI, Y.

Size-selected on agarose gel. Average insert size ~1kb. 5' XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permut Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@ingate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."

ORIGIN

Alignment Scores:
Pred. No.: 5,96e-33 Length: 594
Score: 520.00 Matches: 83
Percent Similarity: 82.0% Conservative: 13
Best Local Similarity: 70.94% Mismatches: 21
Query Match: 76.25% Indels: 0
DB: 6 Gaps: 0

US-10-624-932C-2_COPY_232_348 (1-117) x CA771550 (1-594)

Qy 1 SerAlaSerAlaAlaValIleValTyrValAenGlyGlyTrpSerThrTrpThrGluTrp 20
Db 187 AGCACCACCTGCACCGTCATCTCTACTTGAATGGCGCTGCTCCAGCTGGCAGAGTGG 246
Qy 21 SerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArgSerArgSerCysThrAsn 40
Db 247 TCACCTCTCTCAACCGCTGTGGCGAGGCTGGCAGAACGCGACCTGCACCAAC 306
Qy 41 ProAlaProLeuAenGlyGlyAlaPheCysGluGlyGlnAenValGlnLysThrAlaCys 60
Db 307 CCGCTCCACTCAACGAGGGGCTCTTCGAGGGCCAGGCATTCAGAACCGCCCTGC 366
Qy 61 AlaThrLeuCysProValAspGlySerTrpSerProTrpSerLysTrpSerAlaCysGly 80
Db 367 ACCACCTCTGCCAGTGCATGGGCGTGGAGGAGTGGAGCAAGTGTCAAGCTGCAGC 426
Qy 81 LeuAspCysThrHisTrpArgSerArgGlyCysSerAspProAlaProAraAsnGlyGly 100
Db 427 ACTGAGTGTGCCACTGCGAGTGGCGGAGTGCATGGCGCCGCCACCCAGAACCGAGGC 486
Qy 101 GluGluCysGlnGlyThrAspLeuAspThrArgAenCysThrSerAspLeu 117
Db 487 CGTGACTGCAGGGGACGCTGCTCAGCTCTAAGAACTGCACAGATGGGCTG 537

RESULT 13

LOCUS CN164143 856 bp mRNA linear EST 02-APR-2004
DEFINITION 994266 MARC 4PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION CN164143
VERSION CN164143.1 GI:46178573

KEYWORDS

EST.

SOURCE

Sus scrofa (pig)

ORGANISM

Sus scrofa

REFERENCE

1 (Bases 1 to 856)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Wise, T.A.,

Noneman, D.J., Wray, J.E. and Keele, J.W.

Porcine EST collection using a normalized library constructed from

embryos representing early developmental stages

Unpublished (2003)

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@mail.marc.usda.gov

Single pass sequencing. Bases called with phred v0.020425.c and

trimmed with the aid of the trim_alt option. Vector identified with

cross match v0.990329.

Plate: TM8062 row: N column: 14

Seq primer: GTAATACGACTCATTATAGG.

Location/Qualifiers

1. .856

FEATURES

source

/organism="Sus scrofa"

/mol_type="mRNA"

/db_xref="taxon:9823"

/tissue_type="pooled"

/lab_host="DH10B"

/clone_lib="MARC 4PIG"

/note="Vector: pCDNA3.1; Site_1: EcoRI; Site_2: NotI;

Library made with combined RNA from day-10, day-13,

day-15, day-25, and day-30 whole embryos."

ORIGIN

Alignment Scores:
Pred. No.: 9,28e-32 Length: 856
Score: 508.00 Matches: 81
Percent Similarity: 86.49% Conservative: 15
Best Local Similarity: 72.97% Mismatches: 15
Query Match: 74.49% Indels: 0
DB: 7 Gaps: 0

US-10-624-932C-2_COPY_232_348 (1-117) x CN164143 (1-856)

Qy 1 SerAlaSerAlaAlaValIleValTyrValAenGlyGlyTrpSerThrTrpThrGluTrp 20
Db 524 AGCACAACCGCACTGTCATAGTCTATGTAATGGTGGCTGCTCCACTGGACAGAGTGG 583
Qy 21 SerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArgSerArgSerCysThrAsn 40
Db 584 TCTGTGTGTAATAGCCGCTGTGGACGAGGTATCAGAAGCGCACAAAGACCTGCACCAAT 643
Qy 41 ProAlaProLeuAenGlyGlyAlaPheCysGluGlyGlnAenValGlnLysThrAlaCys 60
Db 644 CCAGCCCCACTCAATGGTGGCTCTCTGTAAGGGCAGAGTGTGCAGAAATAGCCCTGT 703
Qy 61 AlaThrLeuCysProValAspGlySerTrpSerProTrpSerLysTrpSerAlaCysGly 80
Db 704 ACCAGTGTGCCAGTGGATGGCAGATGGACCTCATGAGTAGTGTGACCTGCGGG 763
Qy 81 LeuAspCysThrHisTrpArgSerArgGluCysSerAspProAlaProAraAsnGlyGly 100
Db 764 ACCAGTGCACACACTGGCGCAGAGGAGTGCACAGCACCAGCCCCCAAGAATGGAGGC 823
Qy 101 GluGluCysGlnGlyThrAspLeuAspThrArg 111
Db 824 AAGGACTGCGATGGCTGCTTACAGTCCAAG 856

RESULT 14

LOCUS BF098738

DEFINITION BF098738 678 bp mRNA linear EST 19-OCT-2000

ACCESSION BF098738

VERSION BF098738.1 GI:10881264

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (Bases 1 to 678)

NH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone Distribution by: Incyte Genomics, Inc.

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM9171 row: c column: 19

High quality sequence stop: 634.

Location/Qualifiers

FEATURES

```

source
1. .678
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:3978570"
/tissue_type="tumor, biopsy sample"
/dev_stage="3 months, virgin"
/lab_host="DH10B"
/clone_lib="NCI CGAP Mam1"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sali;
Site 2: Not1; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

ORIGIN
Alignment Scores:
Pred. No.: 1.21e-31 Length: 678
Score: 505.00 Matches: 80
Percent Similarity: 82.73% Conservat: 11
Best Local Similarity: 72.73% Mismatches: 19
Query Match: 74.05% Indels: 0
DB: 2 Gaps: 0

US-10-624-932C-2_COPY_232_348 (1-117) x BF098738 (1-678)

Qy 8 ValtYrVallAenGlyGlyTrrSerThrTrrGluTrrSerValCysSerAlaSerCys 27
Db 2 GTCTATGTGAATGAGGCGTGTCCAGCTGGGCAGAGTGGTCCACCCTGTTCCTCAATCGCTGT 61
Qy 28 GlyArgGlyTrrGlnLysAtrSerArgSerCysThrAenProAlaProLeuAenGlyGly 47
Db 62 GGCCGAGGCTGGCAGAGCGTACTCGGACCTGACCAATCCAGCCCTCACTCAATGGAGGC 121
Qy 48 AlaPheCysGluGlyGlnAenValGlnLysThrAlaCysAlaThrLeuCysProValAasp 67
Db 122 GCCTTCTGTGAGGACAGAGCGCTTCAGAGACAGAGCTTGACACCGTGTGCCAGTGGAT 181
Qy 68 GlySerTrrSerProTrrSerLysTrrSerLysCysGlyLeuAapCysThrHisTrrArg 87
Db 182 GGACGCGTGGACCGAGTGGAGCAAGTGTCTCCCTGCAGACACAGAGTGGCGCACTGGCGC 241
Qy 88 SerArgGluCysSerAppProAlaProArgAenGlyGlyGluCysGlnGlyThrAasp 107
Db 242 AGCCGCGAGTGCATGGCACCCTCCAGACAGAGCGGCGGTGACTGCAGCGGACGCTA 301
Qy 108 LeuAaspThrArgAenCysThrSerAaspLeu 117
Db 302 CTTGACTCCAGAACTGCCTGATGGGCTG 331

RESULT 15
BX872585 746 bp mRNA linear EST 24-MAY-2004
LOCUS BX872585 tcbk Oncorhynchus mykiss cdna clone tcbk0009c.j.16 5prim,
DEFINITION mRNA sequence.
ACCESSION BX872585
VERSION BX872585.2 GI:42787249
KEYWORDS EST.
SOURCE Oncorhynchus mykiss (rainbow trout)
ORGANISM Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 746)
Govoroun,M., Guiguen,Y. and Le Gac,F.
Construction and primary characterization of normalized cdna
libraries in rainbow trout, Oncorhynchus mykiss
Unpublished (2003)
On Dec 17, 2003 this sequence version replaced gi:39999678.
Contact: Guiguen Y
INRA - SCRIBE
Campus de beaulieu, RENNES cedex, 35042, France
Tel: 02.23.48.50.09

Fax: 02.23.48.50.20
Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
sequence.
Plate: 0009 row: j column: 16
Seq primer: M13R.
Location/Qualifiers
1. .746
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
/clone="tcbk0009c.j.16"
/tissue_type="multi-tissues"
/dev_stage="from embryos to adults"
/lab_host="DH10B"
/clone_lib="tcbk"
/notes="Vector: pT73D-pac; AGENAE Rainbow trout
multi-tissues - normalized + 2 subtractions; Clone
distribution : AGENAE Resource centre. Francois PIUMI,
Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et
Etude du genome (LREG), Domaine de Vilvert, 78352,
Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33
(0) 1.34.65.22.73"

ORIGIN
Alignment Scores:
Pred. No.: 2.41e-31 Length: 746
Score: 502.00 Matches: 81
Percent Similarity: 82.91% Conservat: 16
Best Local Similarity: 69.23% Mismatches: 20
Query Match: 73.61% Indels: 0
DB: 5 Gaps: 0

US-10-624-932C-2_COPY_232_348 (1-117) x BX872585 (1-746)

Qy 1 SerAlaSerAlaAlaValIleValTyrValAenGlyGlyTrrSerThrTrrGluTrr 20
Db 331 AGTACCACCTGCTACTGTATTGTCTATGTGAACGGCGCTGTTCGACATGGACAGATGG 390
Qy 21 SerValCysSerAlaSerCysGlyArgGlyTrrGlnLysArgSerArgSerCysThrAen 40
Db 391 TCAGTGTGTAAACAGTCGCTGTGGCGCGGTGTACCAAAAGCGGTACCCGACGCTGTACCAAT 450
Qy 41 ProAlaProLeuAenGlyGlyAlaPheCysGluCylGlnAenValGlnLysThrAlaCys 60
Db 451 CCGCCCGCTCAACGAGGAGGCGCCCTGTGTGAGGACAGGCAACCCAGAGCTGGCCTGC 510
Qy 61 AlaThrLeuCysProValAaspGlySerTrrSerProTrrSerLysTrrSerAlaCysGly 80
Db 511 ACCTCCCTCTGCACCTGTTGACGGGTTGTGGACAGAGTGGAGTAAAGTGTCTACTTGGT 570
Qy 81 LeuAaspCysThrHisTrrArgSerArgGluCysSerAaspProAlaProAenGlyGly 100
Db 571 ACAGAGTGCCTCACTGGCGCAGAGAGAAATGCAATGCCCTGTGCACCAAAATGGAGGC 630
Qy 101 GluGluCysGlnGlyThrAaspLeuAaspThrArgAenCysThrSerAaspLeu 117
Db 631 AAGGACTGCGAGGGGTATGGTCTACAGTCCAGAACTGTACTGACGGACTC 681

Search completed: September 9, 2005, 04:40:39
Job time : 3857.68 secs

```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 8, 2005, 23:47:02; Search time 2077.73 Seconds
(without alignments)
1166.064 Million cell updates/sec

Title: US-10-624-932C-2_COPY_246_295

Perfect score: 290

Sequence: 1 STWTSEVCSASCRGQKQK.....NGGAFCEQNVQTKATCLC 50

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n model -DEV=xlh
-Q=/cgn2_1/USPTO.spool_h/US10624932/runat_08092005_161705_15773/app_query.fasta_1.1386
-DB=GenEmbl -QWMT=fastcap -SUFFIX=rgc -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10624932 @CGN 1.1 7509 @runat_08092005_161705_15773 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

10: gb.ro.*

11: gb.sts.*

12: gb.sw.*

13: gb.un.*

14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	290	100.0	2697	6	AX268596 Sequence
2	290	100.0	2697	6	AX451852 Sequence
3	290	100.0	2697	10	U87305 Rattus norv
4	290	100.0	2752	6	AX449572 Sequence

5	290	100.0	2784	6	CQ730306	Sequence
6	290	100.0	3014	6	BD057524	Netrin re
7	290	100.0	3992	10	MMU487852	Mus muscu
8	290	100.0	4294	10	AK122575	Mus muscu
9	290	100.0	121282	2	AC027318	Homo sapi
c 10	290	100.0	168534	2	AC034209	Homo sapi
c 11	290	100.0	168168	2	AC012283	Homo sapi
c 12	290	100.0	231407	2	AC139592	Rattus no
c 13	290	100.0	242128	2	AC123700	Mus muscu
14	249	85.9	2270	9	BC041156	Homo sapi
15	249	85.9	2612	6	CQ881064	Sequence
16	249	85.9	2780	6	CQ881054	Sequence
17	249	85.9	2962	5	AY187310	Gallus ga
18	249	85.9	2986	6	CQ881052	Sequence
19	249	85.9	3646	6	CQ881060	Sequence
20	249	85.9	3646	9	AF055634	Homo sapi
21	249	85.9	9299	10	MMU72634	Mus muscu
c 22	249	85.9	159206	9	AC098584	Homo sapi
c 23	249	85.9	168940	2	AC102307	Mus muscu
c 24	249	85.9	191935	2	AC114747	Homo sapi
25	244	84.1	9328	10	AB118026	Rattus no
26	244	84.1	250375	2	AC131167	Rattus no
27	243	83.8	2881	6	AX527916	Sequence
28	239	82.4	168	6	AX800695	Sequence
29	239	82.4	2585	6	CQ842137	Sequence
30	239	82.4	2585	9	AK122615	Homo sapi
31	239	82.4	2625	6	CQ721377	Sequence
32	239	82.4	2661	6	AX800717	Sequence
33	239	82.4	2860	6	AX686445	Sequence
34	239	82.4	2860	6	AX686447	Sequence
35	239	82.4	2868	6	AX800719	Sequence
36	239	82.4	2895	6	AX512281	Sequence
37	239	82.4	2995	6	AX497288	Sequence
38	239	82.4	3252	9	AY358147	Homo sapi
39	239	82.4	3770	9	AY126437	Homo sapi
40	239	82.4	3884	6	AX528525	Sequence
41	239	82.4	3884	6	AX464012	Sequence
42	239	82.4	3884	9	AY358351	Homo sapi
43	239	82.4	3933	6	CQ850929	Sequence
44	239	82.4	3933	9	AK128132	Homo sapi
45	239	82.4	3935	9	AB096256	Homo sapi

ALIGNMENTS

RESULT 1	AX268596	Sequence	15 from Patent WO01/5440.	2697 bp	DNA	linear	PAT 29-OCT-2001
LOCUS	AX268596	AX268596					
DEFINITION	AX268596	AX268596					
ACCESSION	AX268596	AX268596					
VERSION	AX268596.1	GI:16541710					
KEYWORDS							
SOURCE	Rattus sp.						
ORGANISM	Rattus sp.						
	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;						
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;						
	Rattus.						
REFERENCE	1						
AUTHORS	Cochran,S.W., Paterson,G.Y., Ohashi,Y.W., Morris,B.Y. and Pratt,J.Y.						
TITLE	Schizophrenia related genes						
JOURNAL	Patent: WO 01/5440-A 15 11-OCT-2001;						
	WELFIDE CORPORATION (JP)						
FEATURES	Location/Qualifiers						
source	1..2697						
	/organism="Rattus sp."						
	/mol_type="unassigned DNA"						
	/db_xref="taxon:10118"						

ORIGIN

Alignment Scores:

Pred. No.:

Score:

1.88e-19

290.00

Length:

2697

Matches:

50

```

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x AX268596 (1-2697)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 736 TCGACGTGGAGTGGTCCGCTGCAGCGCCAGCTGTGGCGTGGTGGCGAGAAACGG 795

Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 796 AGCCGGAGCTGCACCAACCGCGACCTCTCAACGGGGCGCTTCTGTGAGGGGCAGAAAT 855

Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 856 GTCCAGAAACAGAGCTGCGCCACTCTGTGC 885

RESULT 2
AX451652
LOCUS AX451652 2697 bp DNA linear PAT 03-JUL-2002
DEFINITION Sequence 1 from Patent WO0233080.
ACCESSION AX451652
VERSION AX451652.1 GI:21698587
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Koehler, R.H.
TITLE Regulation of human netrin binding membrane receptor unc5h-1
JOURNAL Patent: WO 0233080-A 1 25-APR-2002;
Bayer Aktiengesellschaft (DE)
FEATURES
source
1. 2697
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 1.88e-19 Length: 2697
Score: 290.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x AX451652 (1-2697)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 736 TCGACGTGGAGTGGTCCGCTGCAGCGCCAGCTGTGGCGTGGTGGCGAGAAACGG 795

Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 796 AGCCGGAGCTGCACCAACCGCGCGCTCTCAACGGGGCGCTTCTGTGAGGGGCAGAAAT 855

Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 856 GTCCAGAAACAGAGCTGCGCCACTCTGTGC 885

RESULT 3
RNU87305
LOCUS RNU87305 2697 bp mRNA linear ROD 15-MAY-1997
DEFINITION Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds.
ACCESSION U87305
VERSION U87305.1 GI:2055391
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 2697)
AUTHORS Leonardo, E.D., Hinch, L., Masu, M., Keino-Masu, K., Ackerman, S.L. and Tessier-Lavigne, M.
TITLE Vertebrate homologues of C. elegans UNC-5 are candidate netrin receptors
JOURNAL Nature 386 (6627), 833-838 (1997)
MEDLINE 97271897
PUBMED 9126742
REFERENCE 2 (bases 1 to 2697)
AUTHORS Leonardo, E.D., Hinch, L., Masu, M., Keino-Masu, K. and Tessier-Lavigne, M.
TITLE Direct Submission
JOURNAL Submitted (28-JAN-1997) Anatomy, UCSF, 513 Parnassus, San Francisco, CA 94143-0452, USA
FEATURES
source
1. 2697
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/tissue_type="brain and ventral spinal cord"
/dev_stage="18 day embryo and 13 day embryo"
1. 2697
/codon_start=1
/product="transmembrane receptor UNC5H1"
/protein_id="AA057678.1"
/db_xref="GI:2055392"
/translations="MAVRGLPVLVLLGIVLAALRGSGAQSATVAVPFGANPDLLP
HFLVEPDEVIVKPKVLLVCAPVATQIFKCNQEWVQVHDVIERSTDSGLPTM
EVINVSROQVEKVGLEYNQCVAVSSGTTKSKAYIRIAYLRNFEQPLAKEV
SLRQGVLPKRPPEGIPPAEWEIRNEDLVPSLDENVYITRHSLVVROARLADTAN
YTCVAKNIARRSTSAAVIVYNGWSTWWSKACGLDCTHWRSECDPAPRNGECC
GGAFCEQNVQKTACATLCPDWSWSKACGLDCTHWRSECDPAPRNGECC
RGADLDRNCTSDLCILHATSCPDVALYIGLVAVAVCLFLLALLGLIYCRKEGLDS
VDADSSITLTSQFPVSIKPSKADNPILLTIQDPLSTTTTQGSLSRQDQPGPKFOL
SNGLHSLPLSGSRHTLHSSPTSEADPFVSLSTONYFRSLPRGTSNWAYGTNFNLAG
RLMIPNTGISLLIPDPAIPRKGIYEVYLTLHKEDVRLPLAGCQTLLSPVSCGPGV
LLTRPVILAMDHCGEPSDSEIRLKKQSCGSWEDVHLHGEESPSHLTYCQLGAGAC
YVFTEQLGRFALVGEALVSAATKRLRLLLFPVACTSLSEYNIRVYCLHDTHDALKEV
QLEKQGGQLIQEPRVLHFRLSDYHNLRLSHDVPSSLKSLVYQEIYPFYHWTG
QOYLHCTFTLERINASTDLACKVWQVEGDGQSFNINFTKDTFAELLALSESG
GVPLVGPSPAFKIPFLIRQKI IASLDPPCSRGDWRTLAOKLHLDLSLSPFASKPST
AMILNLWEARHPFNGNLGQLAAVAGLQDPAGLFTVSEAC"

```

```

ACCESSION AX449572
VERSION AX449572.1 GI:21698195
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Padigaru, M., Mezes, P., Mishra, V., Burgess, C., Casman, S.,
Grosse, W.M., Alsobrook, J.P., Lepley, D.M., Gerlach, V.L.,
MacDougall, J.R. and Smithson, G.
TITLE Proteins and nucleic acids encoding same
JOURNAL Patent: WO 0210216-A 1 07-FEB-2002;
Curagen Corporation (US)
FEATURES
source
1..2752
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 1,91e-19 Length: 2752
Score: 290.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x AX449572 (1-2752)
Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 781 TCGACGTGGACCGAGTGGTCCGCTGTCAGCGCCAGCTGTGGCGGGCTGGCAGAAACGG 840
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyAlaPheCysGluGlyClnAsn 40
Db 841 AGCCGGAGCTGCACCAACCGCGCCTCTCAACGGGGCGCTTTCTGTGAGGGGCGAGAAT 900
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 901 GTCCAGAAACAGCCTGCCACCCTGTGTC 930

RESULT 5
LOCUS CQ730306 2784 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 16240 from Patent WO02068579.
ACCESSION CQ730306
VERSION CQ730306.1 GI:42303801
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 16240 06-SEP-2002;
PE Corporation (NY) (US)
FEATURES
source
1..2784
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 1,94e-19 Length: 2784
Score: 290.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

US-10-624-932C-2_COPY_246_295 (1-50) x BD057524 (1-3014)
Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 736 TCGACGTGGACTGAGTGGTCCGCTGTCAGCGCCAGCTGTGGCGGGCTGGCAGAAACGG 795
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyAlaPheCysGluGlyClnAsn 40
Db 796 AGCCGGAGCTGCACCAACCGCGCCTCTCAACGGGGCGCTTTCTGTGAGGGGCGAGAAT 855
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 856 GTCCAGAAACAGCCTGCCACCCTGTGTC 885

RESULT 7

```

```

Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x CQ730306 (1-2784)
Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 823 TCGACGTGGACCGAGTGGTCCGCTGTCAGCGCCAGCTGTGGCGGGCTGGCAGAAACGG 882
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyAlaPheCysGluGlyClnAsn 40
Db 883 AGCCGGAGCTGCACCAACCGCGCCTCTCAACGGGGCGCTTTCTGTGAGGGGCGAGAAT 942
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 943 GTCCAGAAACAGCCTGCCACCCTGTGTC 972

RESULT 6
LOCUS BD057524 3014 bp DNA linear PAT 27-AUG-2002
DEFINITION Netrin receptors.
ACCESSION BD057524
VERSION BD057524.1 GI:22603130
KEYWORDS JP 2001505062-A/1.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 3014)
AUTHORS Lavigne, M.T., Leonardo, D.E., Hinck, L., Masu, M. and Masu, K.K.
TITLE Netrin receptors
JOURNAL Patent: JP 2001505062-A 1 17-APR-2001;
THE REGENTS OF THE UNIV OF CALIFORNIA
COMMENT PN JP 2001505062-A/1
PD 17-APR-2001
PF 19-FEB-1998 JP 1998536840
PR 19-FEB-1997 US 08/089882
PI MARC TESSIER LAVIGNE, DAVID E LEONARDO, LINDSAY HINCK, MASAYUKI
PI MASU,
PI KAZUKO KEINO MASU
PC C07K1/00, C07K14/00, C07K17/00, C07H21/02, C07H21/04, G01N33/53 CC
Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers.
FEATURES
source
1..3014
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Alignment Scores:
Pred. No.: 2,1e-19 Length: 3014
Score: 290.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x BD057524 (1-3014)
Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 736 TCGACGTGGACTGAGTGGTCCGCTGTCAGCGCCAGCTGTGGCGGGCTGGCAGAAACGG 795
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyAlaPheCysGluGlyClnAsn 40
Db 796 AGCCGGAGCTGCACCAACCGCGCCTCTCAACGGGGCGCTTTCTGTGAGGGGCGAGAAT 855
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 856 GTCCAGAAACAGCCTGCCACCCTGTGTC 885

RESULT 7

```

```
MMU487852      3992 bp      mRNA      linear      ROD 24-SEP-2002
LOCUS          Mus musculus mRNA for netrin receptor Unc5h1 (Unc5h1 gene).
ACCESSION      AJ487852
VERSION        GI:22035783
KEYWORDS       netrin receptor Unc5h1; Unc5h1 gene.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
REFERENCE      1
AUTHORS        Engelkamp,D.
TITLE          Cloning of three mouse Unc5 genes and their expression patterns at
JOURNAL        mid-gestation
MEDLINE        Mech. Dev. 118 (1-2), 191-197 (2002)
PUBMED         2239710
REFERENCE      2 (bases 1 to 3992)
AUTHORS        Engelkamp,D.
TITLE          Direct Submission
JOURNAL        Submitted (15-MAY-2002) Neuroanatomy, Max Planck Institute for
Brain Research, Deutschordenstrasse 46, Frankfurt 60528, GERMANY
FEATURES       Location/Qualifiers
source         1..3992
               /organism="Mus musculus"
               /mol_type="mRNA"
               /db_xref="taxon:10090"
               1..3992
               /gene="Unc5h1"
               /size="2928"
               /date="2002"
               /codon_start=1
               /product="netrin receptor Unc5h1"
               /protein_id="CAD32250.1"
               /db_xref="GI:22035784"
               /db_xref="GOA:Q8K1S4"
               /db_xref="UniProt/T/EMBL:Q8K1S4"
               /translation="MAVRPGLWLPALLGIIVLTAWLGRSGAQSATVNPVGNPDLPLP
               HFLVEPDDVIVKNNPVLLVCKVAPATQIFPKNGEWRVQDVHIERSTOGSGSLPTM
               EVRLNVRQVQKVFGLVEYWCQCAWSSSGTKTSQKAYIRIAYLRNFKFEPLAKEV
               SLEQIVLPCRPPEGIIPAEVWLRNEDLDPSLDPNVYITREHSLVVRQARLADTAN
               YTCVAKNIVARRRSAAAVIVVNGMSWTWSEVCSACGCGMKRSRSTNPAPLN
               GGAFCEGQVQKTCATCLCPVDGSMSPSKWSACGLDCTHWRSECSDPAPRNGGEC
               RGADLDTNCTSDCLHTSGSPEDVALYIGLVAVAVCLILLVLLVLYCKKEGLDS
               DVADSSILTSGFQVPSIKPSKADNPHELTIQPDLSITITITTYQGSCLPRQGPSPKQL
               SNHLLSPGSGRHLHSSPTSSEADFVSRKLTQNYFRSLPRGTSNMYATFNFLGG
               RLMTPTNGISILLIPDAIPRGIYIYTLHKPEDVRLPLAGCQTLSPVSCGPPGV
               LLTPRVILMDHCEGSPDWSLRKQSCGSEMEDVHLGESPSPHLYYCOLEAGAC
               YVTEQLGRFALVGEALSVAATKRLRLLPAPVACTSLEYNIRVYCKLHLDHDAKEV
               QLEKLGQQLIQEPRVLHFVDSYHNLRLSHIDVPSSLWKSLLVSYOEIIPYHIWNGT
               QQYHCTFTLERNVASTDLACKVWVQVGDGGSFNINFTNITKDTFRFAEMLALESG
               GVPALVGPSAPKIPFLIRQKIITSLDPPCSRGADWRTLAQKHLHLDLSLSPFASKPSPT
               AMILNLWEARHPFNGLGQLAAAVAGLQPDAGLFTVSEAC"
ORIGIN
Alignment Scores: 2.82e-19 Length: 3992
Pred. No.: 290.00 Matches: 50
Score: 290.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
US-10-624-932C-2_COPY_246_295 (1-50) x MMU487852 (1-3992)
Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 967 TCGACGTGGACCGAGTGGTCCGTCTGCAGTCCAGCTGTGGCGTGGCTGCACAGCG 1026
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyAlaPheCysGluGlyGlnAsn 40
Db 1027 AGCGGAGCTGCACCAACCGGCACCTCTCAACGGGGCGCGCTTCTGTGTGGGGCAGAA 1086
```

```
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 1087 GTCCAGAAAACAGCTGCGCCACTCTGTGC 1116
RESULT 8
LOCUS          AK122575      4294 bp      mRNA      linear      ROD 15-MAR-2003
DEFINITION     Mus musculus mRNA for mKIAA1976 protein.
ACCESSION      AK122575
VERSION        AK122575.1 GI:28972881
KEYWORDS       FLI_CDNA.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
REFERENCE      1
AUTHORS        Okazaki,N., Kikuno,R., Ohara,R., Inamoto,S., Aizawa,H., Yuasa,S.,
               Nakajima,D., Nagase,T., Ohara,O. and Koga,H.
TITLE          Prediction of the coding sequences of mouse homologues of KIAA
               gene: II. The complete nucleotide sequences of 400 mouse
               KIAA-homologous cDNAs identified by screening of terminal sequences
               of cDNA clones randomly sampled from size-fractionated libraries
               DNA Res. 10, 35-48 (2003)
REFERENCE      2 (bases 1 to 4294)
AUTHORS        Okazaki,N., Kikuno,R., Nagase,T., Ohara,O. and Koga,H.
TITLE          Direct Submission
JOURNAL        Submitted (07-FEB-2003) Hisashi Koga, Kazusa DNA Research
               Institute, Laboratory for Genome Informatics; 2-6-7
               Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan
               (E-mail:mouse@kazusa.or.jp, Tel:81-438-52-3919, Fax:81-438-52-3918)
               The CREATE program supported by Japan science and technology
               corporation; cDNA full insert sequencing; Kazusa DNA Research
               Institute; cDNA library construction, clone selection and 5'- &
               3'-end one pass sequencing.
FEATURES       Location/Qualifiers
source         1..4294
               /organism="Mus musculus"
               /mol_type="mRNA"
               /db_xref="taxon:10090"
               /clone="mbh03993"
               /tissue_type="brain"
               /dev_stage="adult"
               /notes="vector:modified pBC SK+"
               1..4294
               /gene="mKIAA1976"
               /size="4294"
               /date="2003"
               /notes="CDS is predicted by in silico analysis. Start codon
               is not identified."
               /codon_start=1
               /evidence=not_experimental
               /product="mKIAA1976 protein"
               /protein_id="BAC65857.1"
               /db_xref="GI:28972882"
               /translation="SLVPIALTKTTLAASSGPEVDVALYIGLVAVAVCLILLVLLV
               LIYCRKKEGLDSVDASSIILTSQFPVSIKPSKADNPHELTIQPDLSITITTYQGSCL
               PRDQGPSKFLQKQLGQQLIQEPRVLHFVDSYHNLRLSHIDVPSSLWKSLLVSYOE
               IPYHIWNGTQQYHCTFTLERNVASTDLACKVWVQVGDGGSFNINFTNITKDTFR
               AEMLALESGVPALVGPSAPKIPFLIRQKIITSLDPPCSRGADWRTLAQKHLHLDL
               SFFASKPSPTAMILNLWEARHPFNGLGQLAAAVAGLQPDAGLFTVSEAC"
ORIGIN
Alignment Scores: 3.04e-19 Length: 4294
Pred. No.: 290.00 Matches: 50
Score: 290.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
US-10-624-932C-2_COPY_246_295 (1-50) x AK122575 (1-4294)
Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
```

```

Db      734 TCGACGTGACCGAGTGGTCCGCTGTCAGCGCCAGCTGTGGCGCGGTGGCGCAGAAACGG 793
      21 SerArgSerCysThrAsnProAlaProLeuAenGlyGlyAlaPheCysGluGlyGlnAen 40
Db      794 AGCCGGAGCTGCACCAACCGGCACCTCTCAACGGGGGGCGCTTCTGTGAGGGGGCAGAAAT 853
      41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db      854 GTCCAGAAAAACAGCTGCGCCACTCTGTGC 883

RESULT 9
AC027318 121282 bp DNA linear PRI 01-DEC-2002
LOCUS Homo sapiens chromosome 5 clone CTC-347K15, complete sequence.
AC027318
AC027318.5 GI:25989047
VERSION HTG.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 121282)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
Unpublished
2 (bases 1 to 121282)
DOE Joint Genome Institute.
TITLE
REFERENCE
AUTHORS
JOURNAL
SUBMITTED (30-MAR-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 121282)
DOE Joint Genome Institute.
TITLE
REFERENCE
AUTHORS
JOURNAL
SUBMITTED (07-MAR-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 121282)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
Unpublished
2 (bases 1 to 121282)
DOE Joint Genome Institute.
TITLE
REFERENCE
AUTHORS
JOURNAL
SUBMITTED (01-DEC-2002) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Dec 1, 2002 this sequence version replaced gi:19224786.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.1.
NOTE: Shatter libraries failed to verify number of repeat copies
13700-15000. Unsure number of repeat copies 13700-15000.
FEATURES
source
Location/Qualifiers
1..121282
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
/clone="CTC-347K15"
13700..15000
misc_feature
/note="NOTE: Shatter libraries failed to verify number of
repeat copies 13700-15000. Unsure number of repeat copies
13700-15000."

ORIGIN
Alignment Scores:
Pred. No.: 9,77e-18 Length: 121282
Score: 290.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-10-624-932C-2_COPY_246_295 (1-50) x AC027318 (1-121282)

```

```

Qy      1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db      12403 TCGACGTGACCGAGTGGTCCGCTGTCAGCGCCAGCTGTGGCGCGGTGGCGCAGAAACGG 12462
      21 SerArgSerCysThrAsnProAlaProLeuAenGlyGlyAlaPheCysGluGlyGlnAen 40
Db      12463 AGCCGGAGCTGCACCAACCGGCACCTCTCAACGGGGGGCGCTTCTGTGAGGGGGCAGAAAT 12522
      41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db      12523 GTCCAGAAAAACAGCTGCGCCACTCTGTGC 12552

RESULT 10
AC034209/c 166534 bp DNA linear HTG 18-JUL-2000
LOCUS Homo sapiens chromosome 5 clone CTC-499E20, WORKING DRAFT SEQUENCE,
12 ordered pieces.
AC034209
AC034209.3 GI:9256723
VERSION HTG; HTGS PHASE2; HTGS_DRAFT.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 166534)
DOE Joint Genome Institute.
TITLE
REFERENCE
AUTHORS
JOURNAL
SUBMITTED (05-APR-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jul 18, 2000 this sequence version replaced gi:8655958.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 376912
Center clone name: CIT-HSPC_499E20
-----
Summary Statistics
Consensus quality: 156088 bases at least Q40
Consensus quality: 162568 bases at least Q30
Consensus quality: 163999 bases at least Q20
Estimated insert size: 169000; pulse field gel estimation
Estimated insert size: 166034; sum-of-contigs estimation
Quality coverage: 8.94 in Q20 bases; pulse field gel estimation
Quality coverage: 9.1 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 12 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
1 3977: contig of 3977 bp in length
3978 4077: gap of unknown length
4078 8171: contig of 4094 bp in length
8172 8271: gap of unknown length
8272 25671: contig of 17400 bp in length
25672 25771: gap of unknown length
25772 41848: contig of 16077 bp in length
41848 41948: gap of unknown length
41948 58436: contig of 16488 bp in length
58436 58537: gap of unknown length
58537 74135: contig of 15599 bp in length
74136 74235: gap of unknown length
74236 81773: contig of 7538 bp in length

```

```

* 81774 81873: gap of unknown length
* 81874 88590: contig of 6717 bp in length
* 88591 88690: gap of unknown length
* 88691 107051: contig of 18361 bp in length
* 107052 107151: gap of unknown length
* 107152 116497: contig of 9346 bp in length
* 116498 116597: gap of unknown length
* 116598 157034: contig of 40437 bp in length
* 157035 157134: gap of unknown length
* 157135 166534: contig of 9400 bp in length.

```

FEATURES

```

source
1. 166534
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
/clones="CTC-499E20"
/clone_lib="CalTech human BAC library C"

```

ORIGIN

```

Alignment Scores:
Pred. No.: 1.36e-17 Length: 166534
Score: 290.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

```

```

US-10-624-932C-2_COPY_246_295 (1-50) x AC034209 (1-166534)

```

```

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 52704 TCGACGTGGACCGAGTGTCTGTCAGCCCGAGCTGTGGCGCGGTGCAGAAACGG 52645
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 52644 AGCCGGAGCTGCACCAACCCGCGCTCTCAACGGCGCGCTTCTGTGAGGGCAGAAAT 52585
Qy 41 ValGlnLysThrAlaCysAlaThrIleuCys 50
Db 52584 GTCCAGAAACAGCGCTGCAGCCACCTGTGC 52555

```

RESULT 11

```

AC012283/c AC012283 168168 bp DNA linear HTG 26-MAY-2000
DEFINITION Homo sapiens clone RP11-1G22, WORKING DRAFT SEQUENCE, 8 unordered
pieces.

```

```

AC012283 AC012283 2 GI:7107835
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 168168)
Birken, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens, clone RP11-1G22
Unpublished
2 (bases 1 to 168168)
Birken, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
Baldwin, J., Barna, N., Beckerly, R., Boguslavskiy, L., Boukhalter, B.,
Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,
Cooke, P., Dearellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,
Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D.,
Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N.,
McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrum, J.,
Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,
Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Teshaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,
Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.

```

TITLE

JOURNAL

COMMENT

```

Direct Submission
Submitted (22-OCT-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Feb 28, 2000 this sequence version replaced gi:6094590.
All repeats were identified using RepeatMasker:
Snitt, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center project name: L2487
Center clone name: 1_G22
----- Summary Statistics
Sequencing vector: M13; M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 125212 bases at least Q40
Consensus quality: 145318 bases at least Q30
Consensus quality: 159522 bases at least Q20
Insert size: 170000; agarose-fp
Quality coverage: 167468; sum-of-contigs
Quality coverage: 4.2 in Q20 bases; agarose-fp
Quality coverage: 4.2 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

```

FEATURES

source

```

1. 168168
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="RP11-1G22"
/clone_lib="RPC1-11 Human Male BAC"
1. 1018
/notes="assembly_fragment"
1119. 3720
/notes="assembly_fragment"
3821. 6477
/notes="assembly_fragment"
6578. 23880
/notes="assembly_fragment"
23981. 47755
/notes="assembly_fragment"
clone end:T7
vector_side:right"
47856. 86463
/notes="assembly_fragment"
86564. 127504
/notes="assembly_fragment"

```

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

```

misc_feature 127605..168168
/note="assembly_fragment
clone_end:SP6
vector_side:left"

ORIGIN
Alignment Scores:
Pred. No.:
Score: 1.37e-17 Length: 168168
290.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x AC012283 (1-168168)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 162355 TCGAGTGTGACCGAGTGTGCTGTGCAGCGCCAGCTGTGGCGCGCTGTGGCAGAAACGG 162296

Qy 21 SerArgSerCysThrAsnProAlaProLeuAenGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 162295 AGCCGGAGTGTGACCAACCGCGGCTCTCAACGGGGCGCTTCTGTGAGGGCGCAGAT 162236

Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 162235 GTCCAGAAACAGCCTGGCGCCACCCTGTGC 162206

RESULT 12
AC139592/c 231407 bp DNA linear HTG 27-MAR-2003
LOCUS Rattus norvegicus clone CH230-12014, WORKING DRAFT SEQUENCE, 54
DEFINITION unorderded pieces.
ACCESSION AC139592
VERSION AC139592.2 GI:28269340
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
1 (bases 1 to 231407)
Murny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Albrooks,S., Amin,A., Anguiano,D.,
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,P.,
Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
Gebregorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
Gunaratne,P., Hagland,W., Hamil,C., Hamilton,C., Hamilton,K.,
Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,
Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
Kovis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
Lorenshewa,L., Loulseghe,H., Lozada,R.J., Lu,X., Ma,J.,
Maheshwari,M., Mahindaratne,M., Mahmoud,M., Malloy,K., Mangum,A.,
Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
Mawhiney,S., McLeod,M., McNeill,T., Meenen,E., Milosavljevic,A.,
Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K.,
Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D.,
Newton,N., Nguyen,N., Norris,S., Nwaokemele,O., Okwuonu,G.,

```

```

Olarnpungagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H.,
Perez,A., Perez,L., Pfannkoch,C., Plopper,F., Poindexter,A.,
Popovic,D., Primus,E., Pu,L.-L., Puazo,M., Quiroz,J., Rachlin,A.,
Reaves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y.,
Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A.,
Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S.,
Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartbeyn,A.,
Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E.,
Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A.,
Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S.,
Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D.,
Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J.,
Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wlaczek,R.,
Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S.,
Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X.,
Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R.,
Holt,R.A., Smith,H.O., Weinstein,G. and Gibbs,R.A.
Direct Submission
Unpublished
2 (bases 1 to 231407)
Worley,K.C.
Direct Submission
Submitted (06-FEB-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 231407)
Worley,K.C.
Direct Submission
Submitted (27-MAR-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Feb 7, 2003 this sequence version replaced gi:28261442.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: KDPU
Center clone name: CH230-12014
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 199497 bases at least Q40
Consensus quality: 205776 bases at least Q30
Consensus quality: 210022 bases at least Q20
Estimated insert size: 207384; sum-of-ctnigs estimation
Quality coverage: 3x in Q20 bases; sum-of-ctnigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 54 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1011: contig of 1011 bp in length
* 1012 1111: gap of unknown length
* 1112 2158: contig of 1047 bp in length
* 2159 2258: gap of unknown length
* 2259 3347: contig of 1089 bp in length
* 3348 3447: gap of unknown length
* 3448 4572: contig of 1125 bp in length
* 4573 5908: contig of 1236 bp in length
* 5909 6008: gap of unknown length
* 6009 7270: contig of 1262 bp in length
* 7271 7370: gap of unknown length
* 7371 8483: contig of 1113 bp in length

```


TITLE
JOURNALREFERENCE
AUTHORS

Direct Submission
Submitted (01-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 242128)
Birren,B., Nuebaum,C., Lander,B., Abouelleil,A., Allen,N., Anderson,M., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y., Collumore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S., Graham,L., Grand-Pierre,N., Hafez,N., Hegopian,D., Hagos,B., Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kanat,A., Karatas,A., Kelle,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,X., Lui,A., Mabbitt,R., MacLean,C., MacDonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M., Melidrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Schauer,S., Schuback,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M., Talamas,J., Testave,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission
Submitted (09-MAR-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 9, 2004 this sequence version replaced gi:28933837.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L26431
Center clone name: 335_A_11

TITLE
JOURNAL

COMMENT

* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 80291: contig of 80291 bp in length
* 80292 80391: gap of 100 bp
* 80392 105410: contig of 25019 bp in length
* 105411 105510: gap of 100 bp
* 105511 172822: contig of 67412 bp in length
* 172923 173022: gap of 100 bp
* 173023 182093: contig of 9071 bp in length
* 182094 182193: gap of 100 bp
* 182194 207358: contig of 25165 bp in length
* 207359 207458: gap of 100 bp
* 207459 222746: contig of 15288 bp in length
* 222747 222846: gap of 100 bp
* 222847 242128: contig of 19282 bp in length.

FEATURES
source

1..242128
/organism="Mus musculus"
/mol_type="Genomic DNA"
/db_xref="taxon:10090"
/chromosome="13"
/map="13"
/clone="RP23-335A11"
/clone_lib="RPC1-23 Female Mouse BAC"

ORIGIN

Alignment Scores:

Pred. No.: 2e-17 Length: 242128
Score: 290.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-624-932c-2_COPY_246_295 (1-50) x AC123700 (1-242128)

Qy 1 SerThrTrrpThrGluTrrpSerValCysSerAlaSerCysGlyArgGlyTrrpGlnLysArg 20

Db 150663 TCGACGTGGACCGAGTGGTCCGTCTGCAGTCCACAGCTGTGGCGGTGGCGGACGGAACGG 150604

Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40

Db 150603 AGCCGGAGTGCACCAACCGCGACCTCTCAACGGGGCGCTTCTGTGAGGGGCAGAAAT 150544

Qy 41 ValGlnLysThrAlaCysAlaThrIleuCys 50

Db 150543 GTCCAGAAAACAGCGCTGCCCACTCTGTGC 150514

RESULT 14

BC041156

LOCUS

DEFINITION

Homo sapiens unc-5 homolog C (C. elegans), mRNA (cDNA clone

MGC:48696 IMAGE:5208108), complete cds.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 2270)

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,

Klausner,R.D., Collins,F.S., Wagner,J., Shenmen,C.M., Schuler,G.D.,

Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,

Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,

Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,

Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,

Scheetz,T.E., Brownstein,M.J., Udín,T.B., Toshiyuki,S.,

Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,

Abramson,K.D., Mullahy,S.J., Bosak,S.A., McGowan,P.J.,

McKernan,R.J., Malek,J.A., Gunaratne,P.H., Richards,S.,

Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,

Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,

Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S.,

Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shevchenko,Y.,

Bohuffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,

Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,

Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,

Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257

12477932

2 (bases 1 to 2270)

Strausberg,R.

Direct Submission

Submitted (16-DEC-2002) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapsb-re@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Institute for Systems Biology

<http://www.systemsbio.org>

contact: amadan@systemsbiology.org

REMARK

COMMENT

Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteaman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK plate: 84 Row: d Column: 5
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 16933524.

FEATURES

Location/Qualifiers
1. .2270
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:48696 IMAGE:5208108"
/tissue_type="Lung, Spleen, fetal, pooled"
/clone_lib="NIH MGC_122"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
1. .2270
/gene="UNC5C"
/note="synonym: UNC5H3"
/db_xref="LocusID:8633"
/db_xref="MIM:603610"
350. .2143
/gene="UNC5C"
/codon_start=1
/product="UNC5C protein"
/protein_id="AAH41156.1"
/db_xref="GI:27370705"
/db_xref="LocusID:8633"
/db_xref="MIM:603610"
/translation="MRKLRTARACGLGLYLLOMLVLPALALLSASGTSGSAQDDDD
FFHLEPTFFSDPEPLPHELIPEERAYIVKKEVNLKYKASPATQIYFKCNSEWHQ
KDHIVDRVDETSGLIVREVSIEISRQOVBEFGPDYWCOCVAMSGAGTTKRRKAY
RIAYLRFTFPEGLPQLEQVLELLQCPPEGIPVAEVLKNEIDIDPVDNRNFI
IIDHNLIIKQALSDTANYTCVAKNIIVAKRSTTATVIVYNGWSTWTSVNCNSRC
GRGQKTRTCTNPAINGGAFCEGQSVOKIACITLCPVDGRTPWKSQTCGTECTH
WRRECTAPAPKNGKDCGLVLQKNCITDGLCMQSFYPISTEQRTONRYGSSAPD
SDDVALYGVIVIAVLCIASVVVALFVYRKNHRDPESDIIDSSALNGGQFPQNIKAA
RQDLUAVPPDLTSAAMRGVYALHDVSDKIPMTNSPILDPNLKIKVNTSGAVT
PQDLSLSEFTKSLSPQTSLENEALSILKNQSLARQTDPSCTAFGFSNLSLGGHLIVPN
SGVSLIIPAGAIPQGRVYEMVTVHRKETWR"
866. .1123
/gene="UNC5C"
/note="IG; Region: Immunoglobulin"
/db_xref="CDD:smart00409"
1136. .1291
/gene="UNC5C"
/note="TSPI; Region: Thrombospondin type 1 repeats"
/db_xref="CDD:smart00209"
1304. .1450
/gene="UNC5C"
/note="TSPI; Region: Thrombospondin type 1 repeats"
/db_xref="CDD:smart00209"
1988. .2140
/gene="UNC5C"
/note="ZUS; Region: Domain present in ZO-1 and Unc5-like
netrin receptors"
/db_xref="CDD:smart00218"

ORIGIN

Alignment Scores:
Pred. No.: 1.99e-15 Length: 2270
Score: 249.00 Matches: 41
Percent Similarity: 94.00% Conservative: 6
Best Local Similarity: 82.00% Mismatches: 3
Query Match: 85.86% Indels: 0
DB: 9 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x BC041156 (1-2270)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
|||||

Db 1139 TCCACCTGGAGCGAGTGTCTGTGTAAACAGCGCTGTGGACGAGGGTATCAGAAACGT 1198
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
:::|||||
Db 1199 ACAAGGACTTGTACCAACCGCGACCACTCAATGGGGTGCTTCTGTGAAGGCGAGGT 1258
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
|||||
Db 1259 GTGCAGAAAATAGCCTGTACTACGTTATGC 1288

RESULT 15

LOCUS CO881064 2612 bp DNA linear PAT 11-OCT-2004
DEFINITION Sequence 13 from Patent WO2004083371.
ACCESSION CO881064
VERSION CO881064.1 GI:54034173
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE

1 Dahl,N.
AUTHORS
TITLE Genes associated with obesity and methods for using the same
JOURNAL Patent: WO 2004083371-A 13 30-SEP-2004;
Astrazeneca AB (SE)

FEATURES

source
1. .2612
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores:
Pred. No.: 2.3e-15 Length: 2612
Score: 249.00 Matches: 41
Percent Similarity: 94.00% Conservative: 6
Best Local Similarity: 82.00% Mismatches: 3
Query Match: 85.86% Indels: 0
DB: 6 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x CO881064 (1-2612)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
|||||
Db 790 TCCACCTGGAGCGAGTGTCTGTGTAAACAGCGCTGTGGACGAGGGTATCAGAAACGT 849
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
:::|||||
Db 850 ACAAGGACTTGTACCAACCGCGACCACTCAATGGGGTGCTTCTGTGAAGGCGAGGT 909

Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
|||||
Db 910 GTGCAGAAAATAGCCTGTACTACGTTATGC 939

Search completed: September 9, 2005, 09:41:08
Job time : 2156.73 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 8, 2005, 20:54:46 ; Search time 258.585 Seconds
(without alignments)
1144.643 Million cell updates/sec

Title: US-10-624-932C-2_COPY_246_295

Perfect score: 290

Sequence: 1 STWTSMVCSASCRGWQKX.....NGGAFCEQNVQKATATLC 50

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool_h/US10624932/runat_08092005_161705_15766/app_query.fasta_1.1386
-DB=N_Geneseq -QFT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNIT8=bits -START=1 -END=1 -MATRIX=BLOSUM62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10624932 @CGN 1 1 1052 @runat_08092005_161705_15766 -NCPU=6 -ICPU=3
-NO_MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_16Dec04:*

1: geneseq1980s:*

2: geneseq1990s:*

3: geneseq2000s:*

4: geneseq2001as:*

5: geneseq2001bs:*

6: geneseq2002as:*

7: geneseq2002bs:*

8: geneseq2003as:*

9: geneseq2003bs:*

10: geneseq2003cs:*

11: geneseq2003ds:*

12: geneseq2004as:*

13: geneseq2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	290	100.0	1002	12 ADH71619	Adh71619 Human gen
2	290	100.0	1009	12 ADH71613	Adh71613 Human gen
3	290	100.0	2697	6 AAS16843	Aas16843 Rat netri
4	290	100.0	2697	6 ABK52891	Abk52891 Human net
5	290	100.0	2752	6 ABK37922	Abk37922 cdna encod

6	290	100.0	2752	12	ADH71617	Adh71617 Human gen
7	290	100.0	2907	4	AAK52261	Aak52261 Human pol
8	290	100.0	3014	2	AAV52940	Aav52940 Rat UNC-5
9	249	85.9	2612	13	ADR99261	Adr99261 Splice va
10	249	85.9	2780	13	ADR99251	Adr99251 Human sRO
11	249	85.9	2796	10	AAL56266	Aal56266 Human thr
12	249	85.9	2986	13	ADR99249	Adr99249 Human lRO
13	249	85.9	3646	5	AA575738	Aa575738 DNA encod
14	249	85.9	3646	13	ADR99257	Adr99257 Human unc
15	243	83.8	993	12	ADH71611	Adh71611 Human gen
16	243	83.8	2880	12	ADH71633	Adh71633 Human gen
17	243	83.8	2881	6	ABK49422	Abk49422 DNA encod
18	243	83.8	2881	10	ADG42568	Adg42568 Novel hum
19	243	83.8	2881	12	ADH71649	Adh71649 Human gen
20	243	83.8	2881	12	ADH71635	Adh71635 Human gen
21	243	83.8	2881	12	ADH71637	Adh71637 Human gen
22	243	83.8	2881	12	ADH71641	Adh71641 Human gen
23	243	83.8	2881	12	ADH71609	Adh71609 Human gen
24	243	83.8	2881	12	ADH71629	Adh71629 Human gen
25	243	83.8	2881	12	ADH71631	Adh71631 Human gen
26	243	83.8	2881	12	ADH71645	Adh71645 Human gen
27	243	83.8	2881	12	ADH71627	Adh71627 Human gen
28	243	83.8	2881	12	ADH71639	Adh71639 Human gen
29	243	83.8	2881	12	ADH71643	Adh71643 Human gen
30	243	83.8	2881	12	ADH71625	Adh71625 Human gen
31	243	83.8	2881	12	ADH71647	Adh71647 Human gen
32	239	82.4	168	10	ADC77399	Adc77399 Human tra
33	239	82.4	2181	8	ABX70460	Abx70460 DNA encod
34	239	82.4	2181	12	ADL24072	Adl24072 Human NOV
35	239	82.4	2585	12	ADQ63623	Adq63623 Novel hum
36	239	82.4	2661	10	ADQ77421	Adq77421 Human tra
37	239	82.4	2860	6	ABT06279	Abt06279 Human NOV
38	239	82.4	2860	6	ABT06280	Abt06280 Human NOV
39	239	82.4	2868	10	ADC77423	Adc77423 Human tra
40	239	82.4	2895	6	ABQ93898	Abq93898 Human tra
41	239	82.4	2898	8	ABX70459	Abx70459 DNA encod
42	239	82.4	2898	12	ADL24070	Adl24070 Human NOV
43	239	82.4	2979	10	ABX17909	Abx17909 cdna encod
44	239	82.4	2995	6	ABK92062	Abk92062 DNA encod
45	239	82.4	3501	11	ADN39805	Adn39805 Cancer/an

ALIGNMENTS

RESULT 1	
ADH71619	
ID	ADH71619 standard; DNA; 1002 BP.
XX	
AC	ADH71619;
XX	
DT	25-MAR-2004 (first entry)
XX	
DE	Human gene of the invention NOV21f SEQ ID NO:515.
XX	
KW	ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW	anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;
KW	vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW	obesity; diabetes; infectious disease; metabolic syndrome X;
XX	dyslipidaemia.
OS	Homo sapiens.
XX	
PN	WO2003102155-A2.
XX	
PD	11-DEC-2003.
XX	
PF	03-JUN-2003; 2003WO-US017430.
XX	
PR	03-JUN-2002; 2002US-0385120P.
PR	04-JUN-2002; 2002US-0385784P.
PR	05-JUN-2002; 2002US-0386041P.
PR	05-JUN-2002; 2002US-0386047P.
PR	06-JUN-2002; 2002US-0386376P.

```
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 06-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-0386796P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387282P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 10-JUN-2002; 2002US-0387535P.
PR 10-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390066P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
PR
PR
XX PA (CURA-) CURAGEN CORP.

XX 06-JUN-2002; 2002US-0386453P.
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Eitenberg S, Gangoli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, McDougall JR;
PI MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigaru M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;
XX WPI; 2004-081935/08.
DR P-PSDB; ADH71620.
DR
XX
PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
PS Example 21; SEQ ID NO 515; 1880pp; English.
XX
CC The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.
XX
SQ Sequence 1002 BP; 193 A; 311 C; 335 G; 163 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.27e-21 Length: 1002
Score: 290.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x ADH71619 (1-1002)
Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 667 TCGAGGTGGACCGAGTGTCCGTCTGCAGCGCCAGCTGTGGCGCGCTGGCAGAAACGG 726
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 727 AGCCGGAGCTGCACCAACCCGCGCCCTCTCAACGGGGCGCTTCTCTGTGAGGGCGAGAAT 786
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 787 GTCCAGAAAACAGCTGCGCACCCCTGTGC 816

RESULT 2
ADH71613
ID ADH71613 standard; DNA; 1009 BP.
XX
AC ADH71613;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human gene of the invention NOV21c SEQ ID NO:509.
XX
ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
```



```
Db      791 GTCCAGAAAACAGCTGCGCCACCTGTGC 820
|||||
RESULT 3
AAS16843 ID AAS16843 standard; cDNA; 2697 BP.
XX
AC AAS16843;
XX
DT 14-FEB-2002 (first entry)
XX
DE Rat netrin receptor UNC5H1 (YSG7) cDNA.
XX
KW YSG; YSG7; schizophrenia; chronic animal model; LCGU; netrin receptor;
KW local cerebral glucose utilisation; phosphodiesterase 1-alpha; UNC5H1;
KW calcium-independent alpha-latrotoxin receptor; CIRL; trkE; synapsin 1A;
KW epithelial discoidin domain receptor 1; synapsin 1B; neuroleptic; ss;
KW tumour necrosis factor alpha; TNF-alpha; rat.
XX
OS Rattus sp.
XX
FH Key Location/Qualifiers
FT CDS 1..2697
FT /tag= a
FT /product= "Rat netrin receptor UNC5H1"
XX
XX WO200175440-A2.
XX
XX 11-OCT-2001.
XX
XX 02-APR-2001; 2001WO-GB001486.
XX
XX 31-MAR-2000; 2000GB-00007880.
XX 26-MAY-2000; 2000GB-00012768.
XX (WELF-) WELFIDE CORP.
XX
XX Cochran S, Paterson G, Ohashi Y, Morris B, Pratt J;
XX WPI; 2002-010813/01.
XX P-PSDB; AAU10543.
XX
XX Novel chronic animal model of schizophrenia, useful for identifying anti-
XX psychotic drugs and genes that are associated with schizophrenia.
XX
XX Claim 1; Fig 8a; 79pp; English.
XX
XX The invention relates to YSG polynucleotide fragments for use in
XX diagnosing and/or developing treatments for schizophrenia using chronic
XX animal models. The polynucleotides and their encoded polypeptides are
XX used for identification of compounds which modulate the expression of YSG
XX molecules, leading to the manufacture of schizophrenia medications. The
XX sequences can also be used for testing candidate compounds for any effect
XX on the polypeptides. Anti-schizophrenic effects of a compound can be
XX determined by measuring local cerebral glucose utilisation (LCGU) or
XX comparing its expression level with that of a control group. The
XX sequences are useful in the identification of genes associated with
XX schizophrenic states and in the development of an antibody. The sequences
XX of the invention include phosphodiesterase 1-alpha, calcium-independent
XX alpha-latrotoxin receptors (CIRL)-1.2&3, epithelial discoidin domain
XX receptor 1 (trkE), netrin receptor (UNC5H1), synapsin 1A and AB and
XX tumour necrosis factor (TNF) alpha. This sequence represents rat netrin
XX receptor UNC5H1 (YSG7) DNA
XX
SQ Sequence 2697 BP; 541 A; 864 C; 766 G; 526 T; 0 U; 0 Other;

Alignment Scores:
Pred. No. : 4.12e-21 Length: 2697
Score: 290.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
```

```
US-10-624-932C-2_COPY_246_295 (1-50) x AAS16843 (1-2697)
Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 736 TCGACGTGGACTGAGTGGTCCGTCCTGCAGCGCCAGCTGTGGCGTGGCTGCAGAAACGG 795
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 796 AGCCGGAGCTGCACCAACCCGGCACCTCTCAACGGGGGGCGCTTCTGTGAGGGGCAGAA 855
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 856 GTCCAGAAAACAGCTGCGCCACTCTGTGC 895
RESULT 4
ABK52891 ID ABK52891 standard; DNA; 2697 BP.
XX
AC ABK52891;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human netrin binding membrane receptor UNC5H-1 DNA sequence #1.
XX
KW Netrin binding membrane receptor; receptor; UNC5H-1; gene; ds; human;
KW neurotropic; neuroprotective; cytostatic; antiparkinsonian;
KW cerebrotective; cancer; central nervous system; CNS; stroke;
KW Parkinson's disease; multiple sclerosis; Alzheimer's disease.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..2697
FT /tag= a
FT /product= "Netrin binding membrane receptor UNC5H-1"
XX
XX WO200233080-A2.
XX
XX 25-APR-2002.
XX
XX 15-OCT-2001; 2001WO-EP011891.
XX 16-OCT-2000; 2000US-0240061P.
XX (FARB ) BAYER AG.
XX
XX Koshler RH;
XX WPI; 2002-463314/49.
XX P-PSDB; AAU97899.
XX
XX Novel human netrin binding membrane receptor polypeptide and
XX polynucleotides for identifying modulating agents useful in treating
XX diseases e.g. Parkinson's disease, multiple sclerosis, stroke,
XX Alzheimer's disease.
XX
XX Claim 1; Fig 1; 94pp; English.
XX
XX This invention relates to the DNA and protein sequences of a novel
XX purified human netrin binding membrane receptor, UNC5H-1. The DNA
XX sequence of the invention is useful as a probe for detecting a nucleic
XX acid encoding the UNC5H-1 protein in a biological sample. The sequences
XX of the invention are useful to screen for agents which decrease the
XX activity of the UNC5H-1 protein. The sequences are also useful for
XX screening agents which regulate (modulate) the activity of the protein of
XX the invention. A pharmaceutical composition containing the protein of the
XX invention or a reagent that modulates the activity of the UNC5H-1 protein
XX may be useful for treating a UNC5H-1 dysfunction related disease such as
XX cancer or a central nervous system (CNS) disorders (e.g. Parkinson's
XX disease, multiple sclerosis, stroke and Alzheimer's disease). Fusion
XX proteins comprising the UNC5H-1 protein are useful for generating
XX antibodies and for in various assay systems, and the protein can be used
```

CC as a bait protein in a two-hybrid assay or three-hybrid assay. The method
CC of the invention is useful for detecting a coding sequence for the UNC5H-
CC 1 protein. The present sequence represents a DNA sequence encoding the
CC human netrin binding membrane receptor UNC5H-1 protein of the invention
XX
SQ Sequence 2697 BP; 503 A; 906 C; 807 G; 481 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.12e-21 Length: 2697
Score: 290.00 Matches: 50
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x ABK52891 (1-2697)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 736 TCGACGTGGACCGAGTGGTCCGTCTGCAGCCGACGCTGTGGCGCGGTGGCAGAAACGG 795
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyClnAsn 40
Db 796 AGCCGGAGCTGCACCAACCCGGCGCTCTCAACGGGGCGCTTTCTGTGGGGGCGAGAAT 855
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 856 GTCCAGAAAACAGCTGCGCCACCTGTGTC 885

RESULT 5

ABK37922
ID ABK37922 standard; cDNA; 2752 BP.

AC ABK37922;

DT 21-MAY-2002 (first entry)

XX cDNA encoding Human protein NOV1.

XX Human; NOVX; ss; gene; cardiomyopathy; atherosclerosis; diabetes;
KW cell signal processing disorder; metabolic disorder; obesity; infection;
KW anorexia; cancer-associated cachexia; cancer; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorders; dyslipidaemia; pain; asthma; hypertension;
KW osteoporosis; Crohn's disease; multiple sclerosis; angina pectoris;
KW myocardial infarction; ulcer; allergy; benign prostatic hypertrophy;
KW psychosis; neurological disorder; anxiety; schizophrenia;
KW manic depression; dementia; dyskinesia; Huntington's disease;
KW Gilles de la Tourette's syndrome; gene therapy.

XX Homo sapiens.

XX WO2000210216-A2.

XX 07-FEB-2002.

XX 30-JUL-2001; 2001WO-US024225.

XX 28-JUL-2000; 2000US-0221409P.

XX 04-AUG-2000; 2000US-0222840P.

XX 04-AUG-2000; 2000US-0223752P.

XX 04-AUG-2000; 2000US-0223762P.

XX 04-AUG-2000; 2000US-0223769P.

XX 04-AUG-2000; 2000US-0223770P.

XX 14-AUG-2000; 2000US-0225146P.

XX 15-AUG-2000; 2000US-0225392P.

XX 15-AUG-2000; 2000US-0225470P.

XX 16-AUG-2000; 2000US-0225697P.

XX 01-FEB-2001; 2001US-0263662P.

XX 05-APR-2001; 2001US-0281645P.

XX (CURA-) CURAGEN CORP.

XX PA

PI Padigaru M, Mezes P, Mishra V, Burgess C, Casman S, Grosse WM;
PI Alsobrook JP, Lopley DM, Gerlach VL, Macdougall JR, Smithson G;
XX
DR WPI: 2002-180074/23.
DR P-PSDB; AU85403.

XX New isolated cytoplasmic, nuclear, membrane bound, or secreted
PT polypeptide, useful for treating cardiomyopathy, atherosclerosis,
PT infections, cancer, neurodegenerative, metabolic, hematopoietic and
PT immune disorders.

PS Claim 9; Page 9-10; 213pp; English.

XX The invention relates to an isolated cytoplasmic, nuclear, membrane
CC bound, or secreted polypeptide (NOVX, x= 1-14) their variants or mature
CC form. Also included are the nucleic acids encoding the NOVX proteins, a
CC vector comprising the nucleic acid, a cell comprising the vector, an anti
CC -NOVX antibody and modulators of NOVX. NOVX, the nucleic acid and the
CC antibody are useful for treating or preventing a NOVX-associated
CC disorder, where the disorder is selected from cardiomyopathy,
CC atherosclerosis, diabetes, a disorder related to cell signal processing
CC and metabolic pathway modulation, metabolic disorders, obesity,
CC infectious disease, anorexia, cancer-associated cachexia, cancer,
CC neurodegenerative disorders, Alzheimer's disease, Parkinson's disease,
CC immune disorders, haematopoietic disorders, and the various
CC dyslipidaemias, metabolic disturbances associated with obesity, the
CC metabolic syndrome X and wasting disorders associated with chronic
CC diseases, bacterial, fungal, protozoal and viral infections, pain,
CC bulimia, asthma, hypertension, urinary retention, osteoporosis, angina
CC disease, multiple sclerosis, Albright Hereditary Osteodystrophy, angina
CC pectoris, myocardial infarction, ulcer, allergy, benign prostatic
CC hypertrophy, and psychotic and neurological disorders, including anxiety,
CC schizophrenia, manic depression, delirium, dementia, and dyskinesias,
CC such as Huntington's disease and Gilles de la Tourette's syndrome. The
CC nucleic acid is useful in gene therapy. The present sequence encodes a
CC NOVX protein

XX SQ Sequence 2752 BP; 505 A; 937 C; 829 G; 481 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4.22e-21 Length: 2752
Score: 290.00 Matches: 50
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x ABK37922 (1-2752)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 781 TCGACGTGGACCGAGTGGTCCGTCTGCAGCCGACGCTGTGGCGCGGTGGCAGAAACGG 840

Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyClnAsn 40
Db 841 AGCCGGAGCTGCACCAACCCGGCGCTCTCAACGGGGCGCTTTCTGTGGGGGCGAGAAT 900

Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50

Db 901 GTCCAGAAAACAGCTGCGCCACCTGTGTC 930

RESULT 6

ADH71617

ID ADH71617 standard; DNA; 2752 BP.

XX ADH71617;

AC ADH71617;

XX 25-MAR-2004 (first entry)

XX Human gene of the invention NOV21e SEQ ID NO:513.

XX ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;

XX anorectic; antidiabetic; antimicrobial; gene therapy;

KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.

XX OS Homo sapiens.

XX PN WO2003102155-A2.

XX PD 11-DEC-2003.

XX PF 03--JUN-2003; 2003WO-US017430.

XX PX 03--JUN-2002; 2002US-0385120P.

PR 04--JUN-2002; 2002US-0385784P.

PR 05--JUN-2002; 2002US-0386041P.

PR 06--JUN-2002; 2002US-0386376P.

PR 06--JUN-2002; 2002US-0386453P.

PR 06--JUN-2002; 2002US-0386864P.

PR 07--JUN-2002; 2002US-0387016P.

PR 07--JUN-2002; 2002US-0386931P.

PR 07--JUN-2002; 2002US-0386942P.

PR 07--JUN-2002; 2002US-0386971P.

PR 07--JUN-2002; 2002US-0387262P.

PR 08--JUN-2002; 2002US-0236960P.

PR 10--JUN-2002; 2002US-0387400P.

PR 10--JUN-2002; 2002US-0387535P.

PR 11--JUN-2002; 2002US-0387610P.

PR 11--JUN-2002; 2002US-0387625P.

PR 11--JUN-2002; 2002US-0387634P.

PR 11--JUN-2002; 2002US-0387688P.

PR 11--JUN-2002; 2002US-0387696P.

PR 11--JUN-2002; 2002US-0387702P.

PR 11--JUN-2002; 2002US-0387836P.

PR 11--JUN-2002; 2002US-0387859P.

PR 12--JUN-2002; 2002US-0387933P.

PR 12--JUN-2002; 2002US-0387934P.

PR 12--JUN-2002; 2002US-0387960P.

PR 12--JUN-2002; 2002US-0388022P.

PR 12--JUN-2002; 2002US-0388036P.

PR 13--JUN-2002; 2002US-0389123P.

PR 14--JUN-2002; 2002US-0389118P.

PR 14--JUN-2002; 2002US-0389120P.

PR 14--JUN-2002; 2002US-0389144P.

PR 14--JUN-2002; 2002US-0389146P.

PR 17--JUN-2002; 2002US-0389729P.

PR 17--JUN-2002; 2002US-0389742P.

PR 18--JUN-2002; 2002US-0389884P.

PR 19--JUN-2002; 2002US-0390066P.

PR 19--JUN-2002; 2002US-0390209P.

PR 21--JUN-2002; 2002US-0390763P.

PR 06--AUG-2002; 2002US-0401628P.

PR 09--AUG-2002; 2002US-0402156P.

PR 09--AUG-2002; 2002US-0402256P.

PR 09--AUG-2002; 2002US-0402389P.

PR 12--AUG-2002; 2002US-0402786P.

PR 12--AUG-2002; 2002US-0402816P.

PR 12--AUG-2002; 2002US-0402821P.

PR 12--AUG-2002; 2002US-0402832P.

PR 13--AUG-2002; 2002US-0403448P.

PR 13--AUG-2002; 2002US-0403459P.

PR 13--AUG-2002; 2002US-0403531P.

PR 13--AUG-2002; 2002US-0403532P.

PR 13--AUG-2002; 2002US-0403563P.

PR 13--AUG-2002; 2002US-0406317P.

PR 15--AUG-2002; 2002US-0403617P.

PR 26--AUG-2002; 2002US-0406182P.

PR 26--AUG-2002; 2002US-0406355P.

PR 27--AUG-2002; 2002US-0406240P.

PR 12-SEP-2002; 2002US-0410084P.

PR 20-SEP-2002; 2002US-0412528P.

PR 23-SEP-2002; 2002US-0412731P.

PR 30-SEP-2002; 2002US-0414801P.

PR 30-SEP-2002; 2002US-0414839P.

PR 30-SEP-2002; 2002US-0414840P.

PR 30-SEP-2002; 2002US-0414954P.

PR 09-OCT-2002; 2002US-0417186P.

PR 23-OCT-2002; 2002US-0417406P.

PR 23-OCT-2002; 2002US-0420639P.

PR 28-OCT-2002; 2002US-0421156P.

PR 31-OCT-2002; 2002US-0422690P.

PR 01-NOV-2002; 2002US-0423330P.

PR 05-NOV-2002; 2002US-00423798.

PR 05-NOV-2002; 2002US-0423798P.

PR 12-NOV-2002; 2002US-0425453P.

XX

FA (CURA-) CURAGEN CORP.

XX

XX Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;

PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;

PI Eitenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;

PI Gusev VI, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;

PI MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;

PI Padigaru M, Patturajan M, Pena CE, Peyman JA, Raha D, Raatelli L;

PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;

PI Smithson G, Spytek KA, Stone DJ, Vernet CM, Voss EZ, Zhong M;

PI Zhong H;

XX

XX WPI; 2004-081935/08.

DR P-PSDB; ADH71618.

DR

XX

PT New NOVX polypeptides and nucleic acid molecules useful for preventing or

PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or

PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

XX

PS Example 21; SEQ ID NO 513; 1880pp; English.

XX

XX The invention relates to a novel isolated polypeptide (NOVX). A

CC polypeptide of the invention has cytostatic, immunomodulator,

CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and

CC antitumour activity, and may have a use in gene therapy, and as a

CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising

CC any of the 303 fully defined nucleotide sequences given in the

CC specification. The polypeptide is useful in the manufacture of a

CC medicament for treating a syndrome associated with a human disease. The

CC polypeptide, polynucleotide and antibody are useful in diagnosing

CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,

CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious

CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are

CC further used as hybridisation probes, in chromosome mapping, tissue

CC typing, preventive medicine, and pharmacogenomics. The present sequence

CC encodes a NOVX polypeptide of the invention.

XX

SQ Sequence 2752 BP; 505 A; 937 C; 829 G; 481 T; 0 U; 0 Other;

Alignment Scores:

Pred No.: 4.22e-21 Length: 2752
Score: 290.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x ADH71617 (1-2752)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20

Db 781 TCGACGTGGACCGAGTGGTCCGTCTGCAGGCCAGCTGTGGCGCGGTGCAGAAACGG 840

Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40

Db 841 AGCCGGAGCTGCACCAACCCGGCGCCTCTTCACGGGGGGCGCTTCTTGTGGGGGCGAGT 900


```
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 901 GTCCAGAAAACAGCTGCGCCACCCTGTGC 930

RESULT 7
AAK52261
ID AAK52261 standard; cDNA; 2907 BP.
XX
AC AAK52261;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 806.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation; ss.
XX
OS Homo sapiens.
XX
PN WO200157190-A2.
XX
FD 09-AUG-2001.
XX
PP 05-FEB-2001; 2001WO-US004098.
XX
PR 03-FEB-2000; 2000US-00496914.
XX
PR 27-APR-2000; 2000US-00560875.
XX
PR 20-JUN-2000; 2000US-00598075.
XX
PR 19-JUL-2000; 2000US-00620325.
XX
PR 01-SEP-2000; 2000US-00654936.
XX
PR 15-SEP-2000; 2000US-00663561.
XX
PR 20-OCT-2000; 2000US-00693325.
XX
PR 30-NOV-2000; 2000US-00728422.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
PI Ma Y, Zhao Q, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
WPI; 2001-476283/51.
DR P-PSDB; AAM79128.
XX
PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT in diagnosis and gene therapy.
XX
PS Claim 1; Page 2691-2694; 6221pp; English.
XX
CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity relating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication
XX
SQ Sequence 2907 BP; 552 A; 966 C; 881 G; 508 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4,51e-21 Length: 2907
Score: 290.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
```

```
US-10-624-932c-2_COPY_246_295 (1-50) x AAK52261 (1-2907)
Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyValGlyTTrpGlnLysArg 20
Db 946 TCGACGTGGACCGAGGTGCTGCTGCGAGCCGACCTGTGGCGCGCTGGCAGAACGG 1005
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 1006 AGCCGGAGCTGCACCAACCCGCGCTCTCAACGGGGCGCTTCTGTGAGGGGAGAAT 1065
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 1066 GTCCAGAAAACAGCTGCGCCACCCTGTGC 1095

RESULT 8
AAV52940
ID AAV52940 standard; cDNA; 3014 BP.
XX
AC AAV52940;
XX
DT 25-MAR-2003 (revised)
DT 21-DEC-1998 (first entry)
XX
DE Rat UNC-5 homologue unc5h-1 cDNA.
XX
KW UNC-5; UNC5H-1; rat; netrin receptor; cell migration; axon guidance;
KW diagnosis; therapy; ds.
XX
OS Rattus sp.
XX
FH Key Location/Qualifiers
FT CDS 1..2697
FT /*tag= a
XX
FN WO9837085-A1.
XX
PD 27-AUG-1998.
XX
PF 19-FEB-1998; 98WO-US003143.
XX
PR 19-FEB-1997; 97US-00808982.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PI Tessier-Lavigne M, Leonardo ED, Hinck L, Masu M, Keino-masu K;
XX
WPI; 1998-495364/42.
DR P-PSDB; AAW78898.
XX
PT Netrin-binding, vertebrate proteins - useful for diagnosis, therapy and
PT the biopharmaceutical industry.
XX
PS Claim 7; Page 15-17; 32pp; English.
XX
CC This cDNA, termed unc5h-1, comprises a rat homologue of Caenorhabditis
CC elegans unc-5. Rat unc5h-1 and unc5h-2 (see AAV52942) cDNAs were isolated
CC from an E18 brain cDNA library. The predicted proteins (see AAW78898 and
CC AAW78900) show similarity with UNC-5. They are predicted to be involved
CC in cell migration and axon guidance, and are characterised as receptor
CC proteins for netrin. Gene expression is observed in regions where
CC differentiating neurons are undergoing axogenesis. Human unc5h-1 (see
CC AAV52941) and unc5h-2 (see AAV52943) cDNAs are also claimed. Vertebrate
CC UNC-5 proteins may be produced recombinantly from transfected host cells
CC by utilising these vertebrate UNC-5 nucleic acids. The invention also
CC provides unc-5 hybridisation probes and primers, vertebrate UNC-5-
CC specific binding agents such as specific antibodies, and methods of
CC making and using the subject compositions in diagnosis (e.g. genetic
CC hybridisation screens for vertebrate unc-5 transcripts), therapy (e.g.
CC gene therapy to modulate vertebrate unc-5 gene expression) and in the
CC biopharmaceutical industry (e.g. as immunogens, reagents for modulating
CC cell guidance, reagents for screening chemical libraries for lead
CC pharmacological agents, etc.). (Updated on 25-MAR-2003 to correct PI
```

```
CC field.)
XX Sequence 3014 BP; 596 A; 977 C; 849 G; 592 T; 0 U; 0 Other;
SQ Alignment Scores:
Pred. No.: 4.7e-21 Length: 3014
Score: 290.00 Matches: 50
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x AAV52940 (1-3014)
Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 736 TCGACGTGGAGTGGTCCGCTCGCAGCCGCCAGCTGTGGCGTGGTGCGACGAAACGG 795
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 796 AGCCGGAGCTGCACCAACCCGGCACCTCTCAACGGGGCGCTTCTGTGAGGGGCAGAAAT 855
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 856 GTCCAGAAACACAGCTGCGCCACTCTGTGC 885

RESULT 9
ADR99261
ID ADR99261 standard; cDNA; 2612 BP.
XX
AC ADR99261;
DT 16-DEC-2004 (first entry)
XX
DE Splice variant human uncoordinated 5C (sUNC5C) protein encoding cDNA.
XX
KW RAR-like orphan receptor alpha 1-uncoordinated 5C; ROR-alpha-1-UNC5C;
KW ROR-alpha-5; obesity; susceptibility; anorectic; antilipaeamic;
KW antiarteriosclerotic; hepatotropic; hypotensive; antidiabetic; cardiant;
KW vasotropic; osteopathic; antiarthritic; cycostatic; gene therapy;
KW hyperlipidaemia; gene; human; ss; sUNC5C.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT CDS 1..1911
FT FT /*tag= a
FT FT /product= "Alternative splice version of human
FT FT uncoordinated 5C (UNC5C) protein"
XX
PN WO2004083371-A2.
XX
XX 30-SEP-2004.
XX
XX 16-MAR-2004; 2004WO-GB001124.
XX
XX 19-MAR-2003; 2003GB-00006185.
XX
XX (ASTR ) ASTRAZENECA AB.
XX (ASTR ) ASTRAZENECA UK LTD.
XX
XX Dahl N;
XX
XX WPI; 2004-691032/67.
XX P-PSDB; ADR99262.
XX
XX New isolated nucleic acid molecule encoding a RAR-like orphan receptor
XX alpha 1-uncoordinated 5C (RORapproximate1al-UNC5C) polypeptide, useful
XX in diagnosing or treating obesity and hyperlipidemia.
XX
XX Disclosure; SEQ ID NO 13; 96pp; English.
XX
XX The invention relates to a novel isolated nucleic acid molecule,
CC
```

```
CC comprising a nucleotide sequence having at least 65% identity to a
CC degenerate variant of a fully defined sequence of 2986, 2780 or 1821 bp
CC (ADR9249, ADR99251 or ADR99255), or the complement of nucleotide
CC sequence with ADR9249, ADR99251 or ADR99255. The invention further
CC comprises: an isolated nucleic acid molecule encoding a RAR-like orphan
CC receptor alpha 1-uncoordinated 5C (ROR-alpha-1-UNC5C) polypeptide; an
CC isolated nucleic acid molecule encoding a ROR-alpha-5 polypeptide; a
CC vector comprising any of the nucleic acid molecules as cited; a host cell
CC comprising the vector; a purified fusion polypeptide of the ROR-alpha-1-
CC UNC5C polypeptide; a purified polypeptide of the ROR-alpha-5 polypeptide;
CC a method for producing a protein comprising culturing the host cell; a
CC method for detecting a polynucleotide which encodes a ROR-alpha-1-UNC5C
CC protein; a method for detecting the presence of an obesity susceptibility
CC gene; a method for detecting the presence of a translocation junction
CC between chromosome 4 at cytoband 4q 22.3 and chromosome 15 at cytoband
CC 15q22.2; a method for identifying a test compound that modulates the
CC expression of an obesity susceptibility gene identified in said method; a
CC method for identifying a test compound that modulates the activity of an
CC obesity protein encoded by the obesity susceptibility gene identified in
CC said method; a method for treating a subject having obesity; a
CC pharmaceutical composition comprising a compound identified in the
CC previous methods, and an adjuvant, diluent or carrier; making a
CC pharmaceutical composition; a method for determining if an obesity
CC susceptibility gene identified in the appropriate method; and a method
CC for diagnosing obesity, or a susceptibility to it in a subject. The
CC isolated nucleic acid molecules and compounds of the invention have the
CC following activities: anorectic, antilipaeamic, antiarteriosclerotic,
CC hepatotropic, hypotensive, antidiabetic, cardiant, vasotropic,
CC osteopathic, antiarthritic, and cycostatic. The isolated nucleic acid
CC molecules and compounds may be used in gene therapy. The compound
CC modulating the activity of an obesity protein or the expression of an
CC obesity susceptibility gene is useful in the preparation of a medicament
CC for the treatment of obesity. The compound is also useful in treating or
CC diagnosing hyperlipidaemia, and the consequences of obesity, such as
CC arteriosclerosis, fatty liver, hypertension, diabetes, coronary heart
CC disease, stroke, gallbladder disease, osteoarthritis and cancer. This
CC polynucleotide sequence represents the gene encoding the alternative
CC splice version of the human uncoordinated 5C (UNC5C) protein of the
CC invention.
XX
SQ Sequence 2612 BP; 666 A; 675 C; 674 G; 597 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9.57e-17 Length: 2612
Score: 249.00 Matches: 41
Percent Similarity: 94.00% Conservativeness: 6
Best Local Similarity: 82.00% Mismatches: 3
Query Match: 85.86% Indels: 0
DB: 13 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x ADR99261 (1-2612)
Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 790 TCCACCTGGACGGAGTGGTCTGTGTGAACAGCGCGCTGTGGACGAGGGTATCAGAAACGT 849
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 850 ACAAGGACTTGTACCAACCCGGCACCTCTCATGGGGTGCCTTCTGTGAAGCGCAGAGT 909
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 910 GTGCAGAAATAGCTGTGCTACTACGTTATGC 939

RESULT 10
ADR99251
ID ADR99251 standard; cDNA; 2780 BP.
XX
AC ADR99251;
DT 16-DEC-2004 (first entry)
XX
XX Human sROR-alpha-1-UNC5C protein encoding cDNA.
```

XX RAR-like orphan receptor alpha 1-uncoordinated 5C; ROR-alpha-1-UNC5C;
KW ROR-alpha-5; obesity; susceptibility; anorectic; antilipemic;
KW antiarteriosclerotic; hepatotropic; hypotensive; antidiabetic; cardiant;
KW vasotropic; osteopathic; antiarthritic; cytostatic; gene therapy;
KW hyperlipidaemia; gene; human; sROR-alpha-1-UNC5C; ss.
XX Homo sapiens.
OS
XX
XX
XX
XX Key Location/Qualifiers
XX 70..2079
XX CDS /tag= a
XX /product= "Human sROR-alpha-1-UNC5C protein"
XX
XX WO2004083371-A2.
XX
XX
XX 30-SEP-2004.
XX
XX 16-MAR-2004; 2004WO-GB001124.
XX
XX 19-MAR-2003; 2003GB-00006185.
XX (ASTR) ASTRAZENECA AB.
XX (ASTR) ASTRAZENECA UK LTD.
XX
XX Dahl N;
XX
XX WPI; 2004-691032/67.
XX P-PSDB; ADR99252.
XX
XX New isolated nucleic acid molecule encoding a RAR-like orphan receptor
XX alpha 1-uncoordinated 5C (RORapproximate) polypeptide, useful
XX in diagnosing or treating obesity and hyperlipidemia.
XX
XX Claim 2; SEQ ID NO 3; 96pp; English.
XX
XX The invention relates to a novel isolated nucleic acid molecule,
XX comprising a nucleotide sequence having at least 65% identity to a
XX degenerate variant of a fully defined sequence of 2986, 2780 or 1821 bp
XX (ADR99249, ADR99251 or ADR99255), or the complement of nucleotide
XX sequence with ADR99249, ADR99251 or ADR99255. The invention further
XX comprises: an isolated nucleic acid molecule encoding a RAR-like orphan
XX receptor alpha 1-uncoordinated 5C (ROR-alpha-1-UNC5C) polypeptide; an
XX isolated nucleic acid molecule encoding a ROR-alpha-5 polypeptide; a
XX vector comprising any of the nucleic acid molecules as cited; a host cell
XX comprising the vector; a purified fusion polypeptide of the ROR-alpha-1-
XX UNC5C polypeptide; a purified polypeptide of the ROR-alpha-5 polypeptide;
XX a method for producing a protein comprising culturing the host cell; a
XX method for detecting a polynucleotide which encodes a ROR-alpha-1-UNC5C
XX protein; a method for detecting the presence of an obesity susceptibility
XX gene; a method for detecting the presence of a translocation junction
XX between chromosome 4 at cytoband 4q 22.3 and chromosome 15 at cytoband
XX 15q22.2; a method for identifying a test compound that modulates the
XX expression of an obesity susceptibility gene identified in said method; a
XX method for identifying a test compound that modulates the activity of an
XX obesity protein encoded by the obesity susceptibility gene identified in
XX said method; a method for treating a subject having obesity; a
XX pharmaceutical composition comprising a compound identified in the
XX previous methods, and an adjuvant, diluent or carrier; making a
XX pharmaceutical composition a method for determining if an obesity
XX susceptibility gene identified in the appropriate method; and a method
XX for diagnosing obesity, or a susceptibility to it in a subject. The
XX isolated nucleic acid molecules and compounds of the invention have the
XX following activities: anorectic, antilipemic, antiarteriosclerotic,
XX hepatotropic, hypotensive, antidiabetic, cardiant, vasotropic,
XX osteopathic, antiarthritic, and cytostatic. The isolated nucleic acid
XX molecules and compounds may be used in gene therapy. The compound
XX modulating the activity of an obesity protein or the expression of an
XX obesity susceptibility gene is useful in the preparation of a medicament
XX for the treatment of obesity. The compound is also useful in treating or
XX diagnosing hyperlipidaemia, and the consequences of obesity, such as
XX arteriosclerosis, fatty liver, hypertension, diabetes, coronary heart
XX disease, stroke, gallbladder disease, osteoarthritis and cancer. This

CC polynucleotide sequence represents the gene encoding the human sROR-alpha
CC -1-UNC5C protein of the invention.
XX
SQ Sequence 2780 BP; 721 A; 727 C; 712 G; 620 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1.03e-16 Length: 2780
Score: 249.00 Matches: 41
Percent Similarity: 94.00% Conservative: 6
Best Local Similarity: 82.00% Mismatches: 3
Query Match: 85.86% Indels: 0
DB: 13 Gaps: 0
US-10-624-932C-2_COPY_246_295 (1-50) x ADR99251 (1-2780)
Qy 1 SerThrTrpThrGluTyrSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 901 TCCACCTGGACGGAGTGGTCTGTGTGTAAACAGCCGCTGTGGACGAGGTATCAGAAAGT 960
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGlyGlyGlnAsn 40
Db 961 ACAAGGAGCTTGTACCAACCCGCGCACCTCAATGGGGTGGCTTCTGTGAAGGGCAGAGT 1020
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 1021 GTGCAGAAATAGCCTGTACTACCTTATGC 1050
RESULT 11
AAL56266
ID AAL56266 standard; DNA; 2796 BP.
XX
AC AAL56266;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human thrombospondin coding sequence.
XX
KW Vector; rAAV; recombinant adeno-associated viral vector;
KW anti-angiogenesis; PEDF; angiogenesis; eye disorder; blindness;
KW retinal degeneration; macular degeneration; neovascularisation;
KW ophthalmological; gene; ds.
XX
OS Homo sapiens.
XX
XX WO2003080648-A2.
XX
XX 02-OCT-2003.
XX
XX 20-MAR-2003; 2003WO-US008667.
XX
XX 20-MAR-2002; 2002US-0366114P.
XX
XX (UYFL) UNIV FLORIDA RES FOUND INC.
XX (UYJO) UNIV JOHNS HOPKINS.
XX
XX Hauswirth WW, Campochiaro PA, Berns KI;
XX WPI; 2003-779243/73.
XX P-PSDB; ABU64297.
XX
XX Novel adeno-associated viral vector comprising polynucleotide encoding
XX pigment epithelium-derived factor, useful for treating choroidal
XX neovascularization, blindness, loss of vision.
XX
XX Claim 19; Page 44-45; Opp; English.
XX
XX The present invention relates to an adeno-associated viral (AAV) vector
XX comprising a polynucleotide that comprises a nucleic acid segment that
XX encodes a choroidal or ocular neovascularisation inhibitory polypeptide
XX operably linked to a promoter that expresses the segment to produce the
XX polypeptide in a selected mammalian host cell. Such a vector is useful
XX for providing a choroidal or ocular neovascularisation inhibitory
XX polypeptide to a mammal, for use in the therapy of ocular

CC neovascularisation, choroidal neovascularisation, retinal
CC neovascularisation, age-related macular degeneration, visual impairment,
CC ocular dysfunction, loss of vision, retinopathy, or blindness in a human.
CC The present sequence is a gene shown in the exemplification of the
CC invention

XX SQ Sequence 2796 BP; 708 A; 734 C; 726 G; 628 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.04e-16 Length: 2796
Score: 249.00 Matches: 41
Percent Similarity: 94.00% Conservative: 6
Best Local Similarity: 82.00% Mismatches: 3
Query Match: 85.86% Indels: 0
DB: 10 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x AAL56266 (1-2796)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 790 TCCACCTGGACGGAGTGTCTGTGTGTACAGCCGCTGTGGACGAGGTATCAGAAACGT 849

Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 850 ACAAGGACTTGTACCAACCCGGCACCCTCAATGGGGTGCCTTCTGTGAAGGCGCAGAGT 909

Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 910 GTGCAGAAATAGCCTGTACTACGTTATGC 939

RESULT 12

ID ADR99249 standard; cDNA; 2986 BP.

XX AC ADR99249;

XX DT 16-DEC-2004 (first entry)

XX DE Human 1ROR-alpha-1-UNC5C protein encoding cDNA.

XX KW RAR-like orphan receptor alpha 1-unc5c protein encoding cDNA;
KW ROR-alpha-5; obesity; susceptibility; anorectic; antilipemic;
KW antiarteriosclerotic; hepatotropic; hypotensive; antidiabetic; cardiant;
KW vasotropic; osteopathic; antiarthritic; cyostatic; gene therapy;
KW hyperlipidaemia; Gene; human; 1ROR-alpha-1-UNC5C; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT CDS 70..2964

FT /tag= a

FT /product= "Human 1ROR-alpha-1-UNC5C protein"

XX WO2004083371-A2.

XX PD 30-SEP-2004.

XX PF 16-MAR-2004; 2004WO-GB001124.

XX PR 19-MAR-2003; 2003GB-00006185.

XX PA (ASTR) ASTRAZENECA AB.

XX PA (ASTR) ASTRAZENECA UK LTD.

XX PI Dahl N;

XX WPI; 2004-691032/67.

XX DR P-PSDB; ADR99250.

XX New isolated nucleic acid molecule encoding a RAR-like orphan receptor

XX PT alpha 1-unc5c protein encoding a RAR-like orphan receptor

XX PT in diagnosing or treating obesity and hyperlipidemia.

PS Claim 2; SEQ ID NO 1; 96pp; English.

XX The invention relates to a novel isolated nucleic acid molecule, a
CC comprising a nucleotide sequence having at least 65% identity to a
CC degenerate variant of a fully defined sequence of 2986, 2780 or 1821 bp
CC (ADR99249, ADR99251 or ADR99255), or the complement of nucleotide
CC sequence with ADR99249, ADR99251 or ADR99255. The invention further
CC comprises an isolated nucleic acid molecule encoding a RAR-like orphan
CC receptor alpha 1-unc5c protein (ROR-alpha-1-UNC5C) polypeptide; an
CC isolated nucleic acid molecule encoding a ROR-alpha-5 polypeptide; a
CC vector comprising any of the nucleic acid molecules as cited; a host cell
CC comprising the vector; a purified fusion polypeptide of the ROR-alpha-1-
CC UNC5C polypeptide; a purified polypeptide of the ROR-alpha-5 polypeptide;
CC a method for producing a protein comprising culturing the host cell; a
CC method for detecting a polynucleotide which encodes a ROR-alpha-1-UNC5C
CC protein; a method for detecting the presence of an obesity susceptibility
CC gene; a method for detecting the presence of a translocation junction
CC between chromosome 4 at cytoband 4q 22.3 and chromosome 15 at cytoband
CC 15q22.2; a method for identifying a test compound that modulates the
CC expression of an obesity susceptibility gene identified in said method; a
CC method for identifying a test compound that modulates the activity of an
CC obesity protein encoded by the obesity susceptibility gene identified in
CC said method; a method for treating a subject having obesity; a
CC pharmaceutical composition comprising a compound identified in the
CC previous methods, and an adjuvant, diluent or carrier; making a
CC pharmaceutical composition; a method for determining if an obesity
CC susceptibility gene identified in the appropriate method; and a method
CC for diagnosing obesity, or a susceptibility to it in a subject. The
CC isolated nucleic acid molecules and compounds of the invention have the
CC following activities: anorectic, antilipemic, antiarteriosclerotic,
CC hepatotropic, hypotensive, antidiabetic, cardiant, vasotropic,
CC osteopathic, antiarthritic, and cyostatic. The isolated nucleic acid
CC molecules and compounds may be used in gene therapy. The compound
CC modulating the activity of an obesity protein or the expression of an
CC obesity susceptibility gene is useful in the preparation of a medicament
CC for the treatment of obesity. The compound is also useful in treating or
CC diagnosing hyperlipidaemia, and the consequences of obesity, such as
CC arteriosclerosis, fatty liver, hypertension, diabetes, coronary heart
CC disease, stroke, gallbladder disease, osteoarthritis and cancer. This
CC polynucleotide sequence represents the gene encoding the human 1ROR-alpha
CC -1-UNC5C protein of the invention.

SQ Sequence 2986 BP; 770 A; 792 C; 770 G; 654 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.12e-16 Length: 2986
Score: 249.00 Matches: 41
Percent Similarity: 94.00% Conservative: 6
Best Local Similarity: 82.00% Mismatches: 3
Query Match: 85.86% Indels: 0
DB: 13 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x ADR99249 (1-2986)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 901 TCCACCTGGACGGAGTGTCTGTGTGTACAGCCGCTGTGGACGAGGTATCAGAAACGT 960

Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 961 ACAAGGACTTGTACCAACCCGGCACCCTCAATGGGGTGCCTTCTGTGAAGGCGCAGAGT 1020

Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50

Db 1021 GTGCAGAAATAGCCTGTACTACGTTATGC 1050

RESULT 13

XX AAS75738

ID AAS75738 standard; cDNA; 3646 BP.

XX AC AAS75738;

XX DT 13-FEB-2002 (first entry)

XX DNA encoding novel human diagnostic protein #11542.
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX Homo sapiens.
XX WO200175067-A2.
XX 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US008631.
XX 31-MAR-2000; 2000US-00540217.
XX 23-AUG-2000; 2000US-00649167.
XX (HYSE-) HYSEQ INC.
XX Drmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
XX P-PSDB; ABG11551.
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity.
XX Claim 1; SEQ ID NO 11542; 103pp; English.
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX sequences. (I) is useful as hybridisation probes, polymerase chain
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX and in recombinant production of (II). The polynucleotides are also used
XX in diagnostics as expressed sequence tags for identifying expressed
XX genes. (I) is useful in gene therapy techniques to restore normal
XX activity of (II) or to treat disease states involving (II). (II) is
XX useful for generating antibodies against it, detecting or quantitating a
XX polypeptide in tissue, as molecular weight markers and as a food
XX supplement. (II) and its binding partners are useful in medical imaging
XX of sites expressing (II). (I) and (II) are useful for treating disorders
XX involving aberrant protein expression or biological activity. The
XX polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
XX coding sequences of the invention. Note: The sequence data for this
XX patent did not appear in the printed specification, but was obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 3646 BP; 930 A; 917 C; 921 G; 877 T; 0 U; 1 Other;
Alignment Scores:
Pred. No.: 1,426-16 Length: 3646
Score: 249.00 Matches: 41
Percent Similarity: 94.00% Conservative: 6
Best Local Similarity: 82.00% Mismatches: 3
Query Match: 85.86% Indels: 0
DB: 5 Gaps: 0
US-10-624-932C-2_COPY_246_295 (1-50) x AAS75738 (1-3646)
Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 944 TCCACCTGGACGGAGTGGTCTGTGTGTAAACCGCTGTGGACGAGGGTATCAGAAACGT 1003
Qy 21 SerArgSerCysThrAsnProAlaProLeuAenGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 1004 ACAAGGACTTGTACCAACCCGACCACTCAATGGGGGTGCTTCTGTGAAGGGCAGAGT 1063

Qy 41 ValGlnLysThrAlaCysAlaThrIleuCys 50
Db 1064 GTGCAGAAATAGCTGTACTACGTTATGC 1093
RESULT 14
ADR99257
ID ADR99257 standard; cDNA; 3646 BP.
XX ADR99257;
XX 16-DEC-2004 (first entry)
XX Human uncoordinated 5C (UNC5C) protein encoding cDNA.
XX RAR-like orphan receptor alpha 1-uncoordinated 5C; ROR-alpha-1-UNC5C;
XX ROR-alpha-5; obesity; susceptibility; anorectic; antilipemic;
XX antiarteriosclerotic; hepatotropic; hypotensive; antidiabetic; cardiant;
XX vasotropic; osteopathic; antiarthritic; cytostatic; gene therapy;
XX hyperlipidaemia; gene; human; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
XX CDS 155..2950
XX /*tag= a
XX /product= "Human uncoordinated 5C (UNC5C) protein"
XX WO2004083371-A2.
XX 30-SEP-2004.
XX 16-MAR-2004; 2004WO-GB001124.
XX 19-MAR-2003; 2003GB-00006185.
XX (ASTR) ASTRAZENECA AB.
XX (ASTR) ASTRAZENECA UK LTD.
XX Dahl N;
XX WPI; 2004-691032/67.
XX P-PSDB; ADR99258.
XX New isolated nucleic acid molecule encoding a RAR-like orphan receptor
XX alpha 1-uncoordinated 5C (RORapproximatelal-UNC5C) polypeptide, useful
XX in diagnosing or treating obesity and hyperlipidemia.
XX Disclosure; SEQ ID NO 9; 96pp; English.
XX The invention relates to a novel isolated nucleic acid molecule,
XX comprising a nucleotide sequence having at least 65% identity to a
XX degenerate variant of a fully defined sequence of 2986, 2780 or 1821 bp
XX (ADR99249, ADR99251 or ADR99255), or the complement of nucleotide
XX sequence with ADR99249, ADR99251 or ADR99255. The invention further
XX comprises an isolated nucleic acid molecule encoding a RAR-like orphan
XX receptor alpha 1-uncoordinated 5C (ROR-alpha-1-UNC5C) polypeptide; an
XX isolated nucleic acid molecule encoding a ROR-alpha-5 polypeptide; a
XX vector comprising any of the nucleic acid molecules as cited; a host cell
XX comprising the vector; a purified fusion polypeptide of the ROR-alpha-1-
XX UNC5C polypeptide; a purified polypeptide of the ROR-alpha-5 polypeptide;
XX a method for producing a protein comprising culturing the host cell; a
XX method for detecting a polynucleotide which encodes a ROR-alpha-1-UNC5C
XX protein; a method for detecting the presence of an obesity susceptibility
XX gene; a method for detecting the presence of a translocation junction
XX between chromosome 4 at cytoband 4q 22.3 and chromosome 15 at cytoband
XX 15q22.2; a method for identifying a test compound that modulates the
XX expression of an obesity susceptibility gene identified in said method; a
XX method for identifying a test compound that modulates the activity of an
XX obesity protein encoded by the obesity susceptibility gene identified in
XX said method; a method for treating a subject having obesity; a
XX pharmaceutical composition comprising a compound identified in the
XX previous methods, and an adjuvant, diluent or carrier; making a
XX pharmaceutical composition; a method for determining if an obesity

CC susceptibility gene identified in the appropriate method; and a method
CC for diagnosing obesity, or a susceptibility to it in a subject. The
CC isolated nucleic acid molecules and compounds of the invention have the
CC following activities: anorectic, antilipemic, antiarteriosclerotic,
CC hepatotropic, hypotensive, antidiabetic, cardiant, vasotropic,
CC osteopathic, antiarthritic, and cytostatic. The isolated nucleic acid
CC molecules and compounds may be used in gene therapy. The compound
CC modulating the activity of an obesity protein or the expression of an
CC obesity susceptibility gene is useful in the preparation of a medicament
CC for the treatment of obesity. The compound is also useful in treating or
CC diagnosing hyperlipidaemia, and the consequences of obesity, such as
CC arteriosclerosis, fatty liver, hypertension, diabetes, coronary heart
CC disease, stroke, gallbladder disease, osteoarthritis and cancer. This
CC polynucleotide sequence represents the gene encoding the human
CC uncoordinated 5C (UNC5C) protein of the invention.

XX

SQ Sequence 3646 BP; 930 A; 917 C; 921 G; 877 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.:	1.42e-16	Length:	3646
Score:	249.00	Matches:	41
Percent Similarity:	94.00%	Conservative:	6
Best Local Similarity:	82.00%	Mismatches:	3
Query Match:	85.86%	Indels:	0
DB:	13	Gaps:	0

US-10-624-932C-2_COPY_246_295 (1-50) x ADR99257 (1-3646)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
|||||
Dy 944 TCCACCTGGACGGAGTGTCTGTGTGTAAACAGCCGCTGTGGACGAGGTATCAGAAACGT 1003
|||||

Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyClnAsn 40
:::|||||
Dy 1004 ACAAGGACTGTACCAACCCGGCCACTCAATGGGGTGCCTTCTGTGAAGGCAGAGT 1063
|||||

Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
|||||
Dy 1064 GTGCAGAAATAGCTGTACTACCTTATGC 1093
|||||

RESULT 15

ID ADH71611 standard; DNA; 993 BP.

XX ADH71611;

AC ADH71611;

XX

DT 25-MAR-2004 (first entry)

XX

XX Human gene of the invention NOV21b SEQ ID NO:507.

DE

XX ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.

XX

OS Homo sapiens.

XX

PN WO2003102155-A2.

XX

XX 11-DEC-2003.

XX

XX 03-JUN-2003; 2003WO-US017430.

XX

XX 03-JUN-2002; 2002US-0385120P.

PR 04-JUN-2002; 2002US-0385784P.

PR 05-JUN-2002; 2002US-0386041P.

PR 05-JUN-2002; 2002US-0386047P.

PR 06-JUN-2002; 2002US-0386376P.

PR 06-JUN-2002; 2002US-0386453P.

PR 06-JUN-2002; 2002US-0386864P.

PR 06-JUN-2002; 2002US-0387016P.

PR 07-JUN-2002; 2002US-0386796P.

PR 07-JUN-2002; 2002US-0386816P.

PR 07-JUN-2002; 2002US-0386911P.

PR 07-JUN-2002; 2002US-0386942P.

PR 07-JUN-2002; 2002US-0386971P.

PR 08-JUN-2002; 2002US-0387262P.

PR 08-JUN-2002; 2002US-0296960P.

PR 10-JUN-2002; 2002US-0387400P.

PR 10-JUN-2002; 2002US-0387535P.

PR 11-JUN-2002; 2002US-0387610P.

PR 11-JUN-2002; 2002US-0387625P.

PR 11-JUN-2002; 2002US-0387634P.

PR 11-JUN-2002; 2002US-0387668P.

PR 11-JUN-2002; 2002US-0387696P.

PR 11-JUN-2002; 2002US-0387702P.

PR 11-JUN-2002; 2002US-0387836P.

PR 11-JUN-2002; 2002US-0387859P.

PR 12-JUN-2002; 2002US-0387933P.

PR 12-JUN-2002; 2002US-0387934P.

PR 12-JUN-2002; 2002US-0387960P.

PR 12-JUN-2002; 2002US-0388022P.

PR 12-JUN-2002; 2002US-0388096P.

PR 13-JUN-2002; 2002US-0389123P.

PR 14-JUN-2002; 2002US-0389118P.

PR 14-JUN-2002; 2002US-0389120P.

PR 14-JUN-2002; 2002US-0389144P.

PR 14-JUN-2002; 2002US-0389146P.

PR 17-JUN-2002; 2002US-0389729P.

PR 17-JUN-2002; 2002US-0389742P.

PR 18-JUN-2002; 2002US-0389884P.

PR 19-JUN-2002; 2002US-0390006P.

PR 19-JUN-2002; 2002US-0390209P.

PR 21-JUN-2002; 2002US-0390763P.

PR 17-JUL-2002; 2002US-0396706P.

PR 06-AUG-2002; 2002US-0401628P.

PR 09-AUG-2002; 2002US-0402156P.

PR 09-AUG-2002; 2002US-0402256P.

PR 09-AUG-2002; 2002US-0402389P.

PR 12-AUG-2002; 2002US-0402786P.

PR 12-AUG-2002; 2002US-0402816P.

PR 12-AUG-2002; 2002US-0402821P.

PR 12-AUG-2002; 2002US-0402832P.

PR 13-AUG-2002; 2002US-0403448P.

PR 13-AUG-2002; 2002US-0403459P.

PR 13-AUG-2002; 2002US-0403531P.

PR 13-AUG-2002; 2002US-0403532P.

PR 13-AUG-2002; 2002US-0403563P.

PR 13-AUG-2002; 2002US-0406317P.

PR 15-AUG-2002; 2002US-0403617P.

PR 26-AUG-2002; 2002US-0406182P.

PR 26-AUG-2002; 2002US-0406355P.

PR 27-AUG-2002; 2002US-0406240P.

PR 12-SEP-2002; 2002US-0410084P.

PR 20-SEP-2002; 2002US-0412528P.

PR 23-SEP-2002; 2002US-0412731P.

PR 30-SEP-2002; 2002US-0414801P.

PR 30-SEP-2002; 2002US-0414839P.

PR 30-SEP-2002; 2002US-0414840P.

PR 30-SEP-2002; 2002US-0414954P.

PR 09-OCT-2002; 2002US-0417186P.

PR 09-OCT-2002; 2002US-0417406P.

PR 23-OCT-2002; 2002US-0420639P.

PR 28-OCT-2002; 2002US-0421156P.

PR 31-OCT-2002; 2002US-0422690P.

PR 01-NOV-2002; 2002US-0423130P.

PR 05-NOV-2002; 2002US-0423798P.

PR 05-NOV-2002; 2002US-0423798P.

PR 12-NOV-2002; 2002US-0425453P.

XX

PA (CURA-) CURAGEN CORP.

XX

XX Alsbrook JP, Alvarez E, Anderson DW, Boldog EL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman X;
PI Ettenberg S, Gangolli EA, Gorman L, Gunther E, Guo X;

PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
 PI MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
 PI Padigaru M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
 PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
 PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
 PI Zhong H;
 XX
 DR WPI; 2004-081935/08.
 DR P-PSDB; ADH71612.
 XX
 XX New NOVX polypeptides and nucleic acid molecules useful for preventing or
 PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
 PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
 XX
 PS Example 21; SEQ ID NO 507; 1880pp; English.
 PS
 XX The invention relates to a novel isolated polypeptide (NOVX). A
 CC polypeptide of the invention has cytostatic, immunomodulator,
 CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
 CC antilipase activity, and may have a use in gene therapy, and as a
 CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
 CC any of the 303 fully defined nucleotide sequences given in the
 CC specification. The polypeptide is useful in the manufacture of a
 CC medicament for treating a syndrome associated with a human disease. The
 CC polypeptide, polynucleotide and antibody are useful in diagnosing,
 CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
 CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
 CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
 CC further used as hybridisation probes, in chromosome mapping, tissue
 CC typing, preventive medicine, and pharmacogenomics. The present sequence
 CC encodes a NOVX polypeptide of the invention.
 XX
 SQ Sequence 993 BP; 187 A; 306 C; 333 G; 167 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.33e-16	Length:	993
Score:	243.00	Matches:	42
Percent Similarity:	89.80%	Conservative:	2
Best Local Similarity:	85.71%	Mismatches:	5
Query Match:	83.79%	Indels:	0
DB:	12	Gaps:	0

US-10-624-932C-2_COPY_246_295 (1-50) x ADH71611 (1-993)

Qy	1	SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg	20
Db	661	TCGACGTGGACCGAGTGGTCCGTCTGCAGCCGACGCTGTGGCGGGCTGCGAGAACGG	720
Qy	21	SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn	40
Db	721	AGCGGAGCTGCACCAACCCGGCGCTCTCAACGGGGCGCTTTCTGTGAGGGGCGAAT	780
Qy	41	ValGlnLysThrAlaCysAlaThrIeu	49
Db	781	GTCCATGACCGCACCGTCTCTCTCTG	807

Search completed: September 9, 2005, 00:42:51
 Job time : 263.585 secs

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 8, 2005, 23:51:22 ; Search time 79.6984 Seconds
(without alignments)
1026.543 Million cell updates/sec

Title: US-10-624-932C-2_COPY_246_295

Perfect score: 290

Sequence: 1 STWTWSVCSACRGWQKR.....NGGAFCEQNVQKTACATLC 50

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool_h/US10624932/runat_08092005_161706_15822/app_query.fasta_1.1386
-DB=Issued_Patents_NA -QWMT=fastcap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USBR=US10624932 @cgn 1 1 187 @runat 08092005_161706_15822 -NCPU=6 -ICPU=3
-NO_MMAP -LARGQUERY -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PTCUS.COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	290	100.0	3014	2	US-08-808-982-1
2	290	100.0	3014	3	US-09-306-902A-1
3	249	85.9	3008	4	US-09-949-016-4794
4	249	85.9	114139	4	US-09-949-016-16536
5	238	82.1	2831	2	US-08-808-982-3
6	238	82.1	2831	3	US-09-306-902A-3
7	147	50.7	2820	4	US-09-854-845-15
8	147	50.7	2865	4	US-09-854-845-13
9	147	50.7	3105	4	US-09-854-845-5
10	147	50.7	3150	4	US-09-854-845-1
11	147	50.7	3237	4	US-09-854-845-7
12	147	50.7	3282	4	US-09-854-845-3

13	147	50.7	3411	4	US-09-854-845-11
14	147	50.7	3456	4	US-09-854-845-9
15	147	50.7	4074	4	US-09-854-845-17
16	139	47.9	3675	3	US-09-930-872-3
17	139	47.9	3675	4	US-10-217-774-3
18	139	47.9	3675	4	US-09-930-872-5
19	139	47.9	4042	4	US-10-217-774-5
20	136	46.9	457	4	US-09-270-767-31598
21	136	46.9	2006	4	US-09-270-767-15258
22	136	46.9	2114	3	US-09-130-491-7
23	132	45.5	4192	3	US-09-122-126B-1
24	132	45.5	4192	4	US-09-634-286A-1
25	132	45.5	4192	4	US-10-247-685-1
26	132	45.5	5722	4	US-09-657-472-1
27	131	45.2	3638	3	US-09-369-364A-8
28	130	44.8	2184	4	US-09-445-023A-2
29	130	44.8	2184	4	US-09-445-023A-13
30	130	44.8	3706	3	US-08-484-970B-58
31	130	44.8	3889	4	US-09-568-559-1
32	130	44.8	4676	3	US-09-130-491-1
33	130	44.8	4858	3	US-09-392-184-1
34	128	44.3	2853	4	US-10-009-332-2
35	128	44.1	7231	4	US-09-919-172-64
36	126	43.4	6659	4	US-09-321-987B-1
37	122	42.1	966	4	US-09-969-532-23
38	122	42.1	999	4	US-09-969-532-21
39	122	42.1	1008	4	US-09-969-532-19
40	122	42.1	1041	4	US-09-969-532-17
41	122	42.1	1659	4	US-09-969-532-7
42	122	42.1	1692	4	US-09-969-532-5
43	122	42.1	1701	4	US-09-969-532-3
44	122	42.1	1734	4	US-09-969-532-1
45	122	42.1	1968	4	US-09-969-532-31

ALIGNMENTS

RESULT 1

US-08-808-982-1
; Sequence 1, Application US/08808982
; Patent No. 5939271
; GENERAL INFORMATION:

; APPLICANT: Tessier-Lavigne, Marc
; APPLICANT: Leonardo, E. David
; APPLICANT: Hink, Lindsay
; APPLICANT: Masu, Masayuki
; APPLICANT: Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,982
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:

```
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3014 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-808-982-1
Alignment Scores:
Pred. No.: 2.36e-24 Length: 3014
Score: 290.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x US-08-808-982-1 (1-3014)
Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 736 TCGACGTGGAGTGGTCCGCTCTGCAGCCCGACCTCTCAACGGGGCGCTTCTGTGAGGGCAGAA 795
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 796 AGCCGGAGCTGCACCAACCGGCACCTCTCAACGGGGCGCTTCTGTGAGGGCAGAA 855
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 856 GTCCAGAAAACAGCTCGCCACTCTGTGC 885

RESULT 2
US-09-306-902A-1
; Sequence 1, Application US/09306902A
; Patent No. 627585
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindsey
; Masu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/306,902A
; FILING DATE: 07-May-1999
; CLASSIFICATION: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3014 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
```

```
US-09-306-902A-1
Alignment Scores:
Pred. No.: 2.36e-24 Length: 3014
Score: 290.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x US-09-306-902A-1 (1-3014)
Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 736 TCGACGTGGAGTGGTCCGCTCTGCAGCCCGACCTCTCAACGGGGCGCTTCTGTGAGGGCAGAA 795
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 796 AGCCGGAGCTGCACCAACCGGCACCTCTCAACGGGGCGCTTCTGTGAGGGCAGAA 855
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 856 GTCCAGAAAACAGCTCGCCACTCTGTGC 885

RESULT 3
US-09-949-016-4794
; Sequence 4794, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4794
; LENGTH: 3008
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-4794
Alignment Scores:
Pred. No.: 1.55e-19 Length: 3008
Score: 249.00 Matches: 41
Percent Similarity: 94.00% Conservative: 6
Best Local Similarity: 82.00% Mismatches: 3
Query Match: 85.86% Indels: 0
DB: 4 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x US-09-949-016-4794 (1-3008)
Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 306 TCCACCTGGACGGAGTGGTCTGTGTGTAAACAGCCGCTGTGGACGAGGTATCAGAAACGT 365
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 366 ACAAGGACTTGTACCAACCGGCACCACTCAATGGGGTGCCTTCTGTGAAGGGCAGAGT 425
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 426 GTGCAGAAAATAGCTGTACTACTACGTATGTC 455

RESULT 4
US-09-949-016-16536
```

```
; Sequence 16536, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR APPLICATION NUMBER: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16536
; LENGTH: 114139
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(114139)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16536

Alignment Scores:
Pred. No.: 1,656-17 Length: 114139
Score: 249.00 Matches: 41
Percent Similarity: 94.00% Conservative: 6
Best Local Similarity: 82.00% Mismatches: 3
Query Match: 85.86% Indels: 0
DB: 4 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x US-09-949-016-16536 (1-114139)
Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 35240 TCCACCTGGACGGAGTGTCTGTGTAAACAGCCGCTGTGGACGAGGGTATCAGAAACGT 35299
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyClnAsn 40
Db 35300 ACAAGGACTTGTACCAACCCGCGACCACTCAATGGGGGTGCTTCTGTGAAGGGCAGAGT 35359
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 35360 GTGCAGAAAATAGCTGTACTACGTTATGC 35389

RESULT 5
US-08-808-982-3
; Sequence 3, Application US/08808982
; Patent No. 5919271
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; APPLICANT: Leonardo, E. David
; APPLICANT: Hink, Lindsey
; APPLICANT: Masu, Masayuki
; APPLICANT: Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

US-09-949-016-16536
; Sequence 16536, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR APPLICATION NUMBER: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16536
; LENGTH: 114139
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(114139)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16536

Alignment Scores:
Pred. No.: 1,656-17 Length: 114139
Score: 249.00 Matches: 41
Percent Similarity: 94.00% Conservative: 6
Best Local Similarity: 82.00% Mismatches: 3
Query Match: 85.86% Indels: 0
DB: 4 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x US-08-808-982-3 (1-2831)
Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 742 TCCAGCTGGCAGAAATGGTCAACCTGTCTTAACCGCTGCGCGCGAGGTTGGCAGAAACGT 801
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyClnAsn 40
Db 802 ACTAGGACCTTGCACCAACCCAGCCCACTCAATGAGGTGCTTCTGCGAGGGACAGGCT 861
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 862 TGCCAGAAAGAGCGCTTGCACCCACCGTGTGC 891

RESULT 6
US-09-306-902A-3
; Sequence 3, Application US/09306902A
; Patent No. 6277585
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; APPLICANT: Leonardo, E. David
; APPLICANT: Hink, Lindsey
; APPLICANT: Masu, Masayuki
; APPLICANT: Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

US-09-306-902A-3
; Sequence 3, Application US/09306902A
; Patent No. 6277585
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; APPLICANT: Leonardo, E. David
; APPLICANT: Hink, Lindsey
; APPLICANT: Masu, Masayuki
; APPLICANT: Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
```


; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 3105
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-854-845-5

Alignment Scores:
Pred. No.: 1.57e-07 Length: 3105
Score: 147.00 Matches: 26
Percent Similarity: 66.67% Conservative: 6
Best Local Similarity: 54.17% Mismatches: 16
Query Match: 50.69% Indels: 0
DB: 4 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x US-09-854-845-5 (1-3105)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 2434 TCCTGCTGGACCTCATGGTCTCCATGCTCAGCTTCCTGTGGTGGGGTCACTATCAACGC 2493
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyClnAsn 40
Db 2494 ACCCGTTCCTGCACAGCCCCGACCCCTCCCGAGGTGAGGACATCTGTCTCGGGCTGCAC 2553
Qy 41 ValGlnLysThrAlaCysAlaThr 48
Db 2554 ACGGAGGAGGACACTATGTGCCACA 2577

RESULT 10
US-09-854-845-1
; Sequence 1, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encod
; FILE REFERENCE: LEX-0177-USA
; CURRENT FILING DATE: 2001-05-14
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3150
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-854-845-1

Alignment Scores:
Pred. No.: 1.6e-07 Length: 3150
Score: 147.00 Matches: 26
Percent Similarity: 66.67% Conservative: 6
Best Local Similarity: 54.17% Mismatches: 16
Query Match: 50.69% Indels: 0
DB: 4 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x US-09-854-845-1 (1-3150)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 2434 TCCTGCTGGACCTCATGGTCTCCATGCTCAGCTTCCTGTGGTGGGGTCACTATCAACGC 2493
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyClnAsn 40
Db 2494 ACCCGTTCCTGCACAGCCCCGACCCCTCCCGAGGTGAGGACATCTGTCTCGGGCTGCAC 2553

Qy 41 ValGlnLysThrAlaCysAlaThr 48
Db 2554 ACGGAGGAGGACACTATGTGCCACA 2577

RESULT 11
US-09-854-845-7
; Sequence 7, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encod
; FILE REFERENCE: LEX-0177-USA
; CURRENT FILING DATE: 2001-05-14
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 3237
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-854-845-7

Alignment Scores:
Pred. No.: 1.66e-07 Length: 3237
Score: 147.00 Matches: 26
Percent Similarity: 66.67% Conservative: 6
Best Local Similarity: 54.17% Mismatches: 16
Query Match: 50.69% Indels: 0
DB: 4 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x US-09-854-845-7 (1-3237)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 2566 TCCTGCTGGACCTCATGGTCTCCATGCTCAGCTTCCTGTGGTGGGGTCACTATCAACGC 2625
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyClnAsn 40
Db 2626 ACCCGTTCCTGCACAGCCCCGACCCCTCCCGAGGTGAGGACATCTGTCTCGGGCTGCAC 2685
Qy 41 ValGlnLysThrAlaCysAlaThr 48
Db 2686 ACGGAGGAGGACACTATGTGCCACA 2709

RESULT 12
US-09-854-845-3
; Sequence 3, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encod
; FILE REFERENCE: LEX-0177-USA
; CURRENT FILING DATE: 2001-05-14
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3282

```
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-854-845-3

Alignment Scores:
Pred. No.:      1.69e-07      Length:      3282
Score:          147.00      Matches:      26
Percent Similarity: 66.67%      Conservative: 6
Best Local Similarity: 54.17%      Mismatches: 16
Query Match:    50.69%      Indels:      0
DB:             4      Gaps:      0

US-10-624-932C-2_COPY_246_295 (1-50) x US-09-854-845-3 (1-3282)
Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 2566 TCCTGCTGGACCTCATGCTCTCCATGCTCAGCTTCCTGTGGGGGTCACTATCAACGC 2625
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyAlaPheCysGluGlyGlnAsn 40
Db 2626 ACCCGTTCTGCACCGACCGCCGACCTCCCGAGGTGAGGACATCTGTCGGGGCTGCAC 2685
Qy 41 ValGlnLysThrAlaCysAlaThr 48
Db 2686 ACGGAGGAGGCATATGTGCCACA 2709

RESULT 13
US-09-854-845-11
; Sequence 11, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encod
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 3411
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-854-845-11

Alignment Scores:
Pred. No.:      1.78e-07      Length:      3411
Score:          147.00      Matches:      26
Percent Similarity: 66.67%      Conservative: 6
Best Local Similarity: 54.17%      Mismatches: 16
Query Match:    50.69%      Indels:      0
DB:             4      Gaps:      0

US-10-624-932C-2_COPY_246_295 (1-50) x US-09-854-845-11 (1-3411)
Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 2740 TCCTGCTGGACCTCATGCTCTCCATGCTCAGCTTCCTGTGGGGGTCACTATCAACGC 2799
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyAlaPheCysGluGlyGlnAsn 40
Db 2800 ACCCGTTCTGCACCGACCGCCGACCTCCCGAGGTGAGGACATCTGTCGGGGCTGCAC 2859
Qy 41 ValGlnLysThrAlaCysAlaThr 48
Db 2860 ACGGAGGAGGCATATGTGCCACA 2883
```

```
RESULT 14
US-09-854-845-9
; Sequence 9, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encod
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 3456
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-854-845-9

Alignment Scores:
Pred. No.:      1.81e-07      Length:      3456
Score:          147.00      Matches:      26
Percent Similarity: 66.67%      Conservative: 6
Best Local Similarity: 54.17%      Mismatches: 16
Query Match:    50.69%      Indels:      0
DB:             4      Gaps:      0

US-10-624-932C-2_COPY_246_295 (1-50) x US-09-854-845-9 (1-3456)
Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 2740 TCCTGCTGGACCTCATGCTCTCCATGCTCAGCTTCCTGTGGGGGTCACTATCAACGC 2799
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyAlaPheCysGluGlyGlnAsn 40
Db 2800 ACCCGTTCTGCACCGACCGCCGACCTCCCGAGGTGAGGACATCTGTCGGGGCTGCAC 2859
Qy 41 ValGlnLysThrAlaCysAlaThr 48
Db 2860 ACGGAGGAGGCATATGTGCCACA 2883

RESULT 15
US-09-854-845-17
; Sequence 17, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encod
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 4074
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-854-845-17

Alignment Scores:
```

Pred. No.: 2.23e-07 Length: 4074
 Score: 147.00 Matches: 26
 Percent Similarity: 66.67% Conservative: 6
 Best Local Similarity: 54.17% Mismatches: 16
 Query Match: 50.69% Indels: 0
 DB: 4 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x US-09-854-845-17 (1-4074)

QY 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
 DB 2930 TCCTGCTGGACCTCATGGTCTCCATGCTCAGCTTCTGGTGGGGGTCACTATCAACGC 2989
 QY 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
 DB 2990 ACCCGTTCCTGCACCGCCCGCAGCCCTCCCGAGGTGAGGACATCTGTCTCGGGCTGCAC 3049
 QY 41 ValGlnLysThrAlaCysAlaThr 48
 DB 3050 ACGGAGGAGGCACCTATGTGCCACA 3073

Search completed: September 9, 2005, 09:51:29
 Job time : 94.6984 secs

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model
Run on: September 9, 2005, 04:41:16 ; Search time 498.956 Seconds
(without alignments)
658.098 Million cell updates/sec
Title: US-10-624-932C-2_COPY_246_295
Perfect score: 290
Sequence: 1 STWTWSVCSACRGWQKR.....NGGAFCEQNVQKTACATLC 50

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0
Searched: 7351250 seqs, 3283620254 residues

Total number of hits satisfying chosen parameters: 14702500

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters: -DEV=xlh
-MODEL=frame+p2n.model -DB=fastap -Q=us10624932/runat_08092005_161709_15882/app_query.fasta_1.1386
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10624932 @CGN 1.1 989 @runat_08092005_161709_15882
-NCPU=6 -ICPU=3 -NO WAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DBG TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US10J_NEW_PUB.seq.*
23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	290	100.0	2697	16	US-10-240-154-15	Sequence 15, Appl
2	290	100.0	2752	10	US-09-918-779-1	Sequence 1, Appli
3	290	100.0	2752	18	US-10-624-932-1	Sequence 1, Appli
4	290	100.0	3014	10	US-09-933-261-1	Sequence 1, Appli
5	290	100.0	3014	14	US-10-256-702-1	Sequence 1, Appli
6	243	83.8	2881	10	US-09-970-944-1	Sequence 31, Appl
7	239	82.4	168	21	US-10-872-681-31	Sequence 117, App
8	239	82.4	2181	17	US-10-094-886-117	Sequence 53, Appl
9	239	82.4	2661	21	US-10-872-681-53	Sequence 1, Appli
10	239	82.4	2860	17	US-10-087-684-1	Sequence 3, Appli
11	239	82.4	2860	17	US-10-087-684-3	Sequence 1, Appli
12	239	82.4	2860	17	US-10-218-779-1	Sequence 3, Appli
13	239	82.4	2860	17	US-10-218-779-3	Sequence 55, Appl
14	239	82.4	2868	21	US-10-872-681-55	Sequence 37, Appl
15	239	82.4	2895	18	US-10-037-417-37	Sequence 115, App
16	239	82.4	2898	17	US-10-094-886-115	Sequence 136, App
17	239	82.4	2979	19	US-10-473-518-136	Sequence 55, Appl
18	239	82.4	2995	11	US-09-972-211-55	Sequence 55, Appl
19	239	82.4	2995	18	US-10-096-625-55	Sequence 18, Appl
20	239	82.4	3485	9	US-09-816-828-18	Sequence 1123, Ap
21	239	82.4	3501	17	US-10-295-027-1123	Sequence 145, App
22	239	82.4	3884	14	US-10-028-072-145	Sequence 145, App
23	239	82.4	3884	14	US-10-140-808-145	Sequence 145, App
24	239	82.4	3884	14	US-10-121-049-145	Sequence 145, App
25	239	82.4	3884	14	US-10-123-904-145	Sequence 145, App
26	239	82.4	3884	14	US-10-140-470-145	Sequence 145, App
27	239	82.4	3884	14	US-10-175-746-145	Sequence 145, App
28	239	82.4	3884	14	US-10-176-918-145	Sequence 145, App
29	239	82.4	3884	14	US-10-176-921-145	Sequence 145, App
30	239	82.4	3884	14	US-10-137-865-145	Sequence 145, App
31	239	82.4	3884	14	US-10-140-474-145	Sequence 145, App
32	239	82.4	3884	14	US-10-142-431-145	Sequence 145, App
33	239	82.4	3884	14	US-10-143-114-145	Sequence 145, App
34	239	82.4	3884	14	US-10-142-419-145	Sequence 145, App
35	239	82.4	3884	14	US-10-123-262-145	Sequence 145, App
36	239	82.4	3884	14	US-10-142-423-145	Sequence 145, App
37	239	82.4	3884	14	US-10-121-050-145	Sequence 145, App
38	239	82.4	3884	14	US-10-141-755-145	Sequence 145, App
39	239	82.4	3884	14	US-10-143-032-145	Sequence 145, App
40	239	82.4	3884	14	US-10-123-108-145	Sequence 145, App
41	239	82.4	3884	14	US-10-123-236-145	Sequence 145, App
42	239	82.4	3884	14	US-10-123-261-145	Sequence 145, App
43	239	82.4	3884	14	US-10-140-921-145	Sequence 145, App
44	239	82.4	3884	14	US-10-140-928-145	Sequence 145, App
45	239	82.4	3884	14	US-10-121-045-145	Sequence 145, App

ALIGNMENTS

RESULT 1
US-10-240-154-15
; Sequence 15, Application US/10240154
; Publication No. US20030175741A1
; GENERAL INFORMATION:
; APPLICANT: Cochran et al.
; TITLE OF INVENTION: SCHIZOPHRENIA RELATED GENES
; FILE REFERENCE: CKFW-P01-006
; CURRENT APPLICATION NUMBER: US/10/240.154
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: PCT/GB01/01486
; PRIOR FILING DATE: 2001-04-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 2697

```
; TYPE: DNA
; ORGANISM: Rattus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2697)
US-10-240-154-15
Alignment Scores:
Pred. No.: 6.16e-27 Length: 2697
Score: 290.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x US-10-240-154-15 (1-2697)
Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 736 TCGACGTGGACTGAGTGGTCCGCTGCGAGCCGACGCTGTGGCGCTGGCAGAAAACGG 795
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 796 AGCCGGAGTGCACCAACCCGCGACCTCTCAACGGGGCGGCTTCTGTGAGGGGCAGAAAT 855
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 856 GTCCAGAAAACAGCCTGCGCCACTCTGTGC 885

RESULT 2
US-09-918-779-1
; Sequence 1, Application US/09918779
; Publication No. US20030064369A1
; GENERAL INFORMATION:
; APPLICANT: Taupier, Raymond
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Rastelli, Luca
; APPLICANT: Spaderna, Steven
; APPLICANT: Shimkets, Richard
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Spytek, Kimberly
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Gusev, Vladimir
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook, John
; APPLICANT: Lepley, Denise
; APPLICANT: Burgess, Catherine
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Smithson, Glennda
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-074 US
; CURRENT APPLICATION NUMBER: US/09/918,779
; CURRENT FILING DATE: 2001-07-30
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/221,409
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/222,840
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,752
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,762
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,770
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,769
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/225,146
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/225,392
; PRIOR FILING DATE: 2000-08-15

; TYPE: DNA
; ORGANISM: Rattus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2697)
US-10-240-154-15
Alignment Scores:
Pred. No.: 6.16e-27 Length: 2697
Score: 290.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x US-09-918-779-1 (1-2752)
Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 781 TCGACGTGGACCGAGTGGTCCGCTGCGAGCCGACGCTGTGGCGCGCTGTGCAGAAAACGG 840
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 841 AGCCGGAGTGCACCAACCCGCGCTCTCAACGGGGCGGCTTCTGTGAGGGGCAGAAAT 900
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 901 GTCCAGAAAACAGCCTGCGCCACTCTGTGC 930

RESULT 3
US-10-624-932-1
; Sequence 1, Application US/10624932
; Publication No. US20040096877A1
; GENERAL INFORMATION:
; APPLICANT: Taupier, Raymond
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Rastelli, Luca
; APPLICANT: Spaderna, Steven
; APPLICANT: Shimkets, Richard
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Spytek, Kimberly
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Gusev, Vladimir
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook, John
; APPLICANT: Lepley, Denise
; APPLICANT: Burgess, Catherine
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Smithson, Glennda
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-074 US
; CURRENT APPLICATION NUMBER: US/10/624,932
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: 09/918,779
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/221,409
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/222,840
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,752
```

```

; APPLICATION NUMBER: 08/808,982
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-933-261-1

Alignment Scores:
Pred. No.: 6,96e-27 Length: 3014
Score: 290.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x US-09-933-261-1 (1-3014)

QY 1 SerThrTpThrGluTpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
DB 736 TCGAGCTGGACTGAGTGTCGCTCGAGCGCCAGCTGTGGGGCGTGGCTGGCAGAACGG 795
QY 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
DB 796 AGCCGGAGCTGCACCAACCCGGCACCTCTCAACGGGGGGCGCCCTTCTGTGTAGGGGGCGAGAT 855
QY 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
DB 856 GTCCAGAAAACAGCCTGCGCCACTCTGTGC 885

RESULT 5
US-10-256-702-1
; Sequence 1, Application US/10256702
; Publication No. US20030059859A1
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindsey
; Masu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/256,702
; FILING DATE: 27-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/933,261
; FILING DATE: 20-Aug-2001
; APPLICATION NUMBER: 08/808,982

```

```
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3014 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-256-702-1

Alignment Scores:
Pred. No.: 6.95e-27 Length: 3014
Score: 290.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x US-10-256-702-1 (1-3014)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 736 TCAGCGTGGAGCTGAGTGGTCCGCTCGCAGCGCCAGCTGTGGCGTGGCTGGCAGAAACGG 795

Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 796 AGCGGAGCTGCACCAACCGCGCACCTCTCAACGGGGGGCGCTTCTCTGTGAGGGGCAGAAAT 855

Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 856 GTCCAGAAAACAGCTGGCCACTCTGTGC 885

RESULT 6
US-09-970-944-1
; Sequence 1, Application US/09970944
; Publication No. US20030204052A1
; GENERAL INFORMATION:
; APPLICANT: Herrman, John L
; APPLICANT: Rastelli, Luca
; APPLICANT: Shimkets, Richard A
; TITLE OF INVENTION: No. US20030204052A1el Proteins and Nucleic Acids Encoding Same an
; FILE REFERENCE: 21402-138
; CURRENT APPLICATION NUMBER: US/09/970,944
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 60/237,862
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2881
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-970-944-1

Alignment Scores:
Pred. No.: 7.01e-21 Length: 2881
Score: 243.00 Matches: 42
Percent Similarity: 89.80% Conservative: 2
Best Local Similarity: 85.71% Mismatches: 5
Query Match: 83.79% Indels: 0
DB: 10 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x US-09-970-944-1 (1-2881)
```

```
Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 822 TCAGCGTGGAGCCAGTGGTCCGCTCGCAGCGCCAGCTGTGGCGCGCTGGCAGAAACGG 881

Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 882 AGCGGAGCTGCACCAACCGCGCGCTCTCAACGGGGGGCGCTTCTCTGTGAGGGGCAGAAAT 941

Qy 41 ValGlnLysThrAlaCysAlaThrLeu 49
Db 942 GTCCATGACCGCACCGCTCTCTCTCTG 968

RESULT 7
US-10-872-681-31
; Sequence 31, Application US/10872681
; Publication No. US20050026251A1
; GENERAL INFORMATION:
; APPLICANT: ARES TRADING LIMITED
; TITLE OF INVENTION: TRANSMEMBRANE PROTEIN
; FILE REFERENCE: P029209W0
; CURRENT APPLICATION NUMBER: US/10/872,681
; CURRENT FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: GB0130721.4
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 31
; LENGTH: 168
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SEQ ID NO:9
US-10-872-681-31

Alignment Scores:
Pred. No.: 9.93e-22 Length: 168
Score: 239.00 Matches: 38
Percent Similarity: 86.00% Conservative: 5
Best Local Similarity: 76.00% Mismatches: 7
Query Match: 82.41% Indels: 0
DB: 21 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x US-10-872-681-31 (1-168)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 15 TCTTCTGGACAGAGTGGTCAGCCTGCAATGTTCCGTGTGTGATGAGGATGGCAGAAACGT 74

Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 75 TCCGGACCTGCACCAACCGCGCACCTCTCTCAATGTTGGGGCGCTTCTCTGTGAGGGGAATGTCA 134

Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 135 GTGCAGAAAATAACCTGCACCTCTCTTTGT 164

RESULT 8
US-10-094-886-117
; Sequence 117, Application US/10094886
; Publication No. US20040002120A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Vernet, Corine A.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Boldog, Ferenc
; APPLICANT: Guo, Xiaojia
```

```

; APPLICANT: Shenoy, Suresh
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Taupier, Raymond J., Jr.
; APPLICANT: Miller, Charles
; APPLICANT: Casman, Stacie
; APPLICANT: Pena, Carol
; APPLICANT: Gangolli, Esha
; APPLICANT: Gusev, Vladimir
; APPLICANT: Smithson, Glennnda
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Gerlach, Valerie
; APPLICANT: Pochart, Pascal
; APPLICANT: Fernandes, Elma
; APPLICANT: Rastelli, Luca
; APPLICANT: Shinkets, Richard
; APPLICANT: Spaderna, Steven
; APPLICANT: LaRochele, William
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-290 B
; CURRENT APPLICATION NUMBER: US/10/094,886
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: 60/274,322
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/313,182
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/288,052
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/318,510
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/274,281
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/314,018
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/274,194
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/274,849
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/296,693
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/313,626
; PRIOR FILING DATE: 2001-08-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 117
; LENGTH: 2181
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (125)..(2162)
US-10-094-886-117

Alignment Scores:
Pred. No.: 1,686-20 Length: 2181
Score: 239.00 Matches: 38
Percent Similarity: 86.00% Conservative: 5
Best Local Similarity: 76.00% Mismatches: 7
Query Match: 82.41% Indels: 0
DB: 17 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x US-10-094-886-117 (1-2181)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 866 TCCTCTGGACAGAGTGGTGCACCTGCAATGTTCCGCTGGTAGAGGATGGCAGAAACGT 925
Qy 21 SerArgSerCysThrAsnProAlaProLeuAenGlyGlyAlaPheCysGluGlyGlnAen 40
Db 926 TCCCGGACCTGCACCAACCCAGCTCTCTCAATGTTGGGGCTTTTGTGAGGGAATGTCA 985
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 41 ValGlnLysThrAlaCysAlaThrLeuCys 50

```

```

Db 986 GTGCAGAAATAAACCTGCACCTTCTCTTTGT 1015
RESULT 9
US-10-872-681-53
; Sequence 53, Application US/10872681
; Publication No. US20050026251A1
; GENERAL INFORMATION:
; APPLICANT: ARES TRADING LIMITED
; TITLE OF INVENTION: TRANSMEMBRANE PROTEIN
; FILE REFERENCE: P029209WO
; CURRENT APPLICATION NUMBER: US/10/872,681
; CURRENT FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: GB0130721.4
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 53
; LENGTH: 2661
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SEQ ID NO:31
US-10-872-681-53

Alignment Scores:
Pred. No.: 2,096-20 Length: 2661
Score: 239.00 Matches: 38
Percent Similarity: 86.00% Conservative: 5
Best Local Similarity: 76.00% Mismatches: 7
Query Match: 82.41% Indels: 0
DB: 21 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x US-10-872-681-53 (1-2661)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 643 TCCTCTGGACAGAGTGGTGCACCTGCAATGTTCCGCTGGTAGAGGATGGCAGAAACGT 702
Qy 21 SerArgSerCysThrAsnProAlaProLeuAenGlyGlyAlaPheCysGluGlyGlnAen 40
Db 703 TCCCGGACCTGCACCAACCCAGCTCTCTCAATGTTGGGGCTTTTGTGAGGGAATGTCA 762
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 763 GTGCAGAAATAAACCTGCACCTTCTCTTTGT 792

RESULT 10
US-10-087-684-1
; Sequence 1, Application US/10087684
; Publication No. US20040029116A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: MacDougall, John R.
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David J.
; APPLICANT: Grosse, William M.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie, J.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Rastelli, Luca
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Zernhusen, Bryan D.
; APPLICANT: Malyankar, Uriel M.

```

```
; APPLICANT: Guo, Xiaojia
; APPLICANT: Miller, Charles E.
; APPLICANT: Gangolli, Esha A.
; TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-214 CIP
; CURRENT APPLICATION NUMBER: US/10/087,684
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: 60/253,834
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,926
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/264,180
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/274,194
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/313,656
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/327,456
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: Curaseqlist version 0.1
; SEQ ID NO 1
; LENGTH: 2860
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (59)..(2857)
US-10-087-684-1

Alignment Scores:
Pred. No.: 2,26e-20 Length: 2860
Score: 239.00 Matches: 39
Percent Similarity: 86.00% Conservative: 4
Best Local Similarity: 78.00% Mismatches: 7
Query Match: 82.41% Indels: 0
DB: 17 Gaps: 0

US-10-624-932c-2_COPY_246_295 (1-50) x US-10-087-684-1 (1-2860)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 806 TCCAGCTGGGCGAGAGTGCTCCACCGCTGTGCGCCGAGGCTGGCAGAGCGC 865

Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 866 ACCCGACCTGCACCAACCCCGCTCCACTCAACGAGGGGGCTTTCTGCGAGGGCCAGGCA 925

Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 926 TTCCAGAAGACCGCTGCACCACCATCTGC 955

RESULT 11
US-10-087-684-3
; Sequence 3, Application US/10087684
; Publication No. US20040029116A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: MacDougall, John R.
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David J.
; APPLICANT: Grosse, William M.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie, J.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Shenoy, Suresh G.
```

```
; APPLICANT: Rastelli, Luca
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Miller, Charles E.
; APPLICANT: Gangolli, Esha A.
; TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-214 CIP
; CURRENT APPLICATION NUMBER: US/10/087,684
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: 60/253,834
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,926
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/264,180
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/274,194
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/313,656
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/327,456
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: Curaseqlist version 0.1
; SEQ ID NO 3
; LENGTH: 2860
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (59)..(2857)
US-10-087-684-3

Alignment Scores:
Pred. No.: 2,26e-20 Length: 2860
Score: 239.00 Matches: 39
Percent Similarity: 86.00% Conservative: 4
Best Local Similarity: 78.00% Mismatches: 7
Query Match: 82.41% Indels: 0
DB: 17 Gaps: 0

US-10-624-932c-2_COPY_246_295 (1-50) x US-10-087-684-3 (1-2860)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 806 TCCAGCTGGGCGAGAGTGCTCCACCGCTGTGCGCCGAGGCTGGCAGAGCGC 865

Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 866 ACCCGACCTGCACCAACCCCGCTCCACTCAACGAGGGGGCTTTCTGCGAGGGCCAGGCA 925

Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 926 TTCCAGAAGACCGCTGCACCACCATCTGC 955

RESULT 12
US-10-218-779-1
; Sequence 1, Application US/10218779
; Publication No. US20040029222A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit
; APPLICANT: MacDougall, John
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David
; APPLICANT: Gerlach, Valerie
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook II, John
; APPLICANT: Lepley, Denise
; APPLICANT: Rieger, Daniel
; APPLICANT: Burgess, Catherine
```

APPLICANT: Casman, Stacie
APPLICANT: Spytek, Kimberly
APPLICANT: Boldog, Ferenc
APPLICANT: Li, Li
APPLICANT: Padigaru, Muralidhara
APPLICANT: Mishra, Vishnu
APPLICANT: Patturajan, Meera
APPLICANT: Shenoy, Suresh
APPLICANT: Rastelli, Luca
APPLICANT: Tchernev, Velizar
APPLICANT: Vernet, Corine
APPLICANT: Zertusen, Bryan
APPLICANT: Malyankar, Uriel
APPLICANT: Guo, Xiaojia
APPLICANT: Miller, Charles
APPLICANT: Gangolli, Esha
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-214
CURRENT APPLICATION NUMBER: US/10/218,779
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: 60/253,834
PRIOR FILING DATE: 2000-11-29
PRIOR APPLICATION NUMBER: 60/250,-926
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 60/264,180
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/313,656
PRIOR FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: 60/327,456
PRIOR FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 216
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 2860
TYPE: DNA
ORGANISM: Homo sapiens
US-10-218-779-1

Alignment Scores:
Pred. No.: 2,26e-20 Length: 2860
Score: 239.00 Matches: 39
Percent Similarity: 86.00% Conservative: 4
Best Local Similarity: 78.00% Mismatches: 7
Query Match: 82.41% Indels: 0
DB: 17 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x US-10-218-779-1 (1-2860)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 806 TCCAGCTGGGCAGAGTGGTCCACCTGCTCCAAACCGCTGTGGCCGAGGCTGGCAGAAGCGC 865
Qy 21 SerArgSerCysThrAsnProAlaProLeuHsngGlyAlaPheCysGluGlyGlnAsn 40
Db 866 ACCCGGACCTGCACCAACCCCGCTCCACTCAACGAGGGGGCTTCTGCGAGGGCCAGGCA 925
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 926 TTCCAGAAGACCGCTGCACCATCTGCG 955

RESULT 13

US-10-218-779-3
Sequence 3, Application US/10218779
Publication No. US2004002922A1
GENERAL INFORMATION:
APPLICANT: Edinger, Shlomit
APPLICANT: MacDougall, John
APPLICANT: Millet, Isabelle
APPLICANT: Ellerman, Karen
APPLICANT: Stone, David
APPLICANT: Gerlach, Valerie
APPLICANT: Grosse, William
APPLICANT: Alsobrook II, John

APPLICANT: Lepley, Denise
APPLICANT: Rieger, Daniel
APPLICANT: Burgess, Catherine
APPLICANT: Casman, Stacie
APPLICANT: Spytek, Kimberly
APPLICANT: Boldog, Ferenc
APPLICANT: Li, Li
APPLICANT: Padigaru, Muralidhara
APPLICANT: Mishra, Vishnu
APPLICANT: Patturajan, Meera
APPLICANT: Shenoy, Suresh
APPLICANT: Rastelli, Luca
APPLICANT: Tchernev, Velizar
APPLICANT: Vernet, Corine
APPLICANT: Zertusen, Bryan
APPLICANT: Malyankar, Uriel
APPLICANT: Guo, Xiaojia
APPLICANT: Miller, Charles
APPLICANT: Gangolli, Esha
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-214
CURRENT APPLICATION NUMBER: US/10/218,779
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: 60/253,834
PRIOR FILING DATE: 2000-11-29
PRIOR APPLICATION NUMBER: 60/250,-926
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 60/264,180
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/313,656
PRIOR FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: 60/327,456
PRIOR FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 216
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 2860
TYPE: DNA
ORGANISM: Homo sapiens
US-10-218-779-3

Alignment Scores:
Pred. No.: 2,26e-20 Length: 2860
Score: 239.00 Matches: 39
Percent Similarity: 86.00% Conservative: 4
Best Local Similarity: 78.00% Mismatches: 7
Query Match: 82.41% Indels: 0
DB: 17 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x US-10-218-779-3 (1-2860)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 806 TCCAGCTGGGCAGAGTGGTCCACCTGCTCCAAACCGCTGTGGCCGAGGCTGGCAGAAGCGC 865
Qy 21 SerArgSerCysThrAsnProAlaProLeuHsngGlyAlaPheCysGluGlyGlnAsn 40
Db 866 ACCCGGACCTGCACCAACCCCGCTCCACTCAACGAGGGGGCTTCTGCGAGGGCCAGGCA 925
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 926 TTCCAGAAGACCGCTGCACCATCTGCG 955

RESULT 14

US-10-872-681-55
Sequence 55, Application US/10872681
Publication No. US2005002625A1
GENERAL INFORMATION:
APPLICANT: ARES TRADING LIMITED
TITLE OF INVENTION: TRANSMEMBRANE PROTEIN
FILE REFERENCE: P029209WO
CURRENT APPLICATION NUMBER: US/10/872,681
CURRENT FILING DATE: 2004-06-21

```
; PRIOR APPLICATION NUMBER: GB0130721.4
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 55
; LENGTH: 2868
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SEQ ID NO:33
US-10-872-681-55

Alignment Scores:
Pred. No.: 2,27e-20 Length: 2868
Score: 239.00 Matches: 38
Percent Similarity: 86.00% Conservative: 5
Best Local Similarity: 76.00% Mismatches: 7
Query Match: 82.41% Indels: 0
DB: 21 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x US-10-872-681-55 (1-2868)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 808 TCTTCTGGACAGAGTGGTCAGCCTGCAATGTTGCTGTGTAGAGGATGGCAGAAACGT 867

Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 868 TCCCGGACCTGCACCAACCCAGCTCCTCAATGTTGGGGCCCTTTGTGAGGGAATGTCA 927

Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 928 GTGCAGAAATAAACCCTGCACCTTCTCTTTGT 957

RESULT 15
US-10-037-417-37
; Sequence 37, Application US/10037417
; Publication No. US20040052806A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Alsobrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Patturajan, Meera
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Sciore, Paul
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Rothenberg, Mark
; APPLICANT: Stone, David J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Anderson, David W
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Miller, Charles E
; APPLICANT: Eisen, Andrew J
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-235
; CURRENT APPLICATION NUMBER: US/10/037,417
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/260,018
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,360
; PRIOR FILING DATE: 2001-01-08

; PRIOR APPLICATION NUMBER: 60/272,411
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/272,817
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/291,186
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/303,231
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/305,060
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/318,405
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/318,700
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 2895
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-037-417-37

Alignment Scores:
Pred. No.: 2,3e-20 Length: 2895
Score: 239.00 Matches: 39
Percent Similarity: 86.00% Conservative: 4
Best Local Similarity: 78.00% Mismatches: 7
Query Match: 82.41% Indels: 0
DB: 18 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x US-10-037-417-37 (1-2895)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 778 TCCAGCTGGGCGAGAGTGGTCACCTGTCTCCAAACCGCTGTGGCCGAGGCTGGCAGAGCGC 837

Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 838 ACCCGACCTGCACCAACCCCGCTCCACTCAACGAGGGGGCTTCTCGAGGGGCCAGGCA 897

Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 898 TTCCAGAGAGCCGCTGCACCAACCATCTGC 927

Search completed: September 9, 2005, 18:52:17
Job time : 502.956 secs
```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 8, 2005, 22:38:37 ; Search time 1645.59 Seconds
(without alignments)
1156.553 Million cell updates/sec

Title: US-10-624-932c-2_copy_246_295

Perfect score: 290

Sequence: 1 STWTWSVCSACRGWQK.....NGGAFCEQNVQKTACATLC 50

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool_h/US10624932/runat_08092005_161706_15792/app_query.fasta_1.1386
-DB=EST -QFMT=fastap -SURFIX=src -MINMATCH=0.1 -LOOPECL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=spct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10624932 @CGN 1 1 8180 @runat_08092005_161706_15792 -NCPU=6 -ICPU=3
-NO.MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hc1:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_g881:*
9: gb_g882:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	290	100.0	500	8 BZ921959	CH240_120
2	287	99.0	548	5 BX452510	EX452510
3	253	87.2	967	5 BU468894	BU468894 603363436
4	249	85.9	351	5 BY020742	BY020742 BY020742
5	249	85.9	602	9 CR012607	CR012607 Reverse s
6	249	85.9	856	7 CN164143	CN164143 994266 MA
7	249	85.9	875	7 CO807001	CO807001 AGENCOURT
8	249	85.9	2791	9 AY406493	AY406493 Mus muscu
9	249	85.9	2802	9 AY406491	AY406491 Homo sapi

10	249	85.9	2802	9	AY406492	Pan trogl
11	249	85.9	3790	3	AK031655	Mus muscu
12	240	82.8	774	5	BU365958	BU365958 603785840
13	239	82.4	594	6	CA771550	CA771550 i072f10_Y
14	239	82.4	681	2	BF313643	BF313643 601900292
15	239	82.4	733	5	BX920046	BX920046 BX920046
C 16	239	82.4	812	5	BX915627	BX915627 BX915627
17	239	82.4	2507	9	AY401470	AY401470 Pan trogl
18	239	82.4	2532	9	AY411747	AY411747 Homo sapi
19	239	82.4	2775	9	AY401469	AY401469 Homo sapi
20	238	82.1	386	6	CB806444	CB806444 AMGNNUC.N
21	238	82.1	678	2	BF098738	BF098738 601750874
22	238	82.1	679	7	CO045001	CO045001 UI-M-G10-
23	238	82.1	693	6	CB246544	CB246544 UI-M-F10-
24	238	82.1	801	7	CV110922	CV110922 AGENCOURT
25	238	82.1	2532	9	AY411749	AY411749 Mus muscu
26	238	82.1	2775	9	AY401471	AY401471 Mus muscu
27	238	82.1	3866	3	AK018177	AK018177 Mus muscu
28	236	81.4	720	1	A1959236	A1959236 fd25g10.Y
C 29	235	81.0	577	7	CO670344	CO670344 DG33-5803
30	229	79.0	354	4	BM257107	BM257107 520613 MA
31	228	78.6	487	5	BQ037844	BQ037844 pgn1c-pk0
32	228	78.6	709	1	AJ729963	AJ729963 AJ729963
33	228	78.6	746	5	BX872585	BX872585 BX872585
34	228	78.6	751	5	BX871388	BX871388 BX871388
C 35	228	78.6	761	5	BX878537	BX878537 BX878537
36	225	77.6	1175	9	CL642218	CL642218 CH213-26B
37	223	76.9	632	2	BE314077	BE314077 601146259
38	219	75.5	459	2	BE700724	BE700724 QV1-NN010
C 39	217	74.8	801	8	BZ880721	BZ880721 CH240_233
40	214	73.8	969	2	BF206813	BF206813 601870209
41	213	73.4	605	5	BX913103	BX913103 BX913103
42	210	72.4	1054	9	CNS02H8B	AL197300 Tetraodon
43	170.5	58.8	2532	9	AY411748	AY411748 Pan trogl
44	165	56.9	453	7	CN626234	CN626234 taes6d02
45	164	56.6	1034	4	BI758231	BI758231 603029876

ALIGNMENTS

RESULT 1
BZ921959/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BZ921959 500 bp DNA linear GSS 12-JUN-2003
CH240_120K19.TJ CHORI-240 Bos taurus genomic clone CH240_120K19,
genomic survey sequence.
BZ921959 GI:31647345
GSS.
Bos taurus (cow)
Bos taurus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1 (bases 1 to 500)
Larkin,D.M., Everts-van der Wind,A., Rebeiz,M., Schweitzer,P.,
Bachman,S., Green,S., Campos,E.J., Benson,L.D., Edwards,J., Liu,L.,
Womack,J.E., de Jong,P.J. and Lewin,H.A.
A Cattle-Human Comparative Map Built with Cattle BAC-ends and Human
Genome Sequence
Unpublished (2003)
Contact: Harris Lewin
Department of Animal Sciences
University of Illinois at Urbana Champaign
1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 217 333 5998
Fax: 217 244 5617
Email: h-lewin@uiuc.edu
Clones are derived from the bovine BAC library CHORI-240
available at <http://www.chori.org/bacpac/bovine240.htm>. For BAC library
availability, please contact Pieter de Jong (pdejong@mail.choi.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering_information.htm). This work
was undertaken as part of the International Bovine BAC Mapping

Consortium (IBBMC) by the University of Illinois at Urbana
Champaign, USA with funds provided by grant No. AG202-34480-11828
from USDA-CSREES and AG99-35205-8534 from USDA/NRI (Livestock
Genome Sequencing Initiative)
Plate: 120 row: K column: 19
Seq primer: SP6
Class: BAC ends.

FEATURES

Location/Qualifiers
1..500
/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="bred: Hereford"
/db_xref="taxon:9913"
/clone="CH240_120K19"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-240"
/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
Hereford bull L1 Domino 99175; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"

ORIGIN

Alignment Scores:
Pred. No.: 1,2e-20 Length: 500
Score: 290.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x BZ921959 (1-500)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 418 TCGAGCTGGAGTCTGCTCTGTCAGCGCCAGCTGTGGCGCGCGTGGCAGAAAAGG 359
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyAlaPheCysGluGlyGlnAsn 40
Db 358 AGCCGGAGCTGCACCAACCCGCGCTCTCAACGGGGGTGCTTCTGTGGGGGCGAGAA 299
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 298 GTCCAGAAAACAGCTGCGCCACCCTGTGTC 269

RESULT 2

BX452510
LOCUS BX452510 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
DEFINITION CS0DN001YE16 5-PRIME, mRNA sequence.
ACCESSION BX452510
VERSION BX452510.2 GI:47063451
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 548)
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 22, 2003 this sequence version replaced gi:31026396.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 3529.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?e=CS0BAG0692F06_CS06574_1&c=3529.f

FEATURES

Location/Qualifiers
1..548
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DN001YE16"
/tissue_type="ADULT BRAIN"
/dev_stage="adult"
/clone_lib="Homo sapiens ADULT BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

ORIGIN

Alignment Scores:
Pred. No.: 2,76e-20 Length: 548
Score: 287.00 Matches: 49
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 98.00% Mismatches: 0
Query Match: 98.97% Indels: 0
DB: 5 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x BX452510 (1-548)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 230 TCGACGTGGACCGAGTGTCTGTCAGCGCCAGCTGTGGCGCGGTGGCAGAAAACGG 289
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyAlaPheCysGluGlyGlnAsn 40
Db 290 AGCCGGAGCTGCACCAACCCGCGCTCTCAACGGGGGTGCTTCTGTGGGGGCGAGAA 349
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 350 GTTCAGAAAACAGCTGCGCCACCCTGTGTC 379

RESULT 3

BX468894
LOCUS BX468894 Gallus gallus CDNA clone ChEST258h9 5', mRNA
DEFINITION 603363436F1 CSEQBN21
ACCESSION BX468894
VERSION BX468894.1 GI:25962471
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 967)
Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
22335534
PUBMED 12445392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

FEATURES

Location/Qualifiers
1..967
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Layer"
/db_xref="taxon:9031"


```

Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 247 ACAAGAACCTGCACCAATCCAGCTCCACTCAATGCGGGGCGCTTCTGTGTGAGGGGCAGAGT 306
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 307 GTGCAGAAATAGCATGCACCTACGTTATGT 336

RESULT 5
LOCUS CR012607 602 bp DNA linear GSS 05-JUL-2004
DEFINITION Reverse strand read from insert in 5'HPRT insertion targeting and
chromosome engineering clone MHPN27n18, genomic survey sequence.
ACCESSION CR012607
VERSION CR012607.1 GI:49745653
KEYWORDS GSS; genome survey sequence; MICR.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 602)
AUTHORS Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
Rogers,J. and Bradley,A.
TITLE Direct Submission
JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. http://www.sanger.ac.uk/MICR
FEATURES
source
location/Qualifiers
1..602
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone_lib="MHPN27n18"
/clone_libs="MHPN"

ORIGIN
Alignment Scores: 3.11e-16 Length: 602
Pred. No.: 249.00 Matches: 41
Score: 94.00% Conservative: 6
Percent Similarity: 82.00% Mismatches: 3
Best Local Similarity: 85.86% Indels: 0
Query Match: 9 Gaps: 0
DB:

US-10-624-932C-2_COPY_246_295 (1-50) x CR012607 (1-602)
Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 451 TCCACCTGGACAGAGTGGTCTGTGTAAACAGCCGCTGTGGCGAGGATATCAGAAACGC 510
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 511 ACAAGAACCTGCACCAACCCAGCCCACTCAATGTTGGGGCGCTTCTGTGTGAGGGGCAGAGT 570
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 571 GTGCAGAAATAGCATGCACCTACGTTATGT 600

RESULT 6
LOCUS CN164143 856 bp mRNA linear EST 02-APR-2004
DEFINITION 994266 MARC 4P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION CN164143
VERSION CN164143.1 GI:46178573
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 856)
AUTHORS Smith,T.P.L., Freking,B.A., Ford,J.J., Vallet,J.L., Wise,T.A.,
Nonneman,D.J., Wray,J.E. and Keele,J.W.

```

```

TITLE Porcine EST collection using a normalized library constructed from
embryos representing early developmental stages
JOURNAL Unpublished (2003)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross match v0.990329.
Plate: TW8062 row: N column: 14
Seq primer: GTAATACGACTCACTATAGG.
FEATURES
source
location/Qualifiers
1..856
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 4P1G"
/note="vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with combined RNA from day-10, day-13,
day-15, day-25, and day-30 whole embryos."

ORIGIN
Alignment Scores: 4.7e-16 Length: 856
Pred. No.: 249.00 Matches: 41
Score: 94.00% Conservative: 6
Percent Similarity: 82.00% Mismatches: 3
Best Local Similarity: 85.86% Indels: 0
Query Match: 7 Gaps: 0
DB:

US-10-624-932C-2_COPY_246_295 (1-50) x CN164143 (1-856)
Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 566 TCCACCTGGACAGAGTGGTCTGTGTAAACAGCCGCTGTGGCGAGGATATCAGAAACGC 625
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 626 ACAAGAACCTGCACCAATCCAGCCCACTCAATGTTGGTGTCTTCTGTGAAGGCAGAGT 685
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 686 GTGCAGAAATAGCATGCCTGTACCACGTTGTGC 715

RESULT 7
LOCUS CO807001 875 bp mRNA linear EST 06-AUG-2004
DEFINITION AGENCOURT 30255333 NIH MGC 257 Mus musculus cDNA clone
IMAGE:30932367 5', mRNA sequence.
ACCESSION CO807001
VERSION CO807001.1 GI:51022265
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 875)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: csapbes-r@mail.nih.gov
Tissue Procurement: Dr. Kathleen Horner, Stanford University
cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

```

DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: NDA1181 row: i column: 16
High quality sequence stop: 671.
Location/Qualifiers

FEATURES

source
1..875
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:3092367"
/lab_host="DH10B Tona"
/clone_lib="NIH_MGC_257"
/note="Organ: oocyte; Vector: pExpress-1; Site 1: EcoRV;
Site 2: NotI; cDNA was primed using oligo-dT primer:
5'-pGACTAGTCTAGATCGGAGCGGCC(T)25-3' and cloned into
the EcoRV/NotI sites of pExpress-1. Size-selection >0.5 kb
resulted in an average insert size of 1.0kb. This is a
normalized library (primary library is NIH_MGC_256) and
was constructed by Express Genomics (Frederick, MD). Note:
this is a NIH_MGC library"

ORIGIN

Alignment Scores:
Pred. No.: 4,828-16 Length: 875
Score: 249.00 Matches: 41
Percent Similarity: 94.00% Conservative: 6
Best Local Similarity: 82.00% Mismatches: 3
Query Match: 85.86% Indels: 0
DB: 7 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x CO807001 (1-875)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
|||||
Db 181 TCCACCTGGACAGAGTGGTCTGTGTAAACAGCCGCTGTGGCGGAGGATATCAGAAACGC 240
|||||
Qy 21 SerArgSerCysThrAsnProAlaProLeuAanGlyGlyAlaPheCysGluGlyGlnAsn 40
|||||
Db 241 ACAAGAACCTGCACCAACCCAGCCCACTCAATGTGGGGCTTCTGTGAGGGGCGAGGT 300
|||||
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
|||||
Db 301 GTGCAGAAATAGCATGCACGTACGTTATGT 330
|||||

RESULT 8
AY406493
LOCUS
DEFINITION
Mus musculus UNC5C gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION
AY406493
VERSION
AY406493.1 GI:39762467
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM

REFERENCE
AY406493 2791 bp DNA linear GSS 15-DEC-2003
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Muridae; Mus.
1 (bases 1 to 2791)
AUTHORS
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios

JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
REFERENCE
2 (bases 1 to 2791)
AUTHORS
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE
Direct Submission

JOURNAL

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment.

FEATURES

source
1..2791
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
<1..>2791
/gene="UNC5C"
/locus_tag="HCW2575"

ORIGIN

Alignment Scores:
Pred. No.: 1,888-15 Length: 2791
Score: 249.00 Matches: 41
Percent Similarity: 94.00% Conservative: 6
Best Local Similarity: 82.00% Mismatches: 3
Query Match: 85.86% Indels: 0
DB: 9 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x AY406493 (1-2791)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
|||||
Db 785 TCCACCTGGACAGAGTGGTCTGTGTAAACAGCCGCTGTGGCGGAGGATATCAGAAACGC 844
|||||
Qy 21 SerArgSerCysThrAsnProAlaProLeuAanGlyGlyAlaPheCysGluGlyGlnAsn 40
|||||
Db 845 ACAAGAACCTGCACCAACCCAGCCCACTCAATGTGGGGCTTCTGTGAGGGGCGAGGT 904
|||||
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
|||||
Db 905 GTGCAGAAATAGCATGCACGTACGTTATGT 934
|||||

RESULT 9
AY406491
LOCUS
DEFINITION
Homo sapiens UNC5C gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION
AY406491
VERSION
AY406491.1 GI:39762465
KEYWORDS
GSS.
SOURCE
Homo sapiens (human)
ORGANISM

REFERENCE
AY406491 2802 bp DNA linear GSS 15-DEC-2003
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 2802)
AUTHORS
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios

JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
REFERENCE
2 (bases 1 to 2802)
AUTHORS
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE
Direct Submission

JOURNAL
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment.

FEATURES

source
1..2802
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1..>2802

gene

```

/ gene="UNC5C"
/ locus_tag="HCM2575"

ORIGIN
Alignment Scores:
Pred. No.: 1.89e-15 Length: 2802
Score: 249.00 Matches: 41
Percent Similarity: 94.00% Conservative: 6
Best Local Similarity: 82.00% Mismatches: 3
Query Match: 85.86% Indels: 0
DB: 9 Gaps: 0

US-10-624-932c-2_COPY_246_295 (1-50) x AY406491 (1-2802)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 796 TCCACCTGGACGGAGTGTCTGTGTAAACAGCCGCTGTGGACGAGGGTATCAGAAACGT 855

Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 856 ACAAGGACTTGTACCAACCCGACCACTCAATGGGGTGCCTTCTGTGAAGGCAGAGT 915

Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 916 GTGCAGAAAATAGCCTGTACTACGTTATGC 945

RESULT 11
AK031655 3790 bp mRNA linear HTC 03-APR-2004
LOCUS Mus musculus 13 days embryo male testis cDNA, RIKEN full-length
DEFINITION enriched library, clone:603047324 product:unc5 homolog (C.
elegans) 3, full insert sequence.
ACCESSION AK031655.1 GI:26327502
VERSION AK031655.1
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
9279253
PUBMED 10349636
2
REFERENCE
3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
PUBMED 11076861
4
REFERENCE
5 The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5
REFERENCE
6 The PANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3790)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,

```



```

US-10-624-932C-2_COPY_246_295 (1-50) x BU365958 (1-774)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
    |||||::|||
Db 320 TCCTCATGGAGCTGAGTGTCTCCAACTGCAACGCGCTGCGGTGCGGGCTGGCAGAGCGCA 379

Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
    |||||::|||
Db 380 TCGGGGACCTGCACCAACCCCTGCCCGCTCAACGAGGGGGCGGTCTCGAGGGGATGTCC 439

Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
    |||||::|||
Db 440 GTGCAGAGATCAGCTGCCTCTCTTTC 469

RESULT 13
LOCUS CA771550
DEFINITION CA771550 594 bp mRNA linear EST 03-DEC-2002
          i072f10.v1 HR85 islet Homo sapiens cDNA clone IMAGE:6131875 5',
          similar to TR:008722 008722 TRANSMEMBRANE RECEPTOR UNCSH2. ;, mRNA
          sequence.
ACCESSION CA771550
VERSION CA771550.1 GI:26008696
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 594)
          Melton, D., Brown, J., Kent, G., Permutt, A., Lee, C., Kaestner, K.,
          Lenishka, I., Scarce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
          Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,
          Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,
          Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R.,
          Williams, T., Jackson, Y., and Bowers, Y.
          Endocrine Pancreas Consortium
          Unpublished (2000)
          Other ESTs: i072f10.x1
          Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
          Endocrine Pancreas Consortium
          Harvard University, Howard Hughes Medical Institute
          Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
          MA 02138
          Tel: 617-495-1812
          Fax: 617-495-8557
          Email: dmelton@biohp.harvard.edu
          Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
          Washington University Genome Sequencing Center For information on
          obtaining a clone please contact: Dr. Hiroshi Inoue
          (hinoue@im.wustl.edu)
          Seq primer: -40RP from Gibco
          High quality sequence stop: 437.
          Location/Qualifiers
            1..594
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="IMAGE:6131875"
              /tissue_type="Purified pancreatic islet"
              /lab_host="DH10B"
              /clone_lib="HR85 islet"
              /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
              NotI; Site_2: XhoI; cDNA made by oligo-dT priming. Directionally
              Size-selected on agarose gel. Average insert size ~1kb. 5'
              XhoI site was destroyed after directional cloning.
              Amplified once. Contact information: Hiroshi Inoue, MD,
              Metabolism Div. (Alan Permutt Lab), Washington University
              School of Medicine, Box 8127, 660 South Euclid Ave., St.
              Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
              314-362-1916, Fax: 314-747-2692."

FEATURES
          source
            1..594
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="IMAGE:6131875"
              /tissue_type="Purified pancreatic islet"
              /lab_host="DH10B"
              /clone_lib="HR85 islet"
              /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
              NotI; Site_2: XhoI; cDNA made by oligo-dT priming. Directionally
              cloned into EcoRI/XhoI sites using the following 5'
              adaptor: GGCACGAG(G). Library constructed by Ling Hong
              in the laboratory of Gerald M. Rubin (University of
              California, Berkeley) using ZAP-cDNA synthesis kit
              (Stratagene) and Superscript II RT (Life Technologies).
              Note: this is a NIH_MGC Library."

ORIGIN
          Alignment Scores:
          Pred. No.: 4.06e-15 Length: 681
          Score: 239.00 Matches: 39
          Percent Similarity: 86.00% Conservative: 4
          Best Local Similarity: 78.00% Mismatches: 7
          Query Match: 82.41% Indels: 0
          DB: 2 Gaps: 0

```


US-10-624-932C-2_COPY_246_295 (1-50) x BF313643 (1-681)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerGlyArgGlyTrpGlnLysArg 20
Db 10 TCCAGCTGGGAGAGTGTTCACCTGTCTCCAAACCCCTGTGGCCGAGGCTGGCAGAGGCG 69
Qy 21 SerArgSerCysThrAsnProAlaProLeuAenGlyAlaPheCysGluGlyGlnAen 40
Db 70 ACCCGGACCTGCACCAACCCCGCTCCACTCAACGAGGGGCGCTTCTGGAGGGCCAGGCA 129
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 130 TTCCAGAGAGCGCGCTGCACCAACCATCTGC 159

RESULT 15
LOCUS BX920046/c
DEFINITION BX920046 Sus Scrofa library (scan) Sus scrofa cDNA clone
scan0009d.p.02 5prim, mRNA sequence.
ACCESSION BX920046
VERSION BX920046.1 GI:41136865
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa

REFERENCE
AUTHORS Bonnet,A., Tosser-Klopp,G., Benne,P., Cabau,C., Villegier,S.,
Soares,M., Ronaldo,F. and Hatey,P.
A Pig Normalised Multi-Tissue cDNA Library
Unpublished (2003)
COMMENT Contact: Tosser-Klopp G
Genetique Animale
Institut National de la Recherche Agronomique
Chemin de Borde-Rouge - Auzerville BP27, 31326 Castanet-Tolosan
cedex, FRANCE
Tel: 33 (0) 5.61.28.51.14
Fax: 33 (0) 5.61.28.53.08
Email: tosser@toulouse.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at signasupport@jouy.inra.fr to obtain the chromatogram of this
sequence.

Plate: 0009 row: p column: 2.

FEATURES
source

Location/Qualifiers
1..733
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="scan0009d.p.02"
/tissue_type="mixed"
/dev_stage="from embryos to adults"
/clone_lib="Sus Scrofa library (scan)"
/note="Tissues: adipose tissue, brain, kidney, liver,
muscle, ovary, testis, heart, hypothalamus, pancreas,
skin, spleen, thymus, placenta, pituitary gland, seminal
vesicle, small intestine, uterus, adrenals, bulbo urethral
gland, cerebral trunk, epididymis, female gonad,
gall-bladder, hippocampus, large intestine, male gonad,
melanocytes, stomach, udder"

ORIGIN

Alignment Scores:

Pred. No.: 4.43e-15 Length: 733
Score: 239.00 Matches: 38
Percent Similarity: 86.00% Conservative: 5
Best Local Similarity: 76.00% Mismatches: 7
Query Match: 82.41% Indels: 0
DB: 5 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x BX920046 (1-733)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerGlyArgGlyTrpGlnLysArg 20

Db 478 TCTTCTCGACAGAGTGGTCAAGCCTGCAATGTTTCGCTGTGTAGAGGATGCAGAAACGT 419
Qy 21 SerArgSerCysThrAsnProAlaProLeuAenGlyAlaPheCysGluGlyGlnAen 40
Db 418 TCCCGGACCTGCACCAATCCAGCTCCTCTCAATGTTGGGGCCTTTTGTGAGGGATGTCA 359
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 358 GTGCAGAAAAATAACCTGCACCTTCTCTCTGT 329

Search completed: September 9, 2005, 04:40:42
Job time : 1648.59 secs

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 8, 2005, 23:47:02 ; Search time 747.981 Seconds
(without alignments)
1166.064 Million cell updates/sec

Title: US-10-624-932C-2_COPY_372_389
Perfect score: 86
Sequence: 1 LVLLLVLLVYCRKKG 18

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+p2n model -DEV=xlh
-Q=/cgn2_1/USPTO_spool_h/US10624932/runat_08092005_161705_15773/app.query.fasta_1.1386
-DB=GenEmbl -QFWT=fastcap -SUPFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=spt -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=pt0 -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10624932 @CGN 1.1 7509 @runat_08092005_161705_15773 -NCPU=6 -ICPU=3
-NO_MMAP -LARGQUERY -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*
1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sv.*
13: gb.un.*
14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	86	100.0	604	AX451656	AX451656 Sequence
2	86	100.0	813	AX054892	AX054892 Sequence
3	86	100.0	1787	BD057525	BD057525 Netrin re
4	86	100.0	2688	BC009333	BC009333 Homo sapi

5	86	100.0	2697	6	AX451652	AX451652 Sequence
6	86	100.0	2752	6	AX449572	AX449572 Sequence
7	86	100.0	2784	6	CQ730306	CQ730306 Sequence
8	86	100.0	2881	6	AX527916	AX527916 Sequence
9	86	100.0	3580	6	AX367094	AX367094 Sequence
10	86	100.0	121282	9	AC027318	AC027318 Homo sapi
c 11	86	100.0	166534	2	AC034209	AC034209 Homo sapi
c 12	86	100.0	168168	2	AC012283	AC012283 Homo sapi
c 13	83	96.5	3844	10	BC058084	BC058084 Mus muscu
c 14	83	96.5	3992	10	MMU487852	AJ487852 Mus muscu
c 15	83	96.5	4294	10	AK122575	AK122575 Mus muscu
c 16	83	96.5	242128	2	AC123700	AC123700 Mus muscu
c 17	82	95.3	349	6	BD204134	BD204134 5'EST and
c 18	68	79.1	2697	6	AX268596	AX268596 Sequence
c 19	68	79.1	2697	10	RNU87305	U87305 Rattus norv
c 20	68	79.1	3014	6	BD057524	BD057524 Netrin re
c 21	68	79.1	171419	2	AC135142	AC135142 Rattus no
c 22	68	79.1	231407	2	AC139592	AC139592 Rattus no
c 23	60	69.8	184142	10	AC132356	AC132356 Mus muscu
c 24	60	69.8	213047	2	AC099622	AC099622 Mus muscu
c 25	59	68.6	174558	10	AC132092	AC132092 Mus muscu
c 26	58	67.4	3743	8	BT003880	BT003880 Arabidops
c 27	58	67.4	5520	6	AX046187	AX046187 Sequence
c 28	58	67.4	87434	8	AB010698	AB010698 Arabidops
c 29	58	67.4	161672	2	AC136667	AC136667 Rattus no
c 30	58	67.4	210514	10	AC117199	AC117199 Mus muscu
c 31	58	67.4	210829	2	AC105851	AC105851 Rattus no
c 32	58	67.4	223446	2	AC098637	AC098637 Rattus no
c 33	58	67.4	231933	2	AC113817	AC113817 Rattus no
c 34	58	67.4	234234	2	AC097194	AC097194 Rattus no
c 35	58	67.4	252127	2	AC108230	AC108230 Rattus no
c 36	58	67.4	257679	2	AC134801	AC134801 Rattus no
c 37	58	67.4	264875	2	AC107101	AC107101 Rattus no
c 38	57	66.3	247780	2	AC106305	AC106305 Rattus no
c 39	56	65.1	441	11	G67418	G67418 Hal196-ar S
c 40	56	65.1	851	6	BD092428	BD092428 Identific
c 41	56	65.1	1024	6	AX787900	AX787900 Sequence
c 42	56	65.1	10860	1	AE000589	AE000589 Helicobac
c 43	56	65.1	39735	5	TRU544609	AJ544609 Takifugu
c 44	56	65.1	66054	2	CEY102G3_3	Continuation (4 of
c 45	56	65.1	122592	3	CEY60A3A_	Continuation (4 of

ALIGNMENTS

RESULT 1	AX451656	Sequence 5 from Patent WO0233080.	604 bp	DNA	linear	PAT 03-JUL-2002
LOCUS	AX451656	Sequence 5 from Patent WO0233080.				
DEFINITION	AX451656	Sequence 5 from Patent WO0233080.				
ACCESSION	AX451656					
VERSION	AX451656.1	GI:21698589				
KEYWORDS						
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	1	Koehler,R.H.				
AUTHORS		Regulation of human netrin binding membrane receptor unc5h-1				
TITLE		Patent: WO 0233080-A 5 25-APR-2002;				
JOURNAL		Bayer Aktiengesellschaft (DE)				
FEATURES		Location/Qualifiers				
source		1..604				
		/organism="Homo sapiens"				
		/mol_type="unassigned DNA"				
		/db_xref="taxon:9606"				
ORIGIN						
Alignment Scores:						
Pred. No.:	0.000173	Length:	604			
Score:	86.00	Matches:	18			
Percent Similarity:	100.00%	Conservative:	0			
Best Local Similarity:	100.00%	Mismatches:	0			

FEATURES

1 LeuValLeuLeuValLeuIleLeuValTyrCvsArgLvsLvsGly 18

US-10-624-1

Query Match:	100.00%		Indels:	0
DB:	6		Gaps:	0
 US-10-624-932C-2_COPY_372_389 (1-18) x AX527916 (1-2881)				
Qy	1 LeuValLeuLeuLeuValLeuLleLeuValTyCyAArgLylySGLUGly 18 			
Db	1203 CTGGTCCTGCTGCTGTGTCCTCATCCCTCGTTATTCGGGAAGAGGGG 1256 			
 RESULT 9				
LOCUS	AX367094	3580 bp	DNA	linear PAT 16-FEB-2002
DEFINITION	Sequence 13 from Patent WO0198354.			
ACCESSION	AX367094			
VERSION	AX367094.1 GI:18855296			
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
TITLE	1 Griffin,J.A., Kallick,D.A., Tribouley,C.M., Yue,H., Nguyen,D.B., Tang,Y.T., Lal,P., Policky,J.L., Azimzai,Y., Lu,D.A., Graul,R., Yao,M.G., Burford,N., Hafalia,A.J., Baughn,M.R., Bandman,O., Patterson,C., Yang,J., Xu,Y., Warren,B.A., Ding,L. and Sanjanwala,M.S. Receptors			
JOURNAL	Patent: WO 0198354-A 13 27-DEC-2001; Incyte Genomics, Inc. (US)			
FEATURES	Location/Qualifiers source 1..3580 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606" /notes="inocyte ID No: 6052371CB1"			
 ORIGIN				
Alignment Scores:				
Pred. No.:	0.000986	Length:	3580	
Score:	86.00	Matches:	18	
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
DB:	6	Gaps:	0	
 US-10-624-932C-2_COPY_372_389 (1-18) x AX367094 (1-3580)				
Qy	1 LeuValLeuLeuLeuValLeuLleLeuValTyCyAArgLylySGLUGly 18 			
Db	949 CTGGTCCTGCTGCTGTGTCCTCATCCCTCGTTATTCGGGAAGAGGGG 1002 			
 RESULT 10				
LOCUS	AC027318	121282 bp	DNA	linear PRI 01-DEC-2002
DEFINITION	Homo sapiens chromosome 5 clone CTC-347K15, complete sequence.			
ACCESSION	AC027318			
VERSION	AC027318.5 GI:259899047			
KEYWORDS	HTG.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
TITLE	1 (bases 1 to 121282) DOE Joint Genome Institute and Stanford Human Genome Center. Direct Submission			
REFERENCE	2 (bases 1 to 121282) Unpublished			
AUTHORS	DOE Joint Genome Institute.			
TITLE	Direct Submission			
JOURNAL	Submitted (30-MAR-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA			
REFERENCE	3 (bases 1 to 121282) DOE Joint Genome Institute.			
AUTHORS	DOE Joint Genome Institute.			

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 8, 2005, 20:54:46 ; Search time 93.0905 Seconds
(without alignments)
1144.643 Million cell updates/sec

Title: US-10-624-932C-2_COPY_372_389
Perfect score: 86
Sequence: 1 LVLLLLLVLYCRKKEG 18

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters: -MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO spool_h/US10624932/runat_08092005 161705 15766/app_query.fasta_1.1386
-DB=N Geneseq -QFWT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10624932 @CGN 1.1 1052 @runat_08092005 161705 15766 -NCPU=6 -ICPU=3
-NO_MMAP -LARGQUERY -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq 16Dec04:*
1: Geneseqn1980a:*
2: Geneseqn1990a:*
3: Geneseqn2000a:*
4: Geneseqn2001a:*
5: Geneseqn2002a:*
6: Geneseqn2003a:*
7: Geneseqn2004a:*
8: Geneseqn2005a:*
9: Geneseqn2006a:*
10: Geneseqn2007a:*
11: Geneseqn2008a:*
12: Geneseqn2009a:*
13: Geneseqn2010a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	86	100.0	390	4 AAh99392	Aah99392 Human pro
2	86	100.0	604	6 ABK52893	Abk52893 Human net
3	86	100.0	813	4 AAC90917	Aac90917 Human UNC
4	86	100.0	1009	12 ADH71615	Adh71615 Human gen
5	86	100.0	1787	2 AAV52941	Aav52941 Human UNC

RESULT 1	
AAH99392	
ID	AAH99392 standard; cDNA; 390 BP.
XX	
AC	AAH99392;
XX	
DT	16-OCT-2001 (first entry)
XX	
DE	Human protein encoding cDNA sequence SEQ
XX	
KW	Human; cancer; ulcer; HIV infection; human
KW	antiinflammatory; antirheumatic; antiarth
KW	antibacterial; endocrine; cardiac; centr
KW	anti-HIV; fungicide; antimutagen; cardio
KW	antiagregant; haemostatic; vulnery; ant
KW	dermatological; antiallergic; antiaasthma
KW	neuroprotective; antidepressant; nootropi
KW	immunostimulant; gene therapy; antisease
KW	antianaphylactic; rheumatoid arthritis; s
KW	cardiac dysfunction; neuropathology; card
KW	genetic disease; haematopoietic disorder;
KW	thrombocytopenia; osteoporosis; severe c
KW	allergic rhinitis; diabetes; multiple scl
KW	Alzheimer's disease; Parkinson's disease;
KW	neurological disorder; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200153455-A2.

ALIGNMENTS

Db 89 CTGGTCCTGCTGCTCTCTCTCATCTCTCGTTATTGCCGGAAGAGGGG 142

RESULT 6

ADH71623

ID ADH71623 standard; DNA; 2463 BP.

XX AC ADH71623;

XX DT 25-MAR-2004 (first entry)

XX DE Human gene of the invention NOV21h SEQ ID NO:519.

XX KW ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;

XX KW anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;

XX KW cancer; cachexia; Alzheimer's disease; Parkinson's disease;

XX KW obesity; diabetes; infectious disease; metabolic syndrome X;

XX KW dyslipidaemia.

XX OS Homo sapiens.

XX PN WO2003102155-A2.

XX PD 11-DEC-2003.

XX PF 03-JUN-2003; 2003WO-US017430.

XX PR 03-JUN-2002; 2002US-0385120P.

PR 04-JUN-2002; 2002US-0385784P.

PR 05-JUN-2002; 2002US-0386041P.

PR 05-JUN-2002; 2002US-0386047P.

PR 06-JUN-2002; 2002US-0386376P.

PR 06-JUN-2002; 2002US-0386864P.

PR 06-JUN-2002; 2002US-0387016P.

PR 07-JUN-2002; 2002US-0386796P.

PR 07-JUN-2002; 2002US-0386816P.

PR 07-JUN-2002; 2002US-0386931P.

PR 07-JUN-2002; 2002US-0386942P.

PR 07-JUN-2002; 2002US-0386971P.

PR 07-JUN-2002; 2002US-0387262P.

PR 08-JUN-2002; 2002US-0296960P.

PR 10-JUN-2002; 2002US-0387400P.

PR 10-JUN-2002; 2002US-0387535P.

PR 11-JUN-2002; 2002US-0387610P.

PR 11-JUN-2002; 2002US-0387625P.

PR 11-JUN-2002; 2002US-0387634P.

PR 11-JUN-2002; 2002US-0387668P.

PR 11-JUN-2002; 2002US-0387696P.

PR 11-JUN-2002; 2002US-0387702P.

PR 11-JUN-2002; 2002US-0387836P.

PR 11-JUN-2002; 2002US-0387859P.

PR 12-JUN-2002; 2002US-0387933P.

PR 12-JUN-2002; 2002US-0387934P.

PR 12-JUN-2002; 2002US-0387960P.

PR 12-JUN-2002; 2002US-0388022P.

PR 12-JUN-2002; 2002US-0388096P.

PR 13-JUN-2002; 2002US-0389123P.

PR 14-JUN-2002; 2002US-0389118P.

PR 14-JUN-2002; 2002US-0389120P.

PR 14-JUN-2002; 2002US-0389144P.

PR 14-JUN-2002; 2002US-0389146P.

PR 17-JUN-2002; 2002US-0389729P.

PR 17-JUN-2002; 2002US-0389742P.

PR 18-JUN-2002; 2002US-0389884P.

PR 19-JUN-2002; 2002US-0390006P.

PR 19-JUN-2002; 2002US-0390209P.

PR 21-JUN-2002; 2002US-0390763P.

PR 17-JUL-2002; 2002US-0396706P.

PR 06-AUG-2002; 2002US-0401628P.

PR 09-AUG-2002; 2002US-0402156P.

PR 09-AUG-2002; 2002US-0402256P.

PR 09-AUG-2002; 2002US-0402389P.

PR 12-AUG-2002; 2002US-0402786P.

PR 12-AUG-2002; 2002US-0402816P.

PR 12-AUG-2002; 2002US-0402821P.

PR 12-AUG-2002; 2002US-0402832P.

PR 13-AUG-2002; 2002US-0403488P.

PR 13-AUG-2002; 2002US-0403459P.

PR 13-AUG-2002; 2002US-0403531P.

PR 13-AUG-2002; 2002US-0403532P.

PR 13-AUG-2002; 2002US-0403563P.

PR 13-AUG-2002; 2002US-0406317P.

PR 15-AUG-2002; 2002US-0403617P.

PR 26-AUG-2002; 2002US-0406182P.

PR 26-AUG-2002; 2002US-0406355P.

PR 27-AUG-2002; 2002US-0406240P.

PR 12-SEP-2002; 2002US-0410084P.

PR 20-SEP-2002; 2002US-0412528P.

PR 23-SEP-2002; 2002US-0412731P.

PR 30-SEP-2002; 2002US-0414801P.

PR 30-SEP-2002; 2002US-0414839P.

PR 30-SEP-2002; 2002US-0414840P.

PR 30-SEP-2002; 2002US-0414954P.

PR 09-OCT-2002; 2002US-0417186P.

PR 09-OCT-2002; 2002US-0417406P.

PR 23-OCT-2002; 2002US-0420639P.

PR 28-OCT-2002; 2002US-0421156P.

PR 31-OCT-2002; 2002US-0422690P.

PR 01-NOV-2002; 2002US-0423130P.

PR 05-NOV-2002; 2002US-00423798.

PR 12-NOV-2002; 2002US-0423798P.

PR 12-NOV-2002; 2002US-0425453P.

XX PA (CURA-) CURAGEN CORP.

XX PI Alsbrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;

PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;

PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;

PI Gusev VI, Herrmann JL, Jekuda R, Li L, Liu X, MacDougall JR;

PI MacLachlan T, Malyankar UM, Mexick AJ, Millet I, Mishra VS;

PI Padigaru M, Patturajan M, Pena CEA, Feyman JA, Raha D, Rastelli L;

PI Rieger DK, Rothenberg ME, Sciore P, Shency SG, Shinkets RA;

PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;

XX Zhong H;

XX WPI; 2004-081935/08.

DR P-PSDB; ADH71624.

XX PT New NOVX polypeptides and nucleic acid molecules useful for preventing or

PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or

PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

XX Example 21; SEQ ID NO 519; 1880pp; English.

PS The invention relates to a novel isolated polypeptide (NOVX). A

CC polypeptide of the invention has cytostatic, immunomodulator,

CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and

CC antilipemic activity, and may have a use in gene therapy, and as a

CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising

CC any of the 303 fully defined nucleotide sequences given in the

CC specification. The polypeptide is useful in the manufacture of a

CC medicament for treating a syndrome associated with a human disease. The

CC polypeptide, polynucleotide and antibody are useful in diagnosing,

CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,

CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious

CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are

CC further used as hybridisation probes, in chromosome mapping, tissue

CC typing, preventive medicine, and pharmacogenomics. The present sequence

CC encodes a NOVX polypeptide of the invention.

XX SQ Sequence 2463 BP; 470 A; 828 C; 721 G; 444 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0.00268 Length: 2463

Score: 86.00 Matches: 18

Percent Similarity: 100.00% Conservative: 0

CC encodes a NOVX polypeptide of the invention.

XX Sequence 2575 BP; 490 A; 873 C; 754 G; 458 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0.00282	Length:	2575
Score:	86.00	Matches:	18
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	12	Gaps:	0

US-10-624-932C-2_COPY_372_389 (1-18) x ADH71621 (1-2575)

Qy 1 LeuValLeuLeuValLeuValLeuValTyrCysArgLysGluGly 18
|||||

Db 921 CTGGTCCTGCTGCTGCTGCTCATCTCGTTATTCGCGGAGAGAGGGG 974
|||||

RESULT 8

ADN95100

ID ADN95100 standard; DNA; 2635 BP.

XX AC ADN95100;

XX 01-JUL-2004 (first entry)

DT Human LEC gene sequence SeqID22.

DE

XX growth; differentiation; blood endothelial cell; BEC;

XX lymphatic endothelial cell; LEC; hereditary lymphoedema; VEGFR-3;

KW lymphatic growth agent; VEGF-C; VEGF-D; antiangiogenic; cytosstatic;

KW vasotrophic; antiinflammatory; gene therapy; endothelial cell disorder;

KW inflammatory disease; cancer metastasis; lymphatic system; gene; ds;

XX human.

XX Homo sapiens.

OS

XX WO2003080640-A1.

XX 02-OCT-2003.

XX 07-MAR-2003; 2003WO-US006900.

PF

XX 07-MAR-2002; 2002US-0363019P.

PR

XX (LUDW-) LUDWIG INST CANCER RES.

PA (LIGN) LICENTIA LTD.

XX Alitalo K, Makinen T, Petrova T, Saharinen P, Saharinen J;

PI

XX WPI; 2003-876899/81.

DR P-PSDB; ADN95115.

XX Claim 23; SEQ ID NO 22; 176pp; English.

PS

CC This invention relates to a method of differentially modulating the growth or differentiation of blood endothelial cells (BEC) or lymphatic endothelial cells (LEC) comprises contacting endothelial cells with a composition comprising an agent that differentially modulates blood or lymphatic endothelial cells. Treating hereditary lymphoedema comprises identifying a human subject with lymphoedema and with a mutation in at least one allele of a gene encoding a LEC protein, where the mutation correlates with lymphoedema in human subjects, and with the proviso that the LEC protein is not VEGFR-3, and administering to the subject a composition comprising a lymphatic growth agent selected from VEGF-C or VEGF-D polypeptides and polynucleotides. The invention may be useful for the development of compounds with an antiangiogenic, cytosstatic, vasotrophic or antiinflammatory activity or for gene therapy. The method is useful in modulating the growth or differentiation of blood endothelial cells or lymphatic endothelial cells, in treating hereditary lymphoedema, in screening for an endothelial cell disorder or predisposition to the disorder or in monitoring the efficacy or toxicity of a drug on endothelial cells. The agent is useful in manufacturing a

CC medicament for the differential modulation of blood vessel endothelial cell or lymphatic vessel endothelial cell growth or differentiation. The lymphatic growth agent may also be used in manufacturing a medicament for the treatment of hereditary lymphoedema resulting from a mutation in a LEC gene or of other diseases involving the lymphatic vessels, such as various inflammatory diseases and cancer metastasis via the lymphatic system. The present sequence is that of a human LEC/BEC differentially expressed gene which is related to the method of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX ftp.wipo.int/pub/published_pct_sequences

XX Sequence 2635 BP; 483 A; 935 C; 722 G; 495 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0.0029	Length:	2635
Score:	86.00	Matches:	18
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	11	Gaps:	0

US-10-624-932C-2_COPY_372_389 (1-18) x ADN95100 (1-2635)

Qy 1 LeuValLeuLeuValLeuValLeuValTyrCysArgLysGluGly 18
|||||

Db 44 CTGGTCCTGCTGCTGCTGCTCATCTCGTTATTCGCGGAGAGAGGGG 97
|||||

RESULT 9

ABK52891

ID ABK52891 standard; DNA; 2697 BP.

XX AC ABK52891;

XX 27-AUG-2002 (first entry)

DT Human netrin binding membrane receptor UNC5H-1 DNA sequence #1.

DE

XX Netrin binding membrane receptor; receptor; UNC5H-1; gene; ds; human;

KW neurotropic; neuroprotective; cytosstatic; antiparkinsonian;

KW cerebroprotective; cancer; central nervous system; CNS; stroke;

KW Parkinson's disease; multiple sclerosis; Alzheimer's disease.

XX Homo sapiens.

OS

XX Key Location/Qualifiers

FT CDS 1..2697

FT /*tag= a

FT /product= "Netrin binding membrane receptor UNC5H-1"

XX WO200233080-A2.

XX 25-APR-2002.

XX 15-OCT-2001; 2001WO-EP011891.

XX 16-OCT-2000; 2000US-0240061P.

XX (FARB) BAYER AG.

XX Koehler RH;

XX WPI; 2002-463314/49.

XX P-PSDB; AAU97899.

XX Novel human netrin binding membrane receptor polypeptide and polynucleotides for identifying modulating agents useful in treating diseases e.g. Parkinson's disease, multiple sclerosis, stroke, Alzheimer's disease.

XX Claim 1; Fig 1; 94pp; English.

PS This invention relates to the DNA and protein sequences of a novel

CC

ADG42568
ID ADG42568 standard; cDNA; 2881 BP.
XX
XX ADG42568;
XX AC
XX AC
XX AC
DT 26-FEB-2004 (first entry)
XX
XX
DE Novel human NOV1 cDNA.
XX
XX cytostatic; gene therapy; NOVX-agonist; NOVX-antagonist; pharmaceutical;
KW NOVX-associated disorder; cancer; human; gene; ss.
KW
XX
XX Homo sapiens.
OS
XX US2003204052-A1.
PN
XX
XX 30-OCT-2003.
PD
XX
XX 04-OCT-2001; 2001US-00970944.
PF
XX
XX 04-OCT-2000; 2000US-0237862P.
PR
XX
XX (HERR/) HERRMANN J L.
PA (RAST/) RASTELLI L.
PA (SHIM/) SHIMKETS R A.
PA
XX
XX Herrmann JL, Rastelli L, Shinkets RA;
PI
XX
XX WPI: 2003-900673/82.
DR P-PSDB; ADG42569.
DR
XX
XX New NOVX gene or NOVX-specific antibody, useful for preparing a
PT composition for treating or preventing a NOVX-associated disorder, e.g.,
PT cancer.
PT
XX
XX Claim 9; SEQ ID NO 1; 118pp; English.
PS
XX
XX The invention describes a new isolated polypeptide comprising: a
CC polypeptide or its mature form comprising a sequence not given in the
CC specification; or a variant of (A), where one or more amino acid residue
CC in the variant differs in no more than 15% from the amino acid sequence
CC of the mature form. The pharmaceutical composition may be administered
CC via oral, transdermal, rectal or parenteral route. The polypeptide,
CC nucleic acid or antibody is useful for preparing a composition for
CC treating or preventing a NOVX-associated disorder, e.g., cancer. This
CC sequence encodes a human NOVX protein.
XX
XX Sequence 2881 BP; 526 A; 987 C; 866 G; 502 T; 0 U; 0 Other;
SQ

Alignment Scores:
Pred. No.: 0.00321 Length: 2881
Score: 86.00 Matches: 18
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-624-932C-2_COPY_372_389 (1-18) x ADG42568 (1-2881)

Qy 1 LeuValLeuLeuValLeuValLeuValLeuValTyrCysArgGlyLysGluGly 18
|||
Db 1203 CTGGTCCTGCTGCTCTGCTCTCATCTCTCGTTATTGCGGAAGAAGAGGGG 1256
|||

RESULT 15
ADH71649
ID ADH71649 standard; DNA; 2881 BP.
XX
XX AC
XX ADH71649;
XX
DT 25-MAR-2004 (first entry)
XX
XX Human gene of the invention NOV21u SEQ ID NO:545.
DE
XX

Job time : 96.0905 secs

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 8, 2005, 23:51:22 ; Search time 28.6914 Seconds
(without alignments)
1026.543 Million cell updates/sec

Title: US-10-624-932C-2_COPY_372_389
Perfect score: 86
Sequence: 1 LVLLLLLVILVCRKKG 18

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool_b/US10624932/runat_08092005_161706_15822/app_query.fasta_1.1366
-DB=Issued_Patents_NA -QFMT=fastcap -SUFFIX=rn1 -MINMATCH=0.1 -LOOPCT=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10624932.cgn1_1.187 @runat_08092005_161706_15822 -NCPU=6 -ICPU=3
-NO_MMAPP -LARGQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PTCUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	86	100.0	1787	2	US-08-808-982-2
2	86	100.0	1787	3	US-09-306-902A-2
3	82	95.3	349	4	US-09-471-276-345
4	68	79.1	3014	2	US-08-808-982-1
5	68	79.1	3014	3	US-09-306-902A-1
6	52	60.5	3111	2	US-09-014-969-12
7	52	60.5	3881	4	US-09-774-528-139
8	51	59.3	1410	4	US-09-270-767-13235
9	51	59.3	138282	4	US-09-949-016-15307
10	49	57.0	866	4	US-09-629-222A-44
11	49	57.0	1514	4	US-09-629-222A-5
12	49	57.0	1854	1	US-08-249-420-1

c 13	49	57.0	1854	2	US-08-737-663-1	Sequence 1, Appli
c 14	49	57.0	37715	4	US-09-949-016-13846	Sequence 13846, A
c 15	49	57.0	44342	4	US-09-949-016-12661	Sequence 12661, A
c 16	48.5	56.4	601	4	US-09-949-016-117417	Sequence 117417, A
c 17	48.5	56.4	601	4	US-09-949-016-117418	Sequence 117418, A
c 18	48.5	56.4	601	4	US-09-949-016-117419	Sequence 117419, A
c 19	48.5	56.4	114842	4	US-09-949-016-14993	Sequence 14993, A
c 20	48	55.8	201	4	US-09-248-796A-9121	Sequence 9121, Ap
c 21	48	55.8	1231	4	US-09-270-767-13014	Sequence 13014, A
c 22	48	55.8	1666	4	US-09-270-767-15102	Sequence 15102, A
c 23	48	55.8	2907	4	US-09-248-796A-3444	Sequence 3444, Ap
c 24	48	55.8	7475	2	US-08-971-036-1	Sequence 1, Appli
c 25	48	55.8	7475	3	US-08-056-570-1	Sequence 1, Appli
c 26	48	55.8	7475	3	US-09-265-617B-1	Sequence 1, Appli
c 27	48	55.8	26335	4	US-09-949-016-17602	Sequence 17602, A
c 28	48	55.8	49559	4	US-09-949-016-12892	Sequence 12892, A
c 29	48	55.8	49559	4	US-09-949-016-17267	Sequence 17267, A
c 30	48	55.8	79858	4	US-09-949-016-16080	Sequence 16080, A
c 31	47.5	55.2	1431	4	US-09-248-796A-5089	Sequence 5089, Ap
c 32	47	54.7	207	4	US-09-248-796A-12822	Sequence 12822, A
c 33	47	54.7	309	4	US-09-248-796A-13696	Sequence 13696, A
c 34	47	54.7	601	4	US-09-949-016-25895	Sequence 25895, A
c 35	47	54.7	601	4	US-09-949-016-25896	Sequence 25896, A
c 36	47	54.7	601	4	US-09-949-016-25897	Sequence 25897, A
c 37	47	54.7	601	4	US-09-949-016-35779	Sequence 35779, A
c 38	47	54.7	601	4	US-09-949-016-35780	Sequence 35780, A
c 39	47	54.7	601	4	US-09-949-016-35857	Sequence 35857, A
c 40	47	54.7	601	4	US-09-949-016-35858	Sequence 35858, A
c 41	47	54.7	601	4	US-09-949-016-35934	Sequence 35934, A
c 42	47	54.7	601	4	US-09-949-016-35935	Sequence 35935, A
c 43	47	54.7	601	4	US-09-949-016-36021	Sequence 36021, A
c 44	47	54.7	601	4	US-09-949-016-36022	Sequence 36022, A
c 45	47	54.7	601	4	US-09-949-016-61325	Sequence 61325, A

ALIGNMENTS

RESULT 1
US-08-808-982-2
; Sequence 2, Application US/08808982
; Patent No. 5939271
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; APPLICANT: Leonardo, E. David
; APPLICANT: Hink, Lindsey
; APPLICANT: Masu, Masayuki
; APPLICANT: Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF INVENTIONS: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,982
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 2:


```

; REFERENCE/DOCKET NUMBER.: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3014 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-306-902A-1

Alignment Scores:
Pred. No.: 0.171 Length: 3014
Score: 68.00 Matches: 14
Percent Similarity: 83.33% Conservative: 1
Best Local Similarity: 77.78% Mismatches: 3
Query Match: 79.07% Indels: 0
DB: 3 Gaps: 0

US-10-624-932C-2_COPY_372_389 (1-18) x US-09-306-902A-1 (1-3014)

Qy 1 LeuValLeuLeuLeuValLeuValLeuValTyrCysArgLysLeuGly 18
Db 1114 CTCCTTCCTGCTGTTGTCGCGCCCTTGACCTCATTTACTGTCGAAGAAGAGGG 1157

```

RESULT 6
US-09-014-969-12
; Sequence 12, Application US/09014969
; Patent No. 5965397
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Racie, Lisa A.

; AFFILIANT: Merberg, David
 ;
 ; APPLICANT: Treacy, Maurice
 ; APPLICANT: Spaulding, Vikki
 ; APPLICANT: Agostino, Michael J.

TITLE OF INVENTION: ENCODING THEM
 NUMBER OF SEQUENCES: 32
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genetics Institute, Inc.
 STREET: 87 CambridgePark Drive
 CITY: Cambridge
 STATE: MA
 COUNTRY: U.S.A.
 ZIP: 02140
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/014,969
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Sprunger, Suzanne A.
 REGISTRATION NUMBER: 41,323
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 498-8284
 TELEFAX: (617) 876-5851
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3111 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA

US-09-014-969-12

Alignment Scores:		
Pred. No.:	74.8	3111
Score:	52.00	9
Percent Similarity:	87.50%	Conservative: 5
Best Local Similarity:	5.25%	Mismatches: 2
Query Match:	60.47%	Indels: 0
DB:	2	Gaps: 0

US-10-624-932C-2 COPY 372 389 (1-18) x US-09-014-969-12 (1-3111)

Qy 1 LeuValLeuLeuLeuValLeuIleLeuValTyrCysArgLys 16
:::|||||::| | | | | | | | | | | | | | | | | | | |
Db 99 ATACTTTGGTTTTGCTGTGTCCTCTTTATATTATTGCAGGGAAG 146

RESULT 7

US-09-774-528-139

```

; Sequence 139, Application US/09774528
; Patent No. 6743619
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Yang, Yonghong
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wang, Dunrui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6743619el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 802
; CURRENT APPLICATION NUMBER: US/09/774,528
; CURRENT FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: pt FL genes Version 2.0

```

; LENGTH: 3881

```

;
; TYPE: DNA
; ORGANISM: Homo sapiens
;
; FEATURE:
;
; NAME/KEY: CDS
; LOCATION: (66)..(2738)
US-09-774-528-139

```

Alignment Scores:

Pred. No.:	98.3	Length:	3891
Score:	52.00	Matches:	9
Percent Similarity:	87.50%	Conservative:	5
Best Local Similarity:	56.25%	Mismatches:	2
Query Match:	60.41%	Indels:	0
DB:	4	Gaps:	0

US-10-624-932C-2 COPY 372 389 (1-18) x US-09-774-528-139 (1-3881)

Qy 1 LeuValLeuLeuLeuValLeuValLeuValTyrCysArgLysLys 16
:::>:::::~:
Dd 1011 ATACTTTGGTTTTGCTGTCTCTCTTTATATTATTCAGAGGAAG 1058

RESULT 8

US-09-270-767-13235/c
; Sequence 13235, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
; FILE REFERENCE: File Reference: 7326-094

```

; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0

```

; LENGTH: 1410
 ; TYPE: DNA
 ; ORGANISM: Drosophila melanogaster
 US-09-270-767-13235

Alignment Scores:

Pred. No.:	40.9	Length:	1410
Score:	51.00	Matches:	9
Percent Similarity:	92.31%	Conservative:	3
Best Local Similarity:	69.23%	Mismatches:	1
Query Match:	59.30%	Indels:	0
DB:	4	Gaps:	0

US-10-624-932C-2 COPY 372 389 (1-18) x US-09-270-767-13235 (1-1410)

QY 1 LeuValLeuLeuLeuValLeuIleLeuValTyrCys 13
:::|||||:::|||||:::|||||
Db 376 ATAGTCCTGCTCCCTTTTGATCTCTGCTGCTTACTGC 338

RESULT 9

US-09-949-016-15307/c
: Sequence 15307, Application US/09949016

; FACEID NO: 0812333
: GENERAL INFORMATION:

1
 2
 3
 4
 5
 6
 7
 8
 9
 10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100
 101
 102
 103
 104
 105
 106
 107
 108
 109
 110
 111
 112
 113
 114
 115
 116
 117
 118
 119
 120
 121
 122
 123
 124
 125
 126
 127
 128
 129
 130
 131
 132
 133
 134
 135
 136
 137
 138
 139
 140
 141
 142
 143
 144
 145
 146
 147
 148
 149
 150
 151
 152
 153
 154
 155
 156
 157
 158
 159
 160
 161
 162
 163
 164
 165
 166
 167
 168
 169
 170
 171
 172
 173
 174
 175
 176
 177
 178
 179
 180
 181
 182
 183
 184
 185
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200
 201
 202
 203
 204
 205
 206
 207
 208
 209
 210
 211
 212
 213
 214
 215
 216
 217
 218
 219
 220
 221
 222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250
 251
 252
 253
 254
 255
 256
 257
 258
 259
 260
 261
 262
 263
 264
 265
 266
 267
 268
 269
 270
 271
 272
 273
 274
 275
 276
 277
 278
 279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500
 501
 502
 503
 504
 505
 506
 507
 508
 509
 510
 511
 512
 513
 514
 515
 516
 517
 518
 519
 520
 521
 522
 523
 524
 525

```

: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/237,768
: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: 60/231,498
: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SEQ ID NOS: 207012
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 15307
: LENGTH: 138282

```

TYPE: DNA
ORGANISM: Human

; ORGANISM: HUMMAN
US-09-949-016-15307

Alignment Scores:

Pred. No.:	1, 2e+04	Length:	138282
Score:	51.00	Matches:	10
Percent Similarity:	87.50%	Conservative:	4
Best Local Similarity:	62.50%	Mismatches:	2
Query Match:	59.30%	Indels:	0
DB:	4	Gaps:	0

US-10-624-932C-2 COPY 372 389 (1-18) X US-09-949-016-15307 (1-138282)

Qy

1 LeuValLeuLeuLeuValLeuValTyrCysArgLysLys 16
|||::|||||:|||:::|||::|||

Dd

120447 TTTATTAATTATAATTATAATTATAACGTGAGACAAGA 12

RESULT, T 10

```

US-09-629-222A-44
; Sequence 44, Application US/09629222A
;
; GENERAL INFORMATION:
; APPLICANT: Bellacosa, Alfonso
; TITLE OF INVENTION: Methods for Detecting
; TITLE OF INVENTION: Single-Nucleotide
; FILE REFERENCE: PCCC 96-21
; CURRENT APPLICATION NUMBER: US/09/629

```

```
; CURRENT FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 09/463,891
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: PCT/US98/15828
; PRIOR FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: 60/053,936
; PRIOR FILING DATE: 1997-07-28
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 866
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-629-222A-44

Alignment Scores:
Pred. No.:      47.7      Length:      866
Score:          49.00     Matches:      10
Percent Similarity: 80.00% Conservative: 2
Best Local Similarity: 66.67% Mismatches: 3
Query Match:    56.98% Indels:      0
DB:             4       Gaps:        0

US-10-624-932C-2_COPY_372_389 (1-18) x US-09-629-222A-44 (1-866)
Qy   1 LeuValLeuLeuValLeuValLeuValTyrCysArgLys 15
Db   87 CTTTCCTTAAGCCTGAAGATTTAAATTACTGTACTGCCGAAAG 131

RESULT 11
US-09-629-222A-5
; Sequence 5, Application US/09629222A
; Patent No. 6599700
; GENERAL INFORMATION:
; APPLICANT: Bellacosa, Alfonso
; TITLE OF INVENTION: Methods for Detection of Transition
; FILE REFERENCE: FCCC 96-21
; CURRENT APPLICATION NUMBER: US/09/629,222A
; CURRENT FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 09/463,891
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: PCT/US98/15828
; PRIOR FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: 60/053,936
; PRIOR FILING DATE: 1997-07-28
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1514
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-629-222A-5

Alignment Scores:
Pred. No.:      95.2      Length:      1514
Score:          49.00     Matches:      10
Percent Similarity: 80.00% Conservative: 2
Best Local Similarity: 66.67% Mismatches: 3
Query Match:    56.98% Indels:      0
DB:             4       Gaps:        0

US-10-624-932C-2_COPY_372_389 (1-18) x US-09-629-222A-5 (1-1514)
Qy   1 LeuValLeuLeuValLeuValLeuValTyrCysArgLys 15
Db   289 CTTTCCTTAAGCCTGAAGATTTAAATTACTGTACTGCCGAAAG 333

RESULT 12
US-08-249-420-1
; Sequence 1, Application US/08249420
; Patent No. 5484724
; GENERAL INFORMATION:
; APPLICANT: El-Sherbeini, Mohamed
; TITLE OF INVENTION: DNA ENCODING GLS1
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christine E. Carty
; STREET: 126 E. Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/249,420
FILING DATE: 26-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Carty, Christine E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 19162
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-6734
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1854 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-249-420-1

Alignment Scores:
Pred. No.:      122      Length:      1854
Score:          49.00     Matches:      8
Percent Similarity: 87.50% Conservative: 6
Best Local Similarity: 50.00% Mismatches: 2
Query Match:    56.98% Indels:      0
DB:             1       Gaps:        0

US-10-624-932C-2_COPY_372_389 (1-18) x US-08-249-420-1 (1-1854)
Qy   3 LeuLeuLeuValLeuLeuValTyrCysArgLysGlugly 18
Db   1714 CTATTGTACTATTACATCATTTATTATTATAAAGACCGGATGGT 1761

RESULT 13
US-08-737-663-1
; Sequence 1, Application US/08737663
; Patent No. 5955337
; GENERAL INFORMATION:
; APPLICANT: El-Sherbeini, Mohamed
; TITLE OF INVENTION: DNA ENCODING GLS1
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Joseph A. Coppola - MERCK & CO., INC.
; STREET: 126 E. Lincoln Avenue - P.O. Box 2000
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/737,663
```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 9, 2005, 04:41:16 ; Search time 179.624 Seconds
(without alignments)
658.098 Million cell updates/sec

Title: US-10-624-932c-2_COPY_372_389
Perfect score: 86
Sequence: 1 LVLLLVLLVYCRKKG 18

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 7351250 seqs, 3283620254 residues

Total number of hits satisfying chosen parameters: 14702500

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool_h/US10624932/runat_08092005.161709_15882/app_query.fasta_1.1386
-DB=Published Applications_NA -QFMT=fastcap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -WMAP=US10624932 @cgn 1 1.989 @runat 08092005.161709_15882
-NCPU=6 -ICPU=3 -NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT_DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications_NA:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	86	100.0	390	18	US-10-296-115-227
2	86	100.0	1787	10	US-09-933-261-2
3	86	100.0	1787	14	US-10-256-702-2
4	86	100.0	2752	18	US-09-918-779-1
5	86	100.0	2752	18	US-10-624-932-1
6	86	100.0	2881	10	US-09-970-944-1
7	86	100.0	3561	20	US-10-643-795A-77
8	86	100.0	3561	21	US-10-948-518-77
9	86	100.0	3580	17	US-10-311-623-13
c 10	86	100.0	9582	9	US-09-764-861-62
c 11	86	100.0	9582	10	US-09-764-861-62
c 12	86	100.0	9582	14	US-10-115-928-62
c 13	86	100.0	18772	9	US-09-764-861-63
c 14	86	100.0	18772	10	US-09-764-861-63
c 15	86	100.0	18772	14	US-10-115-928-63
c 16	82	95.3	349	21	US-10-246-883-345
c 17	68	79.1	2697	16	US-10-240-154-15
c 18	68	79.1	3014	10	US-09-933-261-1
c 19	68	79.1	3014	14	US-10-256-702-1
c 20	56	65.1	851	9	US-09-895-913A-47
c 21	54	62.8	1587	18	US-10-425-114-14571
c 22	54	62.8	1875	20	US-10-739-930-939
c 23	53	61.6	225	17	US-10-242-535A-14360
c 24	53	61.6	225	18	US-10-085-783A-14360
c 25	53	61.6	327	19	US-10-674-124A-5507
c 26	53	61.6	403	18	US-10-424-599-43127
c 27	53	61.6	1594	9	US-09-823-245A-412
c 28	53	61.6	2066	21	US-10-764-420-2078
c 29	53	61.6	3015	15	US-10-033-388-1
c 30	53	61.6	18605	14	US-10-057-726-17
c 31	53	61.6	18855	15	US-10-311-455-584
c 32	53	61.6	20083	20	US-10-723-860-3920
c 33	53	61.6	2731748	19	US-10-297-465A-1
c 34	52	60.5	843	17	US-10-369-493-46895
c 35	52	60.5	978	19	US-10-437-963-49300
c 36	52	60.5	2579	19	US-10-437-963-40594
c 37	52	60.5	3518	17	US-10-437-963-49301
c 38	52	60.5	3881	17	US-10-120-988-139
c 39	52	60.5	3958	17	US-10-172-118-263
c 40	52	60.5	3958	18	US-10-342-887-263
c 41	52	60.5	3958	22	US-10-756-149-520
c 42	51	59.3	218	19	US-10-674-124A-26691
c 43	51	59.3	287	19	US-10-674-124A-13058
c 44	51	59.3	449	19	US-10-674-124A-16394
c 45	51	59.3	643	13	US-10-027-632-47786

ALIGNMENTS

RESULT 1

US-10-296-115-227
; Sequence 227, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296.115
; PRIOR FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488.725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552.317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 227


```

RESULT 5
US-10-624-932-1
; Sequence 1, Application US/10624932
; Publication No. US2004009687A1
; GENERAL INFORMATION:
; APPLICANT: Taupier, Raymond
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Raestelli, Luca
; APPLICANT: Spaderna, Steven
; APPLICANT: Shimkets, Richard
; APPLICANT: Zerkusen, Bryan
; APPLICANT: Spytek, Kimberly
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Guev, Vladimir
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook, John
; APPLICANT: Lepley, Denise
; APPLICANT: Burgess, Catherine
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Smithson, Glennda
; TITLE OF INVENTION: Novel Proteins and Nu
; FILE REFERENCE: 21402-074 US
; CURRENT APPLICATION NUMBER: US/10/624,932
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: 09/918,779
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/221,409
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/222,840
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,752
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,762
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,770
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,769
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/225,146
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/225,392
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/225,470
; PRIOR FILING DATE: 2000-08-15
; Remaining Prior Application data removed
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2752
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-624-932-1

```

Alignment Scores:		
Pred. No.:	0.00335	Length:
Score:	86.00	Matches:
Percent Similarity:	100.00%	Conservative:
Best Local Similarity:	100.00%	Mismatches:
Query Match:	100.00%	Indels:
DB:	18	Gaps:
US-10-624-932C-2	COPY 372 389 (1-18)	x US-10-624-932-1 (1-2752)

QY 1 LeuValLeuLeuValLeuIleLeuValTyrCysArgLysLysGluGly 18

Db 1159 CTGGTCTGCTGCTGTGCTCTCATCTCGTTTATTGCCGGAAGAAGAGGGG 1212

RESULT 6
US-09-970-944-1


```

RESULT 10
US-09-764-861-62/c
; Sequence 62, Application US/09764861
; Publication No. US20020086811A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT204
; CURRENT APPLICATION NUMBER: US/09/764,861
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
; LENGTH: 9582
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-861-62

Alignment Scores:
Pred. No.: 0.0155 Length: 9582
Score: 86.00 Matches: 18
Percent Similarity: 100.00% Conservative: 0

```

```

05-10-115-928-027C
; Sequence 62, Application US/10115928
; Publication No. US20030092615A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ04CL
; CURRENT APPLICATION NUMBER: US/10/115,928
; CURRENT FILING DATE: 2002-04-05
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
; LENGTH: 9582
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-115-928-62

Alignment Scores:
Pred. No.: 0.0155 Length: 9582
Score: 86.00 Matches: 18
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-624-932C-2_COPY_372_389 (1-18) x US-10-115-928-62 (1-9582)
Oy 1 LeuValLeuLeuValLeuValLeuValTyrCysArgLysIysG

```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 8, 2005, 22:38:37 ; Search time 592.413 Seconds
(without alignments)
1156.553 Million cell updates/sec

Title: US-10-624-932c-2_COPY_372_389
Perfect score: 86
Sequence: 1 LVLLLVLLVYCRKEG 18

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-O=/cgn2_1/USPTO spool h/US10624932/runat_08092005_161706_15792/app_query.fasta_1.1386
-DB=EST -QFMT=fastap -SUPFIX=first -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=BLOSUM62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10624932 @CNC 1 1 8180 @runat_08092005_161706_15792 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hcc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gesl:*
9: gb_gses2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	86	100.0	604	2	BE314370 601147261
2	86	100.0	859	2	BF311896 601897733
3	86	100.0	934	2	BF311804 601897316
4	86	100.0	1532	3	BC033727 Homo sapi
5	83	96.5	501	7	CN691436 E0309E05-
6	83	96.5	548	4	BI900830 ib81g04.y
7	83	96.5	675	6	CA315487 UI-M-FW0
8	83	96.5	723	5	BU613458 UI-M-EW0-
9	83	96.5	756	5	BU612387 UI-M-EW0-

10	83	96.5	788	6	CA317532	UI-M-FW0-
11	72	83.7	872	7	CF585872	AGENCOURT
12	70	81.4	608	4	BM487397	pgm2n.pk0
13	66	76.7	514	5	BX522364	BX522364
14	66	76.7	815	7	CK1340529	AGENCOURT
15	65	75.6	531	8	BH657369	BOMFY84TF
16	65	75.6	683	8	BH963887	odh84e02..
17	65	75.6	789	8	BZ445020	BONMX88TF
18	60	69.8	560	1	A1558191	vk25f10.y
19	60	69.8	572	1	AA543602	vk25f10.y
20	58	67.4	405	9	CNS00XJG	Arabidops
21	58	67.4	676	3	CNS08LLI	Single re
22	58	67.4	1008	3	CNS08VZJ	Single re
23	56	65.1	243	8	AZ762451	1M0557P09
24	56	65.1	379	7	CV184054	ta191a12.
25	56	65.1	459	8	BZ674458	PUBXB86TD
26	56	65.1	547	7	CO371148	taht70g05
27	56	65.1	580	5	BP505476	BP505476
28	56	65.1	659	8	CC165132	1189c09.b
29	56	65.1	743	8	BZ822958	PUFAY31TD
30	56	65.1	776	8	BZ822956	PUFAY31TB
31	56	65.1	812	9	CC661906	OGUDY06TV
32	56	65.1	814	8	AQ411942	CPG0921B
33	56	65.1	841	7	CV180913	ta185a08.
34	56	65.1	858	9	CC682181	OGOBM86TH
35	56	65.1	917	9	CNS07DXS	AL441062 T7 end of
36	56	65.1	920	9	CG276138	OG3AG23TV
37	56	65.1	938	9	CNS07D8D	AL440147 T7 end of
38	56	65.1	1009	5	BU857896	AGENCOURT
39	55	64.0	236	1	AV252353	AV252353
40	55	64.0	416	6	CD586290	AK035A3E0
41	55	64.0	552	9	TA232G02P	AL481052 T. brucei
42	55	64.0	582	5	BX872954	BX872954
43	55	64.0	587	5	BX911995	BX911995
44	55	64.0	603	7	CN748091	CN748091
45	55	64.0	684	9	CE274919	tigr-gss-

RESULT 1

BE314370

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

601147261F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3162710 5', mRNA linear EST 26-OCT-2000

mRNA sequence.

BE314370

BE314370.1 GI:9135413

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgaabbs@email.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: Image.llnl.gov

Plate: LLCM122 row: i column: 15

High quality sequence stop: 601.

Location/Qualifiers

1. 604

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone=IMAGE:3162710"

/tissue_type="neuroblastoma"

FEATURES

source

ALIGNMENTS

RESULT 1
BE314370
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BE314370 601147261F1 NIH_MGC_19 Homo sapiens cdna clone IMAGE:3162710 5', mRNA linear EST 26-OCT-2000
mRNA sequence.
BE314370 GI:9135413
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 604)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
plate: LLCml22 row: i column: 15
High quality sequence stop: 601.
Location/Qualifiers
1. .604
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3162710"
/tissue_type="neuroblastoma"

FEATURES
source

```

/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_19"
/notes="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 0.00252 Length: 604
Score: 86.00 Matches: 18
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-624-932C-2_COPY_372_389 (1-18) x BE314370 (1-604)

Qy 1 LeuValLeuLeuLeuValLeuValTyrCysArgLysLysGluGly 18
|||||
Db 25 CTGGTCCTGCTGCTTGTCTCATCTCTGTTATTGCCGGAAGAGAGGGG 78

RESULT 2
BF311896 859 bp mRNA linear EST 21-NOV-2000
LOCUS 601897733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126760 5',
DEFINITION mRNA sequence.
ACCESSION BF311896
VERSION BF311896.1 GI:11259667
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 859)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCMI017 row: b column: 09
High quality sequence stop: 684.
Location/Qualifiers
1. 859
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="neuroblastoma"
/clone_lib="NIH_MGC_19"
/clone_host="DH10B (phage-resistant)"
/notes="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 0.00369 Length: 859
Score: 86.00 Matches: 18
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-624-932C-2_COPY_372_389 (1-18) x BF311804 (1-934)

Qy 1 LeuValLeuLeuLeuValLeuValTyrCysArgLysLysGluGly 18
|||||
Db 45 CTGGTCCTGCTGCTTGTCTCATCTCTGTTATTGCCGGAAGAGAGGGG 98

RESULT 4
BC033727

```

```

Score: 86.00 Matches: 18
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-624-932C-2_COPY_372_389 (1-18) x BF311896 (1-859)

Qy 1 LeuValLeuLeuLeuValLeuValTyrCysArgLysLysGluGly 18
|||||
Db 44 CTGGTCCTGCTGCTTGTCTCATCTCTGTTATTGCCGGAAGAGAGGGG 97

RESULT 3
BF311804 934 bp mRNA linear EST 21-NOV-2000
LOCUS 601897316F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126706 5',
DEFINITION mRNA sequence.
ACCESSION BF311804
VERSION BF311804.1 GI:11259566
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 934)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCMI016 row: p column: 03
High quality sequence stop: 707.
Location/Qualifiers
1. 934
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="neuroblastoma"
/clone_lib="NIH_MGC_19"
/clone_host="DH10B (phage-resistant)"
/notes="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 0.00404 Length: 934
Score: 86.00 Matches: 18
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-624-932C-2_COPY_372_389 (1-18) x BF311804 (1-934)

Qy 1 LeuValLeuLeuLeuValLeuValTyrCysArgLysLysGluGly 18
|||||
Db 45 CTGGTCCTGCTGCTTGTCTCATCTCTGTTATTGCCGGAAGAGAGGGG 98

RESULT 4
BC033727

```


sequence located between the Not-1 site and the polyA tail, is GTCGCGAA. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (EMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

Alignm

Score:	83.00	Matches:	15
Percent Similarity:	100.00%	Conservative:	3
Best Local Similarity:	83.33%	Mismatches:	0
Query Match:	96.51%	Indels:	
DB:	5	Gaps:	0
US-10-624-932C-2_COPY_372_389 (1-18) x BU613458 (1-723)			
Qy	1	LeuValLeuLeuLeuValLeuLeuLeuValTyrCysArgLysLysGluGly	18
Db	609	CTCATCTTCGTGCTGCTGCTCGTCCTCATCTACTGCGCAAGGAAGGAAGA	662

RESULT_9	BU612387	756 bp	mRNA	linear	EST 20-FEB-2003
LOCUS	UI-M-EWO-cax-j-06-0-UI.r1	NIH BMAP_EWO Mus musculus cDNA clone			
DEFINITION	UI-M-EWO-cax-j-06-0-UI 5', mRNA sequence.				
ACCESSION	BU612387				
VERSION	BU612387.1	GI:23278602			
KEYWORDS	EST.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 756)				
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
	Unpublished (1999)				
CONTACT	Robert Strausberg, Ph.D.				
EMAIL	cgapbs-r@mail.nih.gov				
TISSUE	Tissue Procurement: Dr. James Lin, University of Iowa				
COMMENT					

cdna Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

```

FEATURES
source
seq primer: pax-3
Location/Qualifiers
1..756
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="UI-N-EMQ-cax-j-06-0-UI"
/tissue_type="whole brain"
/dev_stage="embryo 15.5 dpc"
/lab_host="DH10B (T1 phage resistant)"

```

/note="Organ: brain; Vector: pYX-Asc; Site 1: Ecor I; Site 2: Not I; The library was constructed" according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with Ecor I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is GTGCTGGAA. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous

primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGACGACG. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

[illegible]

Qy	1	LeuValLeuLeuLeuValLeuLeuLeuValTleuValTtCysArgIysIysGluGly	18
Db	350	CTCATCTTGCTGTGTCGGTCCCTCGTCTCATCTACTACGCCAAGAAGGA	403
RESULT	8		
BU613458			
LOCUS			
DEFINITION		723 bp mRNA linear EST 20-FEB-2003	
		UI-M-EWO-carz-d-10-0-UI.r1 NTH_ENAP_EWO Mus musculus CDNA clone	
		UI-M-EWO-carz-d-10-0-UI 5', mRNA sequence.	
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA sequencing by: Dr. M. Bento Soares, University of Iowa

This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
 Seq primer: pYX-5.
 Location/Qualifiers
 1..723
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"

```

/tissue_type="whole brain"
/dev_stage="embryo 15.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_EWO"
/notes="Organ: Brain; Vector: pYX-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was size selected according to mRNA size fraction,
ligated with EcoR I adaptor, digested with Not I, and then
cloned directionally into pYX-Asc vector. The library tag

```



```

DEFINITION BX522364 Life Tech mouse embryo 8 5dpc 10664019 Mus musculus cDNA clone IMAGE998P091372 ; IMAGE:569336, mRNA sequence.
ACCESSION BX522364
VERSION   BX522364.1 GI:32302310
KEYWORDS EST.
SOURCE    Mus musculus (house mouse)
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 514)
AUTHORS   Heil O., Ebert L., Neubert P., Peters M., Radelof U., Schneider D. and Korn B.
TITLE      Mouse Unigeneset - RZPD2
COMMENT    Unpublished (2003)
           Contact: Ina Rolfs
           RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
           Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
           RZPD; IMAGP998P091372.
           RZPDLIB; I.M.A.G.E. CDNA Clone Collection;
           Mouse Unigeneset - RZPD2 (RZPDLIB No.981)
           http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi?responseLibNo=981 Contact: Ina Rolfs
           RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
           Heubnerweg 6, D-14059 Berlin, Germany
           Tel: +49 30 32639 101
           Fax: +49 30 32639 111
           www.rzpd.de
FEATURES   This clone is available royalty-free from RZPD;
           contact RZPD (clone@rzpd.de) for further information. Seq primer: SP6, Primer sequence: ATTGGTGACACTAG.
           Location/Qualifiers
             1..514
               /organism="Mus musculus"
               /mol_type="mRNA"
               /strain="C57BL/6J"
               /db_xref="taxon:10090"
               /clone="IMAGP998P091372 ; IMAGE:569336"
               /issue_type="embryo"
               /dev_stage="8.5dpc embryos"
               /lab_host="DH10B"
               /clone_lib="Life Tech mouse embryo 8 5dpc 10664019"
               /notes="Organ: whole embryo; Vector: pCMV-SPORT2; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. 8.5dpc embryos. pCMV-SPORT2 vector."
ORIGIN
Alignment Scores:
Pred. No.:          2.73              Length:          514
Score:              66.00            Matches:         13
Percent Similarity: 94.12%           Conservative:     3
Best Local Similarity: 76.47%        Mismatches:      1
Query Match:        76.74%           Indels:          0
DB:                  5                Gaps:            0

US-10-624-932C-2_COPY_372_389 (1-18) x BX522364 (1-514)

Qy      1 LeuValLeuLeuValLeuValLeuValLeuValTyCyseArgLysGlu 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      464 CTCATCTTCGTGCTGCTGCCTCCCTCATCTACTGCGCAAGAAGAA 514

RESULT 14
LOCUS    CK140529
DEFINITION AGENCOURT_16806288 NCI_CGAP_ZEmB3 Danio rerio cDNA clone
IMAGE:7058133 5', mRNA sequence.
ACCESSION CK140529
VERSION   CK140529.1 GI:38651455
KEYWORDS EST.
SOURCE    Danio rerio (zebrafish)
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

```

ORIGIN

Alignment Scores:
Pred. No.: 4.49 Length: 815
Score: 66.00 Matches: 14
Percent Similarity: 88.89% Conservative: 2
Best Local Similarity: 77.78% Mismatches: 2
Query Match: 76.74% Indels: 0
DB: 7 Gaps: 0

US-10-624-932C-2_COPY_372_389 (1-18) x CK140529 (1-815)

Qy 1 LeuValLeuLeuLeuValLeuValLeuValTyrCysArgLysLysGluGly 18
||| |||||||:::|||||:::|||||
Db 122 CTGGCTCTGCTGTCTGTGTCTGTCTGTGTGTACCGCAGGAAGAAGGAGGCT 175

RESULT 15
BH657369
LOCUS BH657369 531 bp DNA linear GSS 19-FEB-2002
DEFINITION BOMFY84TF BO 2.3 KB Brassica oleracea genomic clone BOMFY84,
genomic survey sequence.
ACCESSION BH657369
VERSION BH657369.1 GI:18715746
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 531)
Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 8, 2005, 23:47:02; Search time 4321.67 Seconds
(without alignments)
1166.064 Million cell updates/sec

Title: US-10-624-932C-2_COPY_495_598

Perfect score: 559
Sequence: 1 TSNMTYGTFTNFGRLMIPN.....CCEPSPDSWLRLLKQSCG 104

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO spool_h/US10624932/runat_08092005_161705_15773/app_query.fasta_1.1386
-DB=GenEmbl -QFMT=fastap -SUFFIX=rg -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10624932@cgn2_1.17509 @runat_08092005_161705_15773 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPRLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- GenEmbl.*
1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	559	100.0	2688	9 BC009333	BC009333 Homo sapi
2	559	100.0	2697	6 AX451652	AX451652 Sequence
3	559	100.0	2752	6 AX449572	AX449572 Sequence
4	559	100.0	2881	6 AX527916	AX527916 Sequence

5	559	100.0	3580	6	AX367094	AX367094 Sequence	
6	559	100.0	9700	6	AX054976	AX054976 Sequence	
7	554	99.1	3844	10	BC058084	BC058084 Mus muscu	
8	554	99.1	3992	10	MMU487852	AJ487852 Mus muscu	
9	553	98.9	1787	6	BD057525	BD057525 Netrin re	
10	553	98.9	2697	6	AX268596	AX268596 Sequence	
11	553	98.9	2697	10	RNU87305	U87305 Rattus norv	
12	553	98.9	3014	6	BD057524	BD057524 Netrin re	
13	520	93.0	813	6	AX054892	AX054892 Sequence	
14	465.5	83.3	2784	6	CQ730306	CQ730306 Sequence	
C	15	394.5	70.6	242128	2	AC123700	AC123700 Mus muscu
16	393.5	70.4	6495	9	AB075856	AB075856 Homo sapi	
C	17	393.5	70.4	6522	6	BD186447	BD186447 Novel gen
18	393.5	70.4	121282	9	AC027318	AC027318 Homo sapi	
C	19	393.5	70.4	166534	2	AC034209	AC034209 Homo sapi
C	20	393.5	70.4	168168	2	AC012283	AC012283 Homo sapi
C	21	393.5	70.4	231407	2	AC139592	AC139592 Rattus no
22	374	66.9	604	6	AX451656	AX451656 Sequence	
23	348	62.3	9299	10	MMU72634	U72634 Mus musculu	
24	346	61.9	2962	5	AY187310	AY187310 Gallus ga	
25	345	61.7	9328	10	AB118026	AB118026 Rattus no	
26	337	60.3	2986	6	CQ881052	CQ881052 Sequence	
27	337	60.3	3646	6	CQ881060	CQ881060 Sequence	
28	337	60.3	3646	9	AF055634	AF055634 Homo sapi	
29	333	59.6	1575	6	AX054890	AX054890 Sequence	
30	318	56.9	1393	6	AX054886	AX054886 Sequence	
31	318	56.9	2612	6	CQ881064	CQ881064 Sequence	
32	318	56.9	2780	6	CQ881054	CQ881054 Sequence	
33	318	56.9	4330	5	AY744919	AY744919 Petromyzo	
34	309	55.3	2832	5	AY099459	AY099459 Xenopus l	
35	297	53.1	1438	6	AX054888	AX054888 Sequence	
36	287	51.3	770	6	BD147921	BD147921 Primer fo	
37	287	51.3	770	6	AX867859	AX867859 Sequence	
38	287	51.3	1948	6	BD159676	BD159676 Primer fo	
39	287	51.3	1948	6	AX882354	AX882354 Sequence	
40	287	51.3	1948	9	AX022859	AX022859 Homo sapi	
41	287	51.3	2406	6	AX833115	AX833115 Sequence	
42	287	51.3	2406	9	AK094595	AK094595 Homo sapi	
43	287	51.3	2625	6	CQ721377	CQ721377 Sequence	
44	287	51.3	2860	6	AX686445	AX686445 Sequence	
45	287	51.3	2860	6	AX686447	AX686447 Sequence	

ALIGNMENTS

BC009333	2688 bp	mRNA	linear	PRI 25-MAR-2004
Homo sapiens unc-5 homolog A (C. elegans), mRNA (CDNA clone IMAGE:4126760), partial cds.				
BC009333				
BC009333.2	GI:40226527			
Homo sapiens (human)				
Homo sapiens				
Eukaryota				
Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
1 (bases 1 to 2688)				
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Shat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toehy, T.S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., McKernan, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., Abramson, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,				

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalusz, D.E., Scherch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932
 2 (bases 1 to 2688)
 Strausberg, R.
 Direct Submission
 Submitted (12-JUN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
 NIH-MGC Project URL: <http://mgc.nhl.nih.gov>
 On Dec 19, 2003 this sequence version replaced gi:11424611.
 Contact: MGC help desk
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 Sequencing by: National Institutes of Health Intramural Gaithersburg, Maryland;
 Web site: <http://www.nisec.nih.gov/>
 Contact: nisc_mgc@hgrl.nih.gov
 Akter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granito, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Skantripop, S., Thomas, P.J., Touchman, J.W., Turgeon, C., Vogt, J.D., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAL Plate: 26 Row: g Column: 22.

FEATURES
 source
 1..2688
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4126760"
 /tissue_type="Brain, neuroblastoma"
 /clone_lib="NIH_MGC_19"
 /lab_host="DH10B-R"
 /note="Vector: pOTB7"
 <1..2688
 /gene="UNC5A"
 /note="synonym: UNC5H1"
 /db_xref="locusID:90249"
 /db_xref="MIM:607869"
 <1..1627
 /gene="UNC5A"
 /codon_start=2
 /product="UNC5A protein"
 /protein_id="AAH09333.2"
 /db_xref="GI:40226528"
 /db_xref="LocusID:90249"
 /db_xref="MIM:607869"
 /translation="DVALYVGLIAVAVCLVLLVLLVYCKKGLDSDVDSSILTSGFQVSKPKSKANDPHLLTLOPLDSTTTTYYQSLCPQDGPSPKQLTWGHLLSPLCGGRTLHSSPTSAEFVSRSLSTQNYFRSLPRGTSNMTYGTNFGRLRMIPNTGILSLIPPDAPKGIYIYLLHKPDPVRLPLAGCQTLSPVSCGPGVLLTRPVILAMHDCGSPDSNLFRLKQSCGSEWEDVHLGEEAPSHLYCYOLEASACYFTFQLGRFALVGEALSVAAEKLLKLLFAPVACTSLEYNIRVYCLHDTHDALKEVQLKQGGQLOEPRVLHFQVYHNLRSLTHDPVSSLKSLVSYOEIPFYHWNGTQRYLHCTFTLERSVPSLDLACKLWVQVGDGQSFNINFTKDTFAELLALAESEAGVPALVGPSAFKLPFLRQKLIISLDPPCRGADWRITLAKLHLDLSLFFASKPSPTAMILNWEARHFNPNGLUSQLAAVAGVQPDAGLFTVSEAC"
 413..724
 /gene="UNC5A"

misc_feature
 3.67e-48 Length: 2688
 559.00 Matches: 104
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

ORIGIN
 US-10-624-932C-2_COPY_495_598 (1-104) x BC009333 (1-2688)
 Qy 1 ThrSerAsnMetThrTyrGlyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsn 20
 Db 413 ACCAGCAACATGACCTATGGGACCTTCACTTCCTCGGGGCGGCTGATGATCCCTAAT 472
 Qy 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrGluIle 40
 Db 473 ACAGGAATCAGCCCTCCTCATCCCCCAGATGCCATATCCCGAGGGAAGATCTATGAGATC 532
 Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
 Db 533 TACCTCAGCTGCAACAGCGGAGACGTGAGGTTCGCCCTAGCTGCTGTACACCCCTG 592
 Qy 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
 Db 593 CTGAGTCCCATCGTTAGCTGTGGACCCCTCGGCTGCTGCTACCCGCGCAGTCATCTG 652
 Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
 Db 653 GCTATGGACCACTGTGGGAGCCAGCCCTGACAGCTGGAGCTGCGCCTCAAAAAGCAG 712
 Qy 101 SerCysGluGly 104
 Db 713 TCGTGGAGGGC 724

RESULT 2
 AX451652 2697 bp DNA linear PAT 03-JUL-2002
 DEFINITION Sequence 1 from Patent WO0233080.
 ACCESSION AX451652
 VERSION AX451652.1 GI:21698587
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 Koehler, R.H.
 TITLE Regulation of human netrin binding membrane receptor unc5h-1
 JOURNAL Patent: WO 0233080-A 1 25-APR-2002;
 Bayer Aktiengesellschaft (DE)
 FEATURES
 source
 1..2697
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN
 Alignment Scores: 3.68e-48 Length: 2697
 559.00 Matches: 104
 Pred. No.:
 Score:

/note="ZUS; Region: Domain present in ZO-1 and Unc5-like netrin receptors"
 /db_xref="CDD:smart00218"
 1343..1594
 /gene="UNC5A"
 /note="DEATH; Region: DEATH domain, found in proteins involved in cell death (apoptosis). Alpha-helical domain present in a variety of proteins with apoptotic functions. Some (but not all) of these domains form homotypic and heterotypic dimers"
 /db_xref="CDD:smart00005"

misc_feature

```
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-624-932C-2_COPY_495_598 (1-104) x AX451652 (1-2697)

QY 1 ThrSerAsnMetThrTyrGlyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsn 20
DB 1483 ACCAGCAACATGACCTATGGACCTTCAACTTCTCGGGGGCGGCTGATGATCCCTAAT 1542
QY 21 ThrGlyIleSerLeuLeuLeuProProAspAlaIleProArgGlyIleTyrGluIle 40
DB 1543 ACAGGAATCAGGCTCTCATCCCGCCAGATGCCATACCCGAGGGAAGATCTATGAGATC 1602
QY 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
DB 1603 TACCTCAGCTGACACAGCCGGAAGACGTGAGGTGCCCCCTAGCTGCGTGTGAGACCCCTG 1662
QY 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
DB 1663 CTGAGTCCCATGCTTAGCTGTGGACCCCTGGCGTCTGCTCACCGGGCCAGTCATCCTG 1722
QY 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
DB 1723 GCTATGGACCACTGTGGGGAGCCAGCCCTGCAGCTGAGCGCTGCGCTCAAAAAGCAG 1782
QY 101 SerCysGluGly 104
DB 1783 TCGTGGAGGGC 1794

RESULT 3
AX449572 2752 bp DNA linear PAT 03-JUL-2002
LOCUS AX449572
DEFINITION Sequence 1 from Patent WO0210216.
ACCESSION AX449572
VERSION AX449572.1 GI:21698195
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Padigaru,M., Mezes,P., Mishra,V., Burgess,C., Casman,S.,
Grosse,W.M., Alsbrook,J.P., Lepley,D.M., Gerlach,V.L.,
MacDougall,J.R. and Smithson,G.
TITLE Proteins and nucleic acids encoding same
JOURNAL Patent: WO 0210216-A 1 07-FEB-2002;
Curagen Corporation (US)
FEATURES
source
1..2752
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 3 76e-48 Length: 2752
Score: 559.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-624-932C-2_COPY_495_598 (1-104) x AX449572 (1-2752)

QY 1 ThrSerAsnMetThrTyrGlyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsn 20
DB 1528 ACCAGCAACATGACCTATGGACCTTCAACTTCTCGGGGGCGGCTGATGATCCCTAAT 1587
QY 21 ThrGlyIleSerLeuLeuLeuProProAspAlaIleProArgGlyIleTyrGluIle 40
DB 1588 ACAGGTATCAGGCTCTCATCCCGCCAGATGCCATACCCGAGGGAAGATCTATGAGATC 1647
```

```
QY 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
DB 1648 TACCTCAGCTGACACAGCCGGAAGACGTGAGGTGCCCCCTAGCTGCGTGTGAGACCCCTG 1707
QY 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
DB 1708 CTGAGTCCCATGCTTAGCTGTGGACCCCTGGCGTCTGCTCACCGGGCCAGTCATCCTG 1767
QY 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
DB 1768 GCTATGGACCACTGTGGGGAGCCAGCCCTGCAGCTGAGCGCTGCGCTCAAAAAGCAG 1827
QY 101 SerCysGluGly 104
DB 1828 TCGTGGAGGGC 1839

RESULT 4
AX527916 2881 bp DNA linear PAT 21-NOV-2002
LOCUS AX527916
DEFINITION Sequence 1 from Patent WO0229038.
ACCESSION AX527916
VERSION AX527916.1 GI:25172359
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Herrmann,J.L., Rastelli,L. and Shimkets,R.A.
AUTHORS Novel proteins and nucleic acids encoding same and antibodies
TITLE directed against these proteins
JOURNAL Patent: WO 0229038-A 1 11-APR-2002;
Curagen Corporation (US)
FEATURES
source
1..2881
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 3 94e-48 Length: 2881
Score: 559.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-624-932C-2_COPY_495_598 (1-104) x AX527916 (1-2881)

QY 1 ThrSerAsnMetThrTyrGlyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsn 20
DB 1589 ACCAGCAACATGACCTATGGACCTTCAACTTCTCGGGGGCGGCTGATGATCCCTAAT 1628
QY 21 ThrGlyIleSerLeuLeuLeuProProAspAlaIleProArgGlyIleTyrGluIle 40
DB 1629 ACAGGTATCAGGCTCTCATCCCGCCAGATGCCATACCCGAGGGAAGATCTATGAGATC 1688
QY 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
DB 1689 TACCTCAGCTGACACAGCCGGAAGACGTGAGGTGCCCCCTAGCTGCGTGTGAGACCCCTG 1748
QY 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
DB 1749 CTGAGTCCCATGCTTAGCTGTGGACCCCTGGCGTCTGCTCACCGGGCCAGTCATCCTG 1808
QY 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
DB 1809 GCTATGGACCACTGTGGGGAGCCAGCCCTGCAGCTGAGCGCTGCGCTCAAAAAGCAG 1868
QY 101 SerCysGluGly 104
DB 1869 TCGTGGAGGGC 1879
```


Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.C., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Scherch, A., Schein, D.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932
2 (bases 1 to 3844)
Strausberg, R.
Direct Submission
Submitted (08-SEP-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabbs@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 126 Row: b Column: 11
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 23346570.

FEATURES

source

Location/Qualifiers
1..3844
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="MGC:66671 IMAGE:6813463"
/tissue_type="Brain, mouse, 13.5, 14.5, 16.5, 17.5 dpc"
/clone_lib="NIH BMAP_FW0"
/lab_host="DH108"
/note="Vector: pYX-ASC"
1..3844
/gene="Unc5a"
/db_xref="LocusID:107448"
252..2780
/db_xref="MGI:894682"
/gene="Unc5a"
/codon_start=1
/product="Unc5a protein"
/protein_id="AAH58084.1"
/db_xref="GI:34784159"
/db_xref="LocusID:107448"
/db_xref="MGI:894682"
/translation="NAVRPLGLWALLGLIVLTAWLRGSAQOASATVANPVPANPDLLP
HFLVPEPDIYVKNPVLIVCKAVPATQIFKNGEWRQVDHVERSTDGSSGLPTM
EVRINVSQQVEKVGLEBYWCQCWSSSGTTSQKAYIRIAYLRKNFEQEPKAEV
SLEQIVLPCRPPEGVPAEVEWLNEDLDVPSLDPNVIITREHSLVRQARLADTPN
YTCVAKNTVARRRSASAIVVVDGWSFWKSWACGLDCTHRSRSCSDPAPRNGGE
ECRGADLDRNTCDLCLTSSGPEDVALYIGLVAVAVCLILLIALLVLIYCRKKEGL
DSDVADSLTSGFQPSVKPSKADNPHELLTIQPDLSITTTTYQGSCLCPRODGSPEK
QLSNGHLLSPGSGRHLTHSSPTSEASDFVRLSTQNYFRSLPRGTSNMYAIGTFNPL
GGRLMIPNTGISLLIPDAIPRGKIYEIYLTILHKPEDVRLPLAGCQTLSPVSCGPP

gene

CDS

GVLLTRPVLAMDHCGEPSDPWSLRLKKQCEGSWEDVLHGEPSHLYYCOLEAG
ACYVTEQLGRFALVGEALSVAATKRLRLLPAPVACTSLEYNIYVCLHDTDLALKE
VVOLEKGGQGLIQEPVLVHFADS VHNRLSLTHDVPVSLWKSLLVSVQEI PFYHIW
GTQVYLHCTFTLERVNASTDCLACKVWVQVEGDSQSNINPNIKTDRPAMLALES
EGVPVLVGPASFAKPIFLIRKILITSLDPPGSRGADWRLTQAKLHLDHLSFSFASKPS
PTAMILNLWEARHPFNPNLQGLAAAVAGLGPDPAGLFTVSEAC"
714..926
/gene="Unc5a"
/note="IG; Region: Immunoglobulin"
/db_xref="CDD:smart00409"
984..1130
/gene="Unc5a"
/note="TSPI; Region: Thrombospondin type 1 repeats"
/db_xref="CDD:smart00209"
1566..1877
/gene="Unc5a"
/note="ZU5; Region: Domain present in ZO-1 and Unc5-like
netrin receptors"
/db_xref="CDD:smart00218"
2496..2684
/gene="Unc5a"
/note="DEATH; Region: DEATH domain, found in proteins
involved in cell death (apoptosis); Alpha-helical domain
present in a variety of proteins with apoptotic functions.
Some (but not all) of these domains form homotypic and
heterotypic dimers"
/db_xref="CDD:smart00005"
ORIGIN
Alignment Scores:
Pred. No.: 1,768-47 Length: 3844
Score: 554.00 Matches: 103
Percent Similarity: 99.04% Conservative: 0
Best Local Similarity: 99.04% Mismatches: 1
Query Match: 99.11% Indels: 0
DB: 10 Gaps: 0
US-10-624-932C-2_COPY_495_598 (1-104) x BC058084 (1-3844)
QY 1 ThrSerAenMetThrTyrGlyThrPheAenPheLeuGlyGlyArgLeuMetileProhen 20
Db 1566 ACCAGCAACATGGCCCTATGGGACCTTCAACTTCCTCGGGGGCGGCTGATGATCCCTAAC 1625
QY 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrGluIle 40
Db 1626 ACAGGAATCAGCTCTCTATACCCCGGACGCCATCCCCCGAGGAAAGATCTACGAGATC 1685
QY 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 1686 TACCTCACTCTGCACAGCAGACGCTGAGGTTGCCCTAGCTGGCTGTACAGACCCCTG 1745
QY 61 LeuSerProIleValSerCysGlyProGlyValLeuLeuThrArgProValIleLeu 80
Db 1746 CTGAGTCTCTATCGTTAGCTGTGGGCCCCCAGAGGTCCTGCTACCCGCCAGTCACTCTT 1805
QY 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
Db 1806 GCCATGGACCACTGCGGGAGCCCCAGTCCCGACAGCTGGAGCCTGGGCTCAAAAAGCAG 1865
QY 101 SerCysGluGly 104
Db 1866 TCCTGTGAGGCG 1877
RESULT 8
MMU487852
LOCUS MMU487852 3992 bp mRNA linear ROD 24-SEP-2002
DEFINITION Mus musculus mRNA for netrin receptor Unc5h1 (Unc5h1 gene).
ACCESSION AJ487852
VERSION AJ487852.1 GI:22035783
KEYWORDS netrin receptor Unc5h1; Unc5h1 gene.
SOURCE Mus musculus (house mouse)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
22319710
12351186
2 (bases 1 to 3992)
Engelkamp,D.
Direct Submission
TITLE
JOURNAL
Submitted (15-MAY-2002) Neuroanatomy, Max Planck Institute for
Brain Research, Deutschordenstrasse 46, Frankfurt 60528, GERMANY
Location/Qualifiers
1..3992
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
1..3992
/gene="Unc5h1"
/232..2928
/gene="Unc5h1"
/codon_start=1
/product="netrin receptor Unc5h1"
/protein_id="CAD32250.1"
/db_xref="GI:22035784"
/db_xref="GOA:Q8K1S4"
/db_xref="UniProt/TREMBL:Q8K1S4"
/translation="MAVRPLGMPALLGLVLTAWLRGSGQAQOSTAVNVPFGANPDLLP
HFLVEPDVYIVKQKPVLLVCKVAPATQIFPKNGEWVRQVDHVIERTSSGSLPTM
EVRINRSQKQVPGVGLPEYEWOCVWSSGTSQKAYIRIAYLRKNFQOEPLAKEV
SLEQIVLPKPPSGIPAEVEMLRNEDLVDPSLDPNVYITREHSLVVRQARLADTAN
YTCVAKNIVARRASAAVIVYNGHSTWTEWSCASACGRGQKRSRSTNPAFLN
GGAFCEGNQKATACPCPDVGSWSPKWSACGLDCTHWRSECDPDAPRNGGEEC
RGADLTNRCTSDLCHTSPGDEVALYIGLVAVALILLVLIYCRKGGELS
DVAOSSILTSFQPVSKPADNPILLITIQDLSLTSTTTTQYSLCPRGDPSPKFOL
SNHLLSPGSGRTHLHSSPTSEADFSVRLSTONYPRSLPGTSMNAYGTFFNLGG
RLMPTNGISLIPDAIPCKIYEVILTJLHKPEDVRLPLAGCOTLSPVSCGPPGV
LYTRPVLAMHDCGSPDSWSLRLLKQSCGSMEDVLHGEPSHLYVQLBAGAC
LITFEQGRFALVGEALSVAAATKRLLLFPAPVACTSLEYNIRVYLCHDTHDAKEV
QLEKQLGQLIOEPRLVHFDSKYHNLSDHVPSSKLLSVSYOEIPEYHWTNGT
QOYLHCTPLERVNASDLSACKVWVQVEGDGQSFNFINITKDTFPAEMLALESQ
GVPAIVGPSAFKIPFLRQKITSLDPPCSRGAWRTLAOKLHDSLHSPFASKPSPT
AMILNLWEARHPFNGNLQALAAVAGLQPDAGLFTVSEAC"
ORIGIN
Alignment Scores:
Pred. No.: 1.83e-47 Length: 3992
Score: 554.00 Matches: 103
Percent Similarity: 99.04% Conservative: 0
Best Local Similarity: 99.04% Mismatches: 1
Query Match: 99.11% Indels: 0
DB: 10 Gaps: 0
US-10-624-932C-2_COPY_495_598 (1-104) x MMU487852 (1-3992)
Qy 1 ThrSerAsnMetThrTyGlyThrPheAsnPheLeuGlyArgLeuMetIleProAsn 20
Db 1714 ACCAGCAATGCGCTATGAGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAAC 1773
Qy 21 ThrGlyIleSerLeuIleProProAspAlaIleProArgGlyLysIleTyrGluIle 40
Db 1774 ACAGGAATACGCTCTCTATACCCCGAGCGCATCCCGAGGAAAGATCTACGAGATC 1833
Qy 41 TyrIleuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 1834 TACCTCACTCTGCACACAGCCAGACGCTGAGGTTGCCCTAGCTGGCTGTGACAGCCCTG 1893
Qy 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
Db 1894 CTGAGTCTCATCTAGCTGTGGGGCCCCAGAGTCTCTGCTACCCGGCCAGTATCTCTT 1953
Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Engelkamp,D.
Cloning of three mouse Unc5 genes and their expression patterns at
mid-gestation
Mech. Dev. 118 (1-2), 191-197 (2002)
22319710
12351186
2 (bases 1 to 3992)
Engelkamp,D.
Direct Submission
TITLE
JOURNAL
Submitted (15-MAY-2002) Neuroanatomy, Max Planck Institute for
Brain Research, Deutschordenstrasse 46, Frankfurt 60528, GERMANY
Location/Qualifiers
1..3992
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
1..3992
/gene="Unc5h1"
/232..2928
/gene="Unc5h1"
/codon_start=1
/product="netrin receptor Unc5h1"
/protein_id="CAD32250.1"
/db_xref="GI:22035784"
/db_xref="GOA:Q8K1S4"
/db_xref="UniProt/TREMBL:Q8K1S4"
/translation="MAVRPLGMPALLGLVLTAWLRGSGQAQOSTAVNVPFGANPDLLP
HFLVEPDVYIVKQKPVLLVCKVAPATQIFPKNGEWVRQVDHVIERTSSGSLPTM
EVRINRSQKQVPGVGLPEYEWOCVWSSGTSQKAYIRIAYLRKNFQOEPLAKEV
SLEQIVLPKPPSGIPAEVEMLRNEDLVDPSLDPNVYITREHSLVVRQARLADTAN
YTCVAKNIVARRASAAVIVYNGHSTWTEWSCASACGRGQKRSRSTNPAFLN
GGAFCEGNQKATACPCPDVGSWSPKWSACGLDCTHWRSECDPDAPRNGGEEC
RGADLTNRCTSDLCHTSPGDEVALYIGLVAVALILLVLIYCRKGGELS
DVAOSSILTSFQPVSKPADNPILLITIQDLSLTSTTTTQYSLCPRGDPSPKFOL
SNHLLSPGSGRTHLHSSPTSEADFSVRLSTONYPRSLPGTSMNAYGTFFNLGG
RLMPTNGISLIPDAIPCKIYEVILTJLHKPEDVRLPLAGCOTLSPVSCGPPGV
LYTRPVLAMHDCGSPDSWSLRLLKQSCGSMEDVLHGEPSHLYVQLBAGAC
LITFEQGRFALVGEALSVAAATKRLLLFPAPVACTSLEYNIRVYLCHDTHDAKEV
QLEKQLGQLIOEPRLVHFDSKYHNLSDHVPSSKLLSVSYOEIPEYHWTNGT
QOYLHCTPLERVNASDLSACKVWVQVEGDGQSFNFINITKDTFPAEMLALESQ
GVPAIVGPSAFKIPFLRQKITSLDPPCSRGAWRTLAOKLHDSLHSPFASKPSPT
AMILNLWEARHPFNGNLQALAAVAGLQPDAGLFTVSEAC"
ORIGIN
Alignment Scores:
Pred. No.: 1.83e-47 Length: 3992
Score: 554.00 Matches: 103
Percent Similarity: 99.04% Conservative: 0
Best Local Similarity: 99.04% Mismatches: 1
Query Match: 99.11% Indels: 0
DB: 10 Gaps: 0
US-10-624-932C-2_COPY_495_598 (1-104) x MMU487852 (1-3992)
Qy 1 ThrSerAsnMetThrTyGlyThrPheAsnPheLeuGlyArgLeuMetIleProAsn 20
Db 1714 ACCAGCAATGCGCTATGAGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAAC 1773
Qy 21 ThrGlyIleSerLeuIleProProAspAlaIleProArgGlyLysIleTyrGluIle 40
Db 1774 ACAGGAATACGCTCTCTATACCCCGAGCGCATCCCGAGGAAAGATCTACGAGATC 1833
Qy 41 TyrIleuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 1834 TACCTCACTCTGCACACAGCCAGACGCTGAGGTTGCCCTAGCTGGCTGTGACAGCCCTG 1893
Qy 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
Db 1894 CTGAGTCTCATCTAGCTGTGGGGCCCCAGAGTCTCTGCTACCCGGCCAGTATCTCTT 1953
Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
```

```

RESULT 10
LOCUS AX268596 2697 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 15 from Patent WO0175440.
ACCESSION AX268596
VERSION AX268596.1 GI:16541710
KEYWORDS
SOURCE
ORGANISM
Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 Cochran,S.W., Paterson,G.Y., Ohashi,Y.W., Morris,B.Y. and
AUTHORS Pratt,J.Y.
TITLE Schizophrenia related genes
JOURNAL Patent: WO 0175440-A 15 11-OCT-2001;
WEIPIDE CORPORATION (JP)
FEATURES
Location/Qualifiers
source
1..2697
/organism="Rattus sp."
/mol_type="unassigned DNA"
/db_xref="taxon:10118"
ORIGIN
Alignment Scores:
Pred. No.: 1,54e-47 Length: 2697
Score: 553.00 Matches: 102
Percent Similarity: 99.04% Conservative: 1
Best Local Similarity: 98.08% Mismatches: 1
Query Match: 98.93% Indels: 0
DB: 6 Gaps: 0
US-10-624-932C-2_COPY_495_598 (1-104) x AX268596 (1-2697)
Qy 1 ThrSerAsnMetThrTyrGlyThrPheAsnPhelLeuGlyArgLeuMetIleProAsn 20
Db 1483 ACCAGCAACATGGCTTACGGGACCTTCAACTTCTCGGGGCGGCTGATGATCCTTAAT 1542
Qy 21 ThrGlyIleSerLeuLeuIleProAspAlaIleProArgGlyIleTyrGluIle 40
Db 1543 ACGGGGATCAGCTCCTCATACCCCGGATGCTCCCGGAGGAAGATCTACAGAGATC 1602
Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 1603 TACCTCACATGCACAGCCAGAGACGTGAGTTGCCCTAGCTGGCTGTGACAGCCCTG 1662
Qy 61 LeuSerProIleValSerCysGlyProGlyProGlyValLeuLeuThrArgProValIleLeu 80
Db 1663 CTGAGTCCAGTCTTAGCTGTGGGCCCCCAGAGTCTCTCACCAGGCGCAGTCTATCCTT 1722
Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
Db 1723 GCAATGGACCACTGTGGAGAGCCAGCCCTGACAGCTGAGTCTCGGCTCAAAAAGCAG 1782
Qy 101 SerCysGluGly 104
Db 1783 TCTCGGAGGGC 1794
RESULT 11
LOCUS RNU87305 2697 bp mRNA linear ROD 15-MAY-1997
DEFINITION Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds.
ACCESSION U87305
VERSION U87305.1 GI:2055391
KEYWORDS
SOURCE
Rattus norvegicus (Norway rat)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 2697)

```

```

AUTHORS Leonardo,E.D., Hinck,L., Masu,M., Keino-Masu,K., Ackerman,S.L. and
Tessier-Lavigne,M.
TITLE Vertebrate homologues of C. elegans UNC-5 are candidate netrin
receptors
JOURNAL Nature 386 (6627), 833-838 (1997)
MEDLINE 97271897
PUBMED 9126742
REFERENCE
2 (bases 1 to 2697)
AUTHORS Leonardo,E.D., Hinck,L., Masu,M., Keino-Masu,K. and
Tessier-Lavigne,M.
TITLE Direct Submission
JOURNAL Submitted (28-JAN-1997) Anatomy, UCSF, 513 Parnassus, San
Francisco, CA 94143-0452, USA
FEATURES
Location/Qualifiers
source
1..2697
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/tissue_type="brain and ventral spinal cord"
/dev_stages="18 day embryo and 13 day embryo"
1..2697
/codon_start=1
/product="transmembrane receptor UNC5H1"
/protein_id="AAB57678.1"
/db_xref="GI:2055392"
/translation="MAVRPGLPVLGLGIVLAALRGSGAQOASATVANPVGANPDLLP
HFLVEPDEVIVKPKVLLVCKAVPATQIFPKNGEWRVQDVHVIERTSDSSGLPTM
EVRINVRQOVKEVGLLEEYWCQCVAMSSSGTTKSOKAYIRIAYLRKNFEQEPKLAKEV
SLEQGIVLPCRPPEGIPAEVEMLRNEDLVDPDLDPVYITREHSLVVRQARLADTAN
YTCVAKNIVARRTSAAVYVYNGWSTWENSVCSACGRGWKQRSCNTNPAPLN
GGAFEGNQVQKTACATLCPDVGSSWSKWSACGLDCTHRSRECSQAPRNGEGEC
RGADLTNCTSDLCHTASCPEDVALYIGLVAVALCLLLALLGLLYCRKKEGLDS
DVADSSILTSFGQPVSIKPSKADNPILLITIQDLSLTSTTTTQGSILCSQDQGPSKFLQ
SNGLHSLPLSGRHTLHSSPTSAEDFVSLSTONYFRSLPRGTSNMYGVTFNPLGG
RLMPTNGISLILIPDAIPRGIYEIVLTILKPEDVRLPLAGCOTLLSPVYSCGPPGV
LTLTPVILAMDHCPEPSPWSLRLKQKSCGSWEDVLHLGEESPSHLYYQLEAGAC
YVTFQELGRFALVGEALSVAATLRLLLFAPVACTSLEYINIRVYLDHDTHDALKEVV
QLEQLQGLQITQEPVILFSDYSYHNLRLSIHDVPSLSKSLVSYQIRIPFYHWNGT
QOYLQCTFTLIRINASTDLACKVWVQVGDGQSFNFINITKTDTREAEILLASEG
GVPAIVGPSAPKIPELIRQKTIASLDPPCSRGADWRTLAQKHLHLSLFFASKPSPT
AMILNLEARHPFNGNLQGLAAVAGLQPDAGLFTVSEASC"
ORIGIN
Alignment Scores:
Pred. No.: 1,54e-47 Length: 2697
Score: 553.00 Matches: 102
Percent Similarity: 99.04% Conservative: 1
Best Local Similarity: 98.08% Mismatches: 1
Query Match: 98.93% Indels: 0
DB: 10 Gaps: 0
US-10-624-932C-2_COPY_495_598 (1-104) x RNU87305 (1-2697)
Qy 1 ThrSerAsnMetThrTyrGlyThrPheAsnPhelLeuGlyArgLeuMetIleProAsn 20
Db 1483 ACCAGCAACATGGCTTACGGGACCTTCAACTTCTCGGGGCGGCTGATGATCCTTAAT 1542
Qy 21 ThrGlyIleSerLeuLeuIleProAspAlaIleProArgGlyIleTyrGluIle 40
Db 1543 ACGGGGATCAGCTCCTCATACCCCGGATGCCATCCCGGAGGAAGATCTACAGAGATC 1602
Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 1603 TACCTCACATGCACAGCCAGAGACGTGAGTTGCCCTAGCTGGCTGTGACAGCCCTG 1662
Qy 61 LeuSerProIleValSerCysGlyProGlyProGlyValLeuLeuThrArgProValIleLeu 80
Db 1663 CTGAGTCCAGTCTTAGCTGTGGGCCCCCAGAGTCTCTCACCAGGCGCAGTCTATCCTT 1722
Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
Db 1723 GCAATGGACCACTGTGGAGAGCCAGCCCTGACAGCTGAGTCTCGGCTCAAAAAGCAG 1782

```

```
Qy 101 SerCysGluGly 104
Db 1783 TCCTGCGAGGGC 1794

RESULT 12
BD057524
LOCUS BD057524 3014 bp DNA linear PAT 27-AUG-2002
DEFINITION Netrin receptors.
ACCESSION BD057524
VERSION BD057524.1 GI:22603130
KEYWORDS JP 2001505062-A/1.
SOURCE synthetic construct
ORGANISM Homo sapiens (human)
REFERENCE 1 (bases 1 to 3014)
AUTHORS Lavigne,M.T., Leonardo,D.E., Hinck,L., Masu,M. and Masu,K.K.
TITLE Netrin receptors
JOURNAL Patent: JP 2001505062-A 1 17-APR-2001;
THE REGENTS OF THE UNIV OF CALIFORNIA
COMMENT PN JP 2001505062-A/1
PD 17-APR-2001
PR 19-FEB-1998 JP 1998536840
PI 19-FEB-1997 US 08/808982
PI MARC TESSIER LAVIGNE,DAVID E LEONARDO,LINDSAY HINCK,MASUYUKI
PI MASU,
PI KAZUKO KEINO MASU
PC C07K1/00, C07K14/00, C07K17/00, C07H21/02, C07H21/04, G01N33/53 CC
Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers
FEATURES
source
1..3014
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Alignment Scores:
Pred. No.: 1.73e-47 Length: 3014
Score: 553.00 Matches: 102
Percent Similarity: 99.04% Conservative: 1
Best Local Similarity: 98.08% Mismatches: 1
Query Match: 98.93% Indels: 0
DB: 6 Gaps: 0
US-10-624-932C-2_COPY_495_598 (1-104) x BD057524 (1-3014)
Qy 1 ThrSerAsnMetThrTyrGlyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsn 20
Db 1483 ACCGACACATGGCTACGGACCTTCAACTTCCTCGGGGCGCGCTGATGATCCCTAAT 1542
Qy 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrGluIle 40
Db 1543 ACGGGGATCAGCTCTCATACCCCGGATGCCATCCCGGAGGAAGATCTACGAGATC 1602
Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 1603 TACTTCACATGCAACGACGAGACGTGAGGTGCCCCCTAGCTGGCTGTCAGACCCCTG 1662
Qy 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
Db 1663 CTGAGTCAGTCGTAGTGTGGGCCCCCAGGAGTCTCTGCTCACCGGCCAGTCATCCTT 1722
Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLysGln 100
Db 1723 GCAATGGACCACTGTGGAGAGCCAGCCCTGACAGCTGAGTCTCGGCTCAAAAAGCAG 1782
Qy 101 SerCysGluGly 104
Db 1783 TCCTGCGAGGGC 1794

RESULT 13
AX054892
LOCUS AX054892 813 bp DNA linear PAT 13-JAN-2001
DEFINITION Sequence 7 from Patent WO0073328.
ACCESSION AX054892
VERSION AX054892.1 GI:12228303
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS van Criekeinge,W., Roelens,I., Bogaert,T. and Verwaerde,P.
TITLE Unc-5 constructs and screening methods
JOURNAL Patent: WO 0073328-A 7 07-DEC-2000;
Devgen NV (BE)
FEATURES
Location/Qualifiers
source
1..813
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 1.19e-44 Length: 813
Score: 520.00 Matches: 104
Percent Similarity: 97.20% Conservative: 0
Best Local Similarity: 97.20% Mismatches: 0
Query Match: 93.02% Indels: 3
DB: 6 Gaps: 0
US-10-624-932C-2_COPY_495_598 (1-104) x AX054892 (1-813)
Qy 1 ThrSerAsnMetThrTyrGlyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsn 20
Db 449 ACCAGCAACATGACCTATGGACCTTCAACTTCCTCGGGGCGCGCTGATGATCCCTAAT 508
Qy 21 ThrGlyIle-SerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrGluIle 40
Db 509 ACAGGATCAAGCCTCTCATCCCCCAGATGCCATACCCGAGGAAGATCTATGAT 568
Qy 40 eTyrLeuThr-LeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrL 60
Db 569 CTACCTCAGCTTGCACAAGCGGAGACGTGAGGTGCCCCCTAGCTGGCTGTGAGACCC 628
Qy 60 eLeuSerProIleValSer-CysGlyProProGlyValLeuLeuThrArgProValIle 79
Db 629 TGCTGATGCCATCGTTAGCTTGGACCCCTCGCGCTCTGCTCACCGGCCAGTCATC 688
Qy 80 LeuAlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLysLys 99
Db 689 CTGCTATGGACCACTGTGGGAGCCCGAGCCCTGACAGCTGGAGCCTCGGCTCAAAAAG 748
Qy 100 GlnSerCysGluGly 104
Db 749 CAGTCGTGCGAGGGC 763
RESULT 14
CQ730306
LOCUS CQ730306 2784 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 16240 from Patent WO02068579.
ACCESSION CQ730306
VERSION CQ730306.1 GI:42303801
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 16240 06-SEP-2002;
PE Corporation (NY) (US)
```

FEATURES

Location/Qualifiers
1. .2784
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores:

Pred. No.: 1.93e-38 Length: 2784
Score: 465.50 Matches: 89
Percent Similarity: 85.58% Conservative: 0
Best Local Similarity: 85.58% Mismatches: 15
Query Match: 83.27% Indels: 15
DB: 6 Gaps: 1

US-10-624-932C-2_COPY_495_598 (1-104) x CQ730306 (1-2784)

Qy 1 ThrSerAsnMetThyTyrGlyThrPheAnPheLeuGlyGlyArgLeuMetIleProAn 20
|||||
Db 1615 ACCAGCAACATGACCTATGGGACCTTCAACTTCTCGGGGGCGGCTGATGATCCCTAAT 1674
|||||
Qy 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrGluIle 40
|||||
Db 1675 ACAGGAATCAGCTCTCTATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATC 1734
|||||
Qy 41 TyrLeuThrLeuHisIleProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
|||||
Db 1735 TACCTCAGCTGCACAGCGGAGAC----- 1761
|||||
Qy 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
|||||
Db 1762 -----GTGAGCTGTGGAGCCCTCGCTGCTCACCAGCGGCGCATCTCCTG 1809
|||||
Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
|||||
Db 1810 GCTATGGACCACTGTGGGAGCCAGCCCTGACAGCTGAGCTCGGCTCAAAAGCAG 1869
|||||
Qy 101 SerCysGluGly 104
|||||
Db 1870 TCGTGGAGGCG 1881
|||||

RESULT 15

AC123700/c

LOCUS

AC123700 242128 bp DNA linear HTG 09-MAR-2004
Mus musculus chromosome 13 clone RP23-335A11 map 13, *** SEQUENCING
IN PROGRESS ***, 7 unordered pieces.

ACCESSION

AC123700.4 GI:45268905

HTG; HTGS_PHASE1; HTGS_FULPTOP; HTGS_ACTIVEFIN.

KEYWORDS

Mus musculus (house mouse)

SOURCE

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 242128)

Mus musculus chromosome 13, clone RP23-335A11

Unpublished

2 (bases 1 to 242128)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,

Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavskiy,I.,

Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,

Chazaro,B., Choepel,Y., Collangelo,M., Collins,S., Collumore,A.,

Cook,A., Cooke,P., DeArelano,K., Dewar,K., Diaz,J.S., Dodge,S.,

Paro,S., Ferreira,P., Fitzgerald,M., FitzHugh,W., Gage,D.,

Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L.,

Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I.,

Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K.,

Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Lindblad-Toh,K.,

Liu,G., MacLean,C., MacDonald,P., Major,J., Marquis,N.,

Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrum,J.,

Meneus,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C.,

Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P.,

O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,

TITLE
JOURNALREFERENCE
AUTHORS

Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C.,
Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S.,
Schupback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Teefaye,S.,
Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (01-JUN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 242128)
Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
Anderson,M., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
Boguslavskiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,
Collumore,A., Cook,A., Cooke,P., Corum,B., DeArelano,K.,
Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S.,
Graham,L., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
Lindblad-Toh,K., Liu,X., Lui,A., Mabbitt,R., MacLean,C.,
Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
Meldrum,J., Meneus,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J.,
O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C.,
Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
Talamas,J., Teefaye,S., Theodore,J., Topham,K., Travers,M.,
Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (09-MAR-2004) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 9, 2004 this sequence version replaced gi:28933837.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WTHR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L26431
Center clone name: 335_A_11

TITLE
JOURNAL

COMMENT

* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 80291: contig of 80291 bp in length
* 80292 80391: gap of 100 bp
* 80392 105410: contig of 25019 bp in length
* 105411 105510: gap of 100 bp
* 105511 173922: contig of 67412 bp in length
* 173923 173922: gap of 100 bp
* 173923 182093: contig of 9071 bp in length
* 182094 182193: gap of 100 bp
* 182194 207358: contig of 25165 bp in length
* 207359 207458: gap of 100 bp
* 207459 222746: contig of 15288 bp in length
* 222747 222846: gap of 100 bp
* 222847 224128: contig of 19282 bp in length.

FEATURES

source

1. .242128
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"

/chromosome="13"
/map="13"
/clone="RP23-335A11"
/clone_lib="RPCI-23 Female Mouse BAC"

ORIGIN

Alignment Scores:
Pred. No.: 4.62e-29 Length: 242128
Score: 394.50 Matches: 84
Percent Similarity: 47.46% Conservative: 0
Best Local Similarity: 47.46% Mismatches: 0
Query Match: 70.57% Indels: 93
DB: 2 Gaps: 1

US-10-624-932C-2_COPY_495_598 (1-104) x AC123700 (1-242128)

Qy	21	ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrGluIle	40
Db	145408	ACAGGAATCAGCCTCCTCATACCCCGGACGCCATCCCCCGAGGAAGATCTACGAGATC	145349
Qy	41	TyrLeuThrLeuHisLysProGluAspVal	50
Db	145348	TACCTCACTCTGCACAGCCAGAGACGTGAGGTGTGTGCCCTGCCTGCTGTGTGTGGTGG	145289
Qy	50	-----	50
Db	145288	GGGGGGGGGAGGACCGTCTGTGCTCTCTATCGCTGGAAACACCCCAATTCCCGGCC	145229
Qy	50	-----	50
Db	145228	AGCACTGCTGTACCTGTTCTGACCTGGCCCGAGGGAGCACAGGGGATGAGGCGCACTTAA	145169
Qy	50	-----	50
Db	145168	GCTCACCCCTGATTGCAACTTCCGTCTTACGGTGTCAACCCCACTGCAGAGTCTGT	145109
Qy	50	-----	50
Db	145108	CTCCTAACCCCAACGGTCTCTAGGACTGGCCACTGACGCCITTCCTCTCCACCCATGTTT	145049
Qy	51	-----ArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleValSerCys	67
Db	145048	CCCCACTTGAGTTGCCCTAGCTGGCTGTCTAGACCCCTGTGAGTCTCTATCGTTAGCTGT	144989
Qy	68	GlyProProGlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCysGlyGlu	87
Db	144988	GGGCCCCCAGAGTCTGCTCACCGGCCAGTCTATCTTGCATGGACCACTGCGGGGAG	144929
Qy	88	ProSerProAspSerTrpSerLeuArgLeuLysLysGlnSerCysGluGly	104
Db	144928	CCAGTCCCGACAGCTGGAGCCTGGGCTCTCAAAAGCAGTCTCTGTGAGGGC	144878

Search completed: September 9, 2005, 09:42:25
Job time : 4362.67 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 8, 2005, 20:54:46 ; Search time 537.856 Seconds
(without alignments)
1144.643 Million cell updates/sec

Title: US-10-624-932C-2_COPY_495_598

Perfect score: 559

Sequence: 1 TSNMTYGTFTFLGRLMPN.....CGEPPDSWSRLKKQSCGE 104

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame, p2n.model -DEV=xlh
-Q=/Cgn2_1/USPTO_spool_h/US10624932/runat_08092005_161705_15766/app.query.fasta.1.1386
-DB=N Geneseq -QFMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10624932 @CGN 1.1 1052 @runat_08092005_161705_15766 -NCPU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq_16Dec04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	559	100.0	2463	12	Adh71623 Human gen
2	559	100.0	2575	12	Adh71621 Human gen
3	559	100.0	2635	11	Adn95100 Human LEC
4	559	100.0	2697	6	Abk52891 Human net
5	559	100.0	2752	6	Abk37922 cDNA enco

6	559	100.0	2752	12	ADH71617	Adh71617 Human gen
7	559	100.0	2881	6	ABK49422	Abk49422 DNA enco
8	559	100.0	2881	10	ADG42568	Adg42568 Novel hum
9	559	100.0	2881	12	ADH71649	Adh71649 Human gen
10	559	100.0	2881	12	ADH71635	Adh71635 Human gen
11	559	100.0	2881	12	ADH71637	Adh71637 Human gen
12	559	100.0	2881	12	ADH71641	Adh71641 Human gen
13	559	100.0	2881	12	ADH71609	Adh71609 Human gen
14	559	100.0	2881	12	ADH71629	Adh71629 Human gen
15	559	100.0	2881	12	ADH71645	Adh71645 Human gen
16	559	100.0	2881	12	ADH71627	Adh71627 Human gen
17	559	100.0	2881	12	ADH71639	Adh71639 Human gen
18	559	100.0	2881	12	ADH71643	Adh71643 Human gen
19	559	100.0	2881	12	ADH71625	Adh71625 Human gen
20	559	100.0	2881	12	ADH71647	Adh71647 Human gen
21	559	100.0	3561	12	ADL06497	Adl06497 Human tum
22	559	100.0	3580	6	ABK15169	Abk15169 Human RSP
23	559	100.0	9700	4	AAC90958	Aac90958 Plasmid p
24	555	99.3	2881	12	ADH71631	Adh71631 Human gen
25	554	99.1	2880	12	ADH71633	Adh71633 Human gen
26	553	98.9	1787	2	AAV52941	Aav52941 Human UNC
27	553	98.9	2697	6	AAV16843	Aav16843 Rat netri
28	553	98.9	3014	2	AAV52940	Aav52940 Rat UNC-5
29	520	93.0	813	4	AAC90917	Aac90917 Human UNC
30	503	90.0	1321	4	AAH99530	Aah99530 Human pro
31	465.5	83.3	2907	4	AAK52261	Aak52261 Human pol
32	393.5	70.4	6522	8	AAI51204	Aai51204 Human gen
33	393.5	70.4	9582	4	AAD16560	Aad16560 Human nov
34	393.5	70.4	9582	6	ABS64150	Abs64150 Human apo
35	393.5	70.4	9582	10	AAD60459	Aad60459 Human sec
36	393.5	70.4	18772	4	AAD16561	Aad16561 Human nov
37	393.5	70.4	18772	6	ABS64151	Abs64151 Human apo
38	393.5	70.4	18772	10	AAD60460	Aad60460 Human sec
39	374	66.9	604	6	ABK52893	Abk52893 Human net
40	337	60.3	2796	10	AAI56266	Aai56266 Human thr
41	337	60.3	2986	13	ADR95249	Adr95249 Human lro
42	337	60.3	3646	5	AA575738	Aa575738 DNA enco
43	337	60.3	3646	13	ADR99257	Adr99257 Human unc
44	333	59.6	1575	4	AAC90916	Aac90916 Human UNC
45	318	56.9	1393	4	AAC90914	Aac90914 Human UNC

ALIGNMENTS

RESULT 1
ADH71623
ID ADH71623 standard; DNA; 2463 BP.
XX
AC ADH71623;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human gene of the invention NOV21h SEQ ID NO:519.
XX
KW ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX
OS Homo sapiens.
XX
PN WO2003102155-A2.
XX
PD 11-DEC-2003.
XX
PF 03-JUN-2003; 2003WO-US017430.
XX
PR 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 05-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.

PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 06-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-0387696P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0388123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390066P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402158P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
XX

(CURA-) CURAGEN CORP.

XX Alsbrook JP, Alvarez E, Anderson DW, Boldog FI, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI MacLachlan T, Malvankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigaru M, Patturajan M, Pena CE, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shinkets RA;
PI Smithson G, Spytek KA, Stone DU, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;
XX WPI; 2004-081935/08.
DR P-PSDB; ADH71624.
XX
PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
PS Example 21; SEQ ID NO 519; 1880pp; English.
XX
CC The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.
XX
SQ Sequence 2463 BP; 470 A; 828 C; 721 G; 444 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 5.23e-53 Length: 2463
Score: 559.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0
US-10-624-932C-2_COPY_495_598 (1-104) x ADH71623 (1-2463)
Qy 1 ThrSerAsnMetThrTyrGlyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsn 20
Db 1246 ACCAGCAACATGACCTATGGACCTTCACTTCCTCGGGGCGGCTGATCCCTAAT 1305
Qy 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrGluIle 40
Db 1306 ACAGGAATCAGCTCCTCATCCCCCAGATGCCATACCCGAGGGAAGATCTATGAGATC 1365
Qy 41 TyrLeuThrIleuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrIleu 60
Db 1366 TACCTCAGCTGCAACAGCGGAAGAGGTGAGGTGGCCCTAGCTGGCTGTGCACACCTG 1425
Qy 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
Db 1426 CTGAGTCCCATCGTTAGCTGTGGACCCCTCGCTGCTCACC CGGCCATCATCTG 1485
Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
Db 1486 GCTATGGACCACTGTGGGAGCCCGAGCCCTGACAGCTGGAGCTCGCCCTCAAAAAGCAG 1545
Qy 101 SerCysGluGly 104
Db 1546 TCGTGGCAGGGC 1557
XX

RESULT 2

ADH71621	ADH71621 standard; DNA; 2575 BP.	
ID	ADH71621 standard; DNA; 2575 BP.	
XX		
AC	ADH71621;	
DT	25-MAR-2004 (first entry)	
XX		
DE	Human gene of the invention NOV21g SEQ ID NO:517.	
XX		
KW	ds; gene; human; cytostatic; immunomodulator; neuroprotective; nontropic;	
KW	anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;	
KW	vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;	
KW	obesity; diabetes; infectious disease; metabolic syndrome X;	
KW	dyslipidaemia.	
XX		
OS	Homo sapiens.	
XX		
PN	WO2003102155-A2.	
XX		
PD	11-DEC-2003.	
XX		
PF	03-JUN-2003; 2003WO-US017430.	
XX		
PR	03-JUN-2002; 2002US-0385120P.	
PR	04-JUN-2002; 2002US-0385784P.	
PR	05-JUN-2002; 2002US-0386041P.	
PR	05-JUN-2002; 2002US-0386047P.	
PR	06-JUN-2002; 2002US-0386376P.	
PR	06-JUN-2002; 2002US-0386453P.	
PR	06-JUN-2002; 2002US-0386864P.	
PR	06-JUN-2002; 2002US-0387016P.	
PR	07-JUN-2002; 2002US-0386796P.	
PR	07-JUN-2002; 2002US-0386811P.	
PR	07-JUN-2002; 2002US-0386931P.	
PR	07-JUN-2002; 2002US-0386942P.	
PR	07-JUN-2002; 2002US-0386971P.	
PR	07-JUN-2002; 2002US-0387262P.	
PR	08-JUN-2002; 2002US-0296960P.	
PR	10-JUN-2002; 2002US-0387400P.	
PR	10-JUN-2002; 2002US-0387535P.	
PR	11-JUN-2002; 2002US-0387610P.	
PR	11-JUN-2002; 2002US-0387625P.	
PR	11-JUN-2002; 2002US-0387634P.	
PR	11-JUN-2002; 2002US-0387668P.	
PR	11-JUN-2002; 2002US-0387696P.	
PR	11-JUN-2002; 2002US-0387702P.	
PR	11-JUN-2002; 2002US-0387836P.	
PR	11-JUN-2002; 2002US-0387859P.	
PR	12-JUN-2002; 2002US-0387933P.	
PR	12-JUN-2002; 2002US-0387934P.	
PR	12-JUN-2002; 2002US-0387960P.	
PR	12-JUN-2002; 2002US-0388022P.	
PR	12-JUN-2002; 2002US-0388096P.	
PR	13-JUN-2002; 2002US-0389123P.	
PR	14-JUN-2002; 2002US-0389118P.	
PR	14-JUN-2002; 2002US-0389120P.	
PR	14-JUN-2002; 2002US-0389144P.	
PR	14-JUN-2002; 2002US-0389146P.	
PR	17-JUN-2002; 2002US-0389729P.	
PR	17-JUN-2002; 2002US-0389742P.	
PR	18-JUN-2002; 2002US-0389884P.	
PR	19-JUN-2002; 2002US-0390006P.	
PR	19-JUN-2002; 2002US-0390209P.	
PR	21-JUN-2002; 2002US-0390763P.	
PR	17-JUL-2002; 2002US-0396706P.	
PR	06-AUG-2002; 2002US-0401628P.	
PR	09-AUG-2002; 2002US-0402156P.	
PR	09-AUG-2002; 2002US-0402256P.	
PR	09-AUG-2002; 2002US-0402389P.	
PR	12-AUG-2002; 2002US-0402786P.	
PR	12-AUG-2002; 2002US-0402816P.	
PR	12-AUG-2002; 2002US-0402821P.	
PR	12-AUG-2002; 2002US-0402832P.	
PR		
PA	(CURA-) CURAGEN CORP.	
XX		
XX	Alsbrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;	
PI	Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;	
PI	Etenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;	
PI	Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;	
PI	MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;	
PI	Padigaru M, Patturajan M, Pena CE, Peyman JA, Raha D, Rastelli L;	
PI	Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shinkets RA;	
PI	Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;	
PI	Zhong H;	
XX		
XX	WPI: 2004-081935/08.	
XX	P-PSDB; ADH71622.	
DR		
XX		
PT	New NOVX polypeptides and nucleic acid molecules useful for preventing or	
PT	treating NOVX-associated disorders, e.g. cancer, diabetes, infection or	
XX	obesity, and in chromosome mapping, tissue typing or pharmacogenomics.	
PS	Example 21; SEQ ID NO 517; 1880pp; English.	
XX		
CC	The invention relates to a novel isolated polypeptide (NOVX). A	
CC	polypeptide of the invention has cytostatic, immunomodulator,	
CC	neuroprotective, nontropic, anorectic, antidiabetic, antimicrobial, and	
CC	antilipemic activity, and may have a use in gene therapy, and as a	
CC	vaccine. The polypeptides are encoded by NOVX polynucleotides comprising	
CC	any of the 303 fully defined nucleotide sequences given in the	
CC	specification. The polypeptide is useful in the manufacture of a	
CC	medicament for treating a syndrome associated with a human disease. The	
CC	polypeptide, polynucleotide and antibody are useful in diagnosing,	
CC	treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,	
CC	Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious	

```
US-10-624-932C-2_COPY_495_598 (1-104) x ADH71621 (1-2575)
Qy 1 ThrSerAenMetThrTyrGlyThrPheAenPheLeuGlyArgLeuMetIleProAen 20
Db 1290 ACCAGCAACATGACCTATGGACCTTCAACTTCCTCGGGGCGCGCTGATCCCTAAT 1349
Qy 21 ThrGlyIleSerLeuLeuIleProAenPheAenPheLeuGlyArgLeuMetIleProAen 40
Db 1350 ACAGGAATCAGCTTCCTATCCCTCCAGATGCCATACCCAGGAGAGATCTATGAGATC 1409
Qy 41 TyrLeuThrLeuHisLeuValSerCysGlyProGlyValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 1410 TACCTCAGCTGTCACAGCCGAGACGCTGAGTGGCTGCCCTAGCTGGCTGTCACAGCCCTG 1469
Qy 61 LeuSerProIleValSerCysGlyProGlyValLeuLeuThrArgProValIleLeu 80
Db 1470 CTGAGTCCCATCGTTAGCTGTGGACCCCTGGCTGCTGCTCACCAGGCGCAGTCACTCTG 1529
Qy 81 AlaMetAenHisCysGlyGluProSerProAenSerTrpSerLeuArgLeuIleGln 100
Db 1530 GCTATGGACCACTGTGGGAGCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAG 1589
Qy 101 SerCysGluGly 104
Db 1590 TCGTGGAGGGC 1601
RESULT 3
ID ADN95100
XX ADN95100 standard; DNA; 2635 BP.
XX AC ADN95100;
XX DT 01-JUL-2004 (first entry)
XX DE Human LEC gene sequence SeqID22.
XX KW growth; differentiation; blood endothelial cell; BEC;
KW lymphatic endothelial cell; LEC; hereditary lymphoedema; VEGFR-3;
KW lymphatic growth agent; VEGF-C; VEGF-D; antiangiogenic; cytoskeletal;
KW vasotrophic; antiinflammatory; gene therapy; endothelial cell disorder;
KW inflammatory disease; cancer metastasis; lymphatic system; gene; ds;
XX KW human.
XX OS Homo sapiens.
XX PN WO2003080640-A1.
XX PD 02-OCT-2003.
XX PF 07-MAR-2003; 2003WO-US006900.
XX PR 07-MAR-2002; 2002US-0363019P.
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX PA (LICN) LICENTIA LTD.
XX PI Alitalo K, Makinen T, Petrova T, Saharinen P, Saharinen J;
XX WPI; 2003-876899/81.
XX DR P-PSDB; ADN95115.
XX PS Claim 23; SEQ ID NO 22; 176pp; English.
XX CC This invention relates to a method of differentially modulating the
CC growth or differentiation of blood endothelial cells (BEC) or lymphatic
CC endothelial cells (LEC) comprises contacting endothelial cells with a
CC composition comprising an agent that differentially modulates blood or
CC lymphatic endothelial cells. Treating hereditary lymphoedema comprises
CC identifying a human subject with lymphoedema and with a mutation in at
CC least one allele of a gene encoding a LEC protein, where the mutation
CC correlates with lymphoedema in human subjects, and with the proviso that
CC the LEC protein is not VEGFR-3; and administering to the subject a
```

```
composition comprising a lymphatic growth agent selected from VEGF-C or
VEGF-D polypeptides and polynucleotides. The invention may be useful for
the development of compounds with an antiangiogenic, cytoskeletal,
vasotrophic or antiinflammatory activity or for gene therapy. The method
is useful in modulating the growth or differentiation of blood
endothelial cells or lymphatic endothelial cells, in treating hereditary
lymphoedema, in screening for an endothelial cell disorder or
predisposition to the disorder or in monitoring the efficacy or toxicity
of a drug on endothelial cells. The agent is useful in manufacturing a
medicament for the differential modulation of blood vessel endothelial
cell or lymphatic vessel endothelial cell growth or differentiation. The
lymphatic growth agent may also be used in manufacturing a medicament for
the treatment of hereditary lymphoedema resulting from a mutation in a
LEC gene or of other diseases involving the lymphatic vessels, such as
various inflammatory diseases and cancer metastasis via the lymphatic
system. The present sequence is that of a human LEC/BEC differentially
expressed gene which is related to the method of the invention. Note: The
sequence data for this patent did not form part of the printed
specification but was obtained in electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences
```

XX SQ Sequence 2635 BP; 483 A; 935 C; 722 G; 495 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5,71e-53 Length: 2635
Score: 559.00 Matches: 104
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-10-624-932C-2_COPY_495_598 (1-104) x ADN95100 (1-2635)

```
Qy 1 ThrSerAenMetThrTyrGlyThrPheAenPheLeuGlyArgLeuMetIleProAen 20
Db 413 ACCAGCAACATGACCTATGGACCTTCAACTTCCTCGGGGCGCGCTGATCCCTAAT 472
Qy 21 ThrGlyIleSerLeuLeuIleProAenPheAenPheLeuGlyArgLeuMetIleProAen 40
Db 473 ACAGGAATCAGCTTCCTATCCCTCCAGATGCCATACCCAGGAGAGATCTATGAGATC 532
Qy 41 TyrLeuThrLeuHisLeuValSerCysGlyProGlyValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 533 TACCTCAGCTGTCACAGCCGAGACGCTGAGGTTGCCCTAGCTGGCTGTCACAGCCTG 592
Qy 61 LeuSerProIleValSerCysGlyProGlyValLeuLeuThrArgProValIleLeu 80
Db 593 CTGAGTCCCATCGTTAGCTGTGGACCCCTGGCTGCTCACCAGGCGCAGTCACTCTG 652
Qy 81 AlaMetAenHisCysGlyGluProSerProAenSerTrpSerLeuArgLeuIleGln 100
Db 653 GCTATGGACCACTGTGGGAGCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAG 712
Qy 101 SerCysGluGly 104
Db 713 TCGTGGAGGGC 724
```

RESULT 4
ABK52891
ID ABK52891 standard; DNA; 2697 BP.
XX AC ABK52891;
XX DT 27-AUG-2002 (first entry)
XX DE Human netrin binding membrane receptor UNC5H-1 DNA sequence #1.
XX KW Netrin binding membrane receptor; receptor; UNC5H-1; gene; ds; human;
KW neurotrophic; neuroprotective; cytoskeletal; antiparkinsonian;
KW cerebroprotective; cancer; central nervous system; CNS; stroke;
KW Parkinson's disease; multiple sclerosis; Alzheimer's disease.
XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX FT 1. :2697
XX FT /*tag= a
XX FT /product= "Netrin binding membrane receptor UNC5H-1"
XX PN WO200233080-A2.
XX PD 25-APR-2002.
XX PF 15-OCT-2001; 2001WO-EP011891.
XX PR 16-OCT-2000; 2000US-0240061P.
XX PA (FARB) BAYER AG.
XX PI Koehler RH;
XX PD WPI; 2002-463314/49.
XX DR P-PSDB; AAU97899.
XX PT Novel human netrin binding membrane receptor polypeptide and
XX PT polynucleotides for identifying modulating agents useful in treating
XX PT diseases e.g. Parkinson's disease, multiple sclerosis, stroke,
XX PT Alzheimer's disease.
XX PS Claim 1; Fig 1; 94pp; English.
XX CC This invention relates to the DNA and protein sequences of a novel
XX CC purified human netrin binding membrane receptor, UNC5H-1. The DNA
XX CC acid encoding the invention is useful as a probe for detecting a nucleic
XX CC of the invention is useful in a biological sample. The sequences
XX CC of the invention are useful to screen for agents which decrease the
XX CC activity of the UNC5H-1 protein. The sequences are also useful for
XX CC screening agents which regulate (modulate) the activity of the protein of
XX CC the invention. A pharmaceutical composition containing the protein of the
XX CC invention or a reagent that modulates the activity of the UNC5H-1 protein
XX CC may be useful for treating a UNC5H-1 dysfunction related disease such as
XX CC cancer or a central nervous system (CNS) disorders (e.g. Parkinson's
XX CC disease, multiple sclerosis, stroke and Alzheimer's disease). Fusion
XX CC proteins comprising the UNC5H-1 protein are useful for generating
XX CC antibodies and for in various assay systems, and the protein can be used
XX CC as a bait protein in a two-hybrid assay or three-hybrid assay. The method
XX CC of the invention is useful for detecting a coding sequence for the UNC5H-
XX CC 1 protein. The present sequence represents a DNA sequence encoding the
XX CC human netrin binding membrane receptor UNC5H-1 protein of the invention
XX SQ Sequence 2697 BP; 503 A; 906 C; 807 G; 481 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5.88e-53 Length: 2697
Score: 559.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-624-932c-2_copy_495_598 (1-104) x ABK52891 (1-2697)

QY 1 ThrSerAnMetThrTyGlyThrPheAnPheLeuGlyGlyArgLeuMetIleProAn 20
DB 1483 ACCAGCAACATGACCTATGGGACCTTCACTTCCTCGGGGGCGGCTGATCCCTAAT 1542
QY 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyfGluIle 40
DB 1543 ACAGGATCAGGCTCTCTATCCCCCAGATGCCATACCCCGAGGAGGATCTATGAGATC 1602
QY 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
DB 1603 TACCTCAGCTGCACAAGCCGGAAGACGTGAGGTTTGCCCTAGCTGGCTGTACAGACCTG 1662
QY 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80

Db 1663 CTGAGTCCCATCGTTAGCTGTGGACCCCTCGGCTCTCTGCTACCCGGCCAGTCAATCCTG 1722
QY 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
Db 1723 GCTATGGACCACTGTGGGAGCCCGAGCCCTGACAGCTGGAGCTGGCCTCAAAAAGCAG 1782
QY 101 SerCysGluGly 104
Db 1783 TCGTGCAGGGC 1794
RESULT 5
ABK37922
ID ABK37922 standard; cDNA; 2752 BP.
XX AC ABK37922;
XX DT 21-MAY-2002 (first entry)
XX DE cDNA encoding Human protein NOV1.
XX KW Human; NOVX; ss; gene; cardiomyopathy; atherosclerosis; diabetes;
XX KW cell signal processing disorder; metabolic disorder; obesity; infection;
XX KW anorexia; cancer-associated cachexia; cancer; neurodegenerative disorder;
XX KW Alzheimer's disease; Parkinson's disease; immune disorder;
XX KW haematopoietic disorders; dyslipidaemia; pain; asthma; hypertension;
XX KW osteoporosis; Crohn's disease; multiple sclerosis; angina pectoris;
XX KW myocardial infarction; ulcer; allergy; benign prostatic hypertrophy;
XX KW psychosis; neurological disorder; anxiety; schizophrenia;
XX KW manic depression; dementia; dyskinesia; Huntington's disease;
XX KW Gilles de la Tourette's syndrome; gene therapy.
XX OS Homo sapiens.
XX PN WO200210216-A2.
XX PD 07-FEB-2002.
XX PF 30-JUL-2001; 2001WO-US024225.
XX PR 28-JUL-2000; 2000US-0221409P.
XX PR 04-AUG-2000; 2000US-0222840P.
XX PR 04-AUG-2000; 2000US-0223752P.
XX PR 04-AUG-2000; 2000US-0223762P.
XX PR 04-AUG-2000; 2000US-0223769P.
XX PR 14-AUG-2000; 2000US-0223770P.
XX PR 15-AUG-2000; 2000US-0225146P.
XX PR 15-AUG-2000; 2000US-0225392P.
XX PR 16-AUG-2000; 2000US-0225470P.
XX PR 16-AUG-2000; 2000US-0225697P.
XX PR 01-FEB-2001; 2001US-0263662P.
XX PR 05-APR-2001; 2001US-0281645P.
XX (CURA-) CURAGEN CORP.
XX PI Padigaru M, Mezes P, Mishra V, Burgess C, Casman S, Groese WM;
XX PI Alsbrook JP, Lepley DM, Gerlach VL, Macdougall JR, Smithson G;
XX WPI; 2002-180074/23.
XX DR P-PSDB; AAU85403.
XX PT New isolated cytoplasmic, nuclear, membrane bound, or secreted
XX PT polypeptide, useful for treating cardiomyopathy, atherosclerosis,
XX PT infections, cancer, neurodegenerative, metabolic, hematopoietic and
XX PT immune disorders.
XX PS Claim 9; Page 9-10; 213pp; English.
XX CC The invention relates to an isolated cytoplasmic, nuclear, membrane
XX CC bound, or secreted polypeptide (NOVX, x= 1-14) their variants or mature
XX CC form. Also included are the nucleic acids encoding the NOVX proteins, a
XX CC vector comprising the nucleic acid, a cell comprising the vector, an anti
XX CC -NOVX antibody and modulators of NOVX. NOVX, the nucleic acid and the
XX CC antibody are useful for treating or preventing a NOVX-associated

CC disorder, where the disorder is selected from cardiomyopathy,
CC atherosclerosis, diabetes, a disorder related to cell signal processing
CC and metabolic pathway modulation, metabolic disorders, obesity,
CC infectious disease, anorexia, cancer-associated cachexia, cancer,
CC neurodegenerative disorders, Alzheimer's disease, Parkinson's disease,
CC immune disorders, haematopoietic disorders, and the various
CC dyslipidaemias, metabolic disturbances associated with obesity, the
CC metabolic syndrome X and wasting disorders associated with chronic
CC diseases, bacterial, fungal, protozoal and viral infections, pain,
CC bulimia, asthma, hypertension, urinary retention, osteoporosis, Crohn's
CC disease, multiple sclerosis, Albright Hereditary Osteodystrophy, angina
CC pectoris, myocardial infarction, ulcer, allergy, benign prostatic
CC hypertrophy, and psychotic and neurological disorders, including anxiety,
CC schizophrenia, manic depression, delirium, dementia, and dyskinesias,
CC such as Huntington's disease and Gilles de la Tourette's syndrome. The
CC nucleic acid is useful in gene therapy. The present sequence encodes a
CC NOVX protein

SQ Sequence 2752 BP; 505 A; 937 C; 829 G; 481 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 6.04e-53 Length: 2752
Score: 559.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-624-932C-2_COPY_495_598 (1-104) x ABK37922 (1-2752)

QY 1 ThrSerAenMetThrTyrGlyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsn 20
DB 1528 ACCAGCAACATGACCTATGGGACCTTCACTTCCTGGGGGGCCGGCTGATGATCCCTAAT 1587
QY 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrGluIle 40
DB 1588 ACAGGTATCAGCTCCTCATCCCCCAGATGCCATACCCGAGGGAGATCTATGAGATC 1647
QY 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrIleu 60
DB 1648 TACTCAGCTGCAACAGCCGAGACGTGAGGTGGCCCTAGCTGGCTGTCAGACCCCTG 1707
QY 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
DB 1708 CTGAGTCCCATCGTTAGCTGTGGACCCCTGGCGCTCTGCTACCGGCCAGTCTCTCTG 1767
QY 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
DB 1768 GCTATGGACCACTGTGGGGAGCCAGCCCTGACAGCTGGAGCCTCGGCTCAAAAAGCAG 1827
QY 101 SerCysGluGly 104
DB 1828 TCGTGGAGGGC 1839

RESULT 6

ADH71617

ID ADH71617 standard; DNA; 2752 BP.

AC ADH71617;

XX

XX 25-MAR-2004 (first entry)

DT

XX Human gene of the invention NOV21e SEQ ID NO:513.

DE

XX ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antidiabetic; antilipemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.

XX

OS Homo sapiens.

XX

XX WO2003102155-A2.

FN

XX 11-DEC-2003.
PD 03-JUN-2003; 2003WO-US017430.
XX 03-JUN-2002; 2002US-0385120P.
XX 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 06-JUN-2002; 2002US-0386376P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 07-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-038796P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 08-JUN-2002; 2002US-0387262P.
PR 10-JUN-2002; 2002US-038760P.
PR 10-JUN-2002; 2002US-0387400P.
PR 11-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 12-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 13-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 15-AUG-2002; 2002US-0403617P.
PR 15-AUG-2002; 2002US-0403618P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 23-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.

PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 09-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
XX (CURA-) CURAGEN CORP.
XX
XX Alsobrook JP, Alvarez E, Anderson DM, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JU, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigar M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shinkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;
XX
XX WPI: 2004-081935/08.
DR P-PSDB; ADH71618.
XX
XX New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
XX Example 21; SEQ ID NO 513; 1880pp; English.
XX
XX The invention relates to a novel isolated polypeptide (NOVX) . A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.
XX
SQ Sequence 2752 BP; 505 A; 937 C; 829 G; 481 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.04e-53 Length: 2752
Score: 559.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-10-624-932C-2_COPY_495_598 (1-104) x ADH71617 (1-2752)

QY 1 ThrSerAsnMetThrTyrglyThrPheAsnPhLeuGlyArgLeuMetileProhen 20
DB 1528 ACCAGCAACATGACCTATGGGACCTTCACTTCTCGGGGGCGGCTGATGATCCCTAAT 1587
QY 21 ThrGlyIleSerLeuLeuileProProAspAlaIleProArgGlyLysIleTyrgluile 40
DB 1588 ACAGGTATCAGCTCTCTATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATC 1647
QY 41 TyrLeuThrLeuHigLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
DB 1648 TACCTCAGCTGCACAAAGCGGAGAGCTGAGGTGGCTTACCTAGCTGGCTGCAGACCTG 1707
QY 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
DB 1708 CTGAGTCCCATCGTTAGCTGTGGACCCCTCGCTGCTCACCCTGGCCAGTCATCCTG 1767

QY 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysLysGln 100
DB 1768 GCTATGGACCACTGTGGGAGGCCAGCCCTGACAGCTGGAGCTGGCCCTCAAAAGCAG 1827
QY 101 SerCysGluGly 104
DB 1828 TCGTGCAGGGC 1839
RESULT 7
ABK49422
ID ABK49422 standard; DNA; 2881 BP.
XX
XX AC ABK49422;
XX
XX 15-JUL-2002 (first entry)
XX
XX DNA encoding human UNC5-like protein NOV1.
XX
XX Human; NOVX polypeptide; cardiomyopathy; atherosclerosis; cancer;
KW cell signal processing; metabolic pathway modulation; cancerous tissue;
KW antibody; diabetes; transgenic animal; UNC5-like protein; NOV1;
KW chromosome 13; gene; ds.
XX
XX Homo sapiens.
XX
XX FH Key Location/Qualifiers
FT CDS 87..2786
FT /*tag= a
FT /product= "Human UNC5-like protein NOV1"
XX
XX WO200229038-A2.
XX
XX 11-APR-2002.
XX
XX 04-OCT-2001; 2001WO-US031377.
XX
XX 04-OCT-2000; 2000US-0237862P.
XX (CURA-) CURAGEN CORP.
XX
XX Herrmann JU, Rastelli L, Shinkets RA;
PI WPI: 2002-340104/37.
DR P-PSDB; AAU79939.
XX
XX Novel isolated NOVX polypeptide, and encoded polynucleotide, useful for
PT treating cardiomyopathy, atherosclerosis, and cancer.
XX
XX Claim 8; Page 7-8; 180pp; English.
XX
XX The present invention relates to a new NOVX polypeptide having a 900
CC (NOV1), 4349 (NOV2), 940 (NOV3), 798 (NOV4), 865 (NOV5), or 331 (NOV6)
CC residue amino acid sequence, as given in the specification. The novel
CC polypeptide, and its encoding polynucleotide, are used to treat
CC cardiomyopathy, atherosclerosis, cancer or a disease related to cell
CC signal processing and metabolic pathway modulation, in a human. Detecting
CC the polypeptide or polynucleotide is useful for identifying cancerous
CC tissue. The antibody can be used to treat diabetes or cancer. The host
CC cells can be used to produce non-human transgenic animals useful in drug
CC screening. The present nucleic acid sequence is that of the human UNC5-
CC like NOV1 gene located on chromosome 13. This sequence encodes the human
CC UNC5-like protein NOV1 of the invention
XX
SQ Sequence 2881 BP; 526 A; 985 C; 868 G; 502 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.4e-53 Length: 2881
Score: 559.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

XX Human gene of the invention NOV21n SEQ ID NO:531.
DE
XX ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipaeamic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX Homo sapiens.
OS
XX WO2003102155-A2.
FN
XX 11-DEC-2003.
PD
XX 03-JUN-2003; 2003WO-US017430.
PF
XX 03-JUN-2002; 2002US-0385120P.
XX 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 05-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 06-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-0387969P.
PR 07-JUN-2002; 2002US-0388169P.
PR 07-JUN-2002; 2002US-0388931P.
PR 07-JUN-2002; 2002US-0386943P.
PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 13-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.

PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417406P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
XX (CURA-) CURAGEN CORP.
FA
XX Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Caterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Erttenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI Maciachian T, Malyankar UM, Mezick AU, Millet I, Mishra VS;
PI Padigaru M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shinkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;
XX
XX WPI; 2004-081935/08.
DR P-PSDB; ADH71636.
XX
XX New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
XX Example 21; SEQ ID NO 531; 1880pp; English.
PS
XX The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaeamic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing.
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.
XX
SQ Sequence 2881 BP; 527 A; 985 C; 867 G; 502 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 6.4e-53 Length: 2881
Score: 559.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0
US-10-624-932C-2_COPY_495_598 (1-104) x ADH71635 (1-2881)
Qy 1 ThrSerAsnMetThrTyrGlyThrPheAsnPheLeuGlyArgLeuMetIleProAsn 20
Db 1569 ACCAGCAACATGACCTATGGACCTTCACTTCCTCGGGGCGCGGTATGATCCCTAAT 1628

CC antilipaeamic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.

SQ Sequence 2881 BP; 527 A; 985 C; 867 G; 502 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.4e-53 Length: 2881
Score: 559.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-10-624-932C-2_COPY_495_598 (1-104) x ADH71637 (1-2881)

Qy 1 ThrSerAsnMetThrTyrGlyThrPheAsnPhetLeuGlyArgLeuMetIleProAsn 20
Db 1569 ACCAGCAACATGACCTATGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAAT 1628
Qy 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrGluIle 40
Db 1629 ACAGGTATCAGCCTCCTCATCCCCCAGATGCCATACCCGAGGGAGATCTATGAGATC 1688
Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrIleu 60
Db 1689 TACCTCAGCTGCACAGCCGAGACGTCGAGGTTCGCCCTAGCTGGCTGTGCAGACCCCTG 1748
Qy 61 LeuSerProIleValSerCysGlyProGlyValLeuLeuThrArgProValIleIeu 80
Db 1749 CTGAGTCCCATCTGTTAGCTGTGGACCCCTCGCGCTGCTCACCCGCCAGTCATCTCTG 1808
Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
Db 1809 GCTATGGACCACTGTGGGAGCCCGACCCCTGCAGCTGGAGCCTCGCGCTCAAAAGCAG 1868
Qy 101 SerCysGluGly 104
Db 1869 TCGTCCGAGGGC 1880

RESULT 12

ID ADH71641 standard; DNA; 2881 BP.

XX AC ADH71641;

XX XX 25-MAR-2004 (first entry)

XX DE Human gene of the invention NOV21q SEQ ID NO:537.

XX KW ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
XX KW anorectic; antidiabetic; antimicrobial; antilipaeamic; gene therapy;
XX KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
XX KW obesity; diabetes; infectious disease; metabolic syndrome X;
XX KW dyslipidaemia.

XX OS Homo sapiens.

XX XX WO2003102155-A2.

XX XX 11-DEC-2003.

XX XX 03-JUN-2003; 2003WO-US017430.

XX

PR 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 06-JUN-2002; 2002US-0386376P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 06-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-038796P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 11-JUN-2002; 2002US-038735P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387688P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 21-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-040617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.

PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton B, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangoli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VV, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI MacLachlan T, Malyankar UM, Mezick AJ, Millet J, Mishra VS;
PI Padigar M, Ratturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shmiks RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;
XX
XX WPI: 2004-081935/08.
DR P-FSDB; ADH71642.
XX
XX New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
XX Example 21; SEQ ID NO 537; 1880pp; English.
XX
XX The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.
XX
SQ Sequence 2881 BP; 526 A; 986 C; 867 G; 502 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.4e-53 Length: 2881
Score: 559.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-10-624-932C-2_COPY_495_598 (1-104) x ADH71641 (1-2881)

QY 1 ThrSerAnMetThrTyrglyThrPheAnPheLeuGlyArgLeuMetIleProAsn 20
Db 1569 ACCAGCAACATGACCTATGGGACCTTCACTTCTCGGGGGCGGCTGATGCTCCTAAT 1628

QY 21 ThrGlyIleSerLeuLeuProAspAlaIleProArgGlyLysIleTyrcGlutle 40
Db 1629 ACAGGTATCAGCTCTCTATCCCCCAGATGTCATACCCGAGGGAAGATCTATGAGATC 1688

QY 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 1689 TACCTCAGCTGCACACGCGGAGACGTCGTAGTTGGCCCTAGCTGGCTGCAGACCTG 1748

QY 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
Db 1749 CTGAGTCCCATGCTGTAGCTGTGGACCCCTGCTGCTCCTCACCCTGCGCCATCATCTG 1808

QY 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
Db 1809 GCTATGAGCCACTGTGGGAGCCCGAGCCCTGTGACGTGAGCTGCGCTCAAAAGCAG 1869

QY 101 SerCysGluGly 104
Db 1869 TCGTCCGAGGCG 1880
RESULT 13
ADH71609
ID ADH71609 standard; DNA; 2881 BP.
XX
XX ADH71609;
XX
XX 25-MAR-2004 (first entry)
XX
XX Human gene of the invention NOV21a SEQ ID NO:505.
XX
XX ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX
XX Homo sapiens.
OS
XX WO2003102155-A2.
PN
XX 11-DEC-2003.
PD
XX
XX 03-JUN-2003; 2003WO-US017430.
XX
XX 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 06-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 06-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-0386796P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389146P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390066P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.

PR 09-AUG-2002; 2002US-0402389P.
 PR 12-AUG-2002; 2002US-0402786P.
 PR 12-AUG-2002; 2002US-0402816P.
 PR 12-AUG-2002; 2002US-0402821P.
 PR 12-AUG-2002; 2002US-0402832P.
 PR 13-AUG-2002; 2002US-0403448P.
 PR 13-AUG-2002; 2002US-0403459P.
 PR 13-AUG-2002; 2002US-0403531P.
 PR 13-AUG-2002; 2002US-0403532P.
 PR 13-AUG-2002; 2002US-0403563P.
 PR 13-AUG-2002; 2002US-0406317P.
 PR 15-AUG-2002; 2002US-0403617P.
 PR 26-AUG-2002; 2002US-0406182P.
 PR 26-AUG-2002; 2002US-0406355P.
 PR 27-AUG-2002; 2002US-0406240P.
 PR 12-SEP-2002; 2002US-0410084P.
 PR 20-SEP-2002; 2002US-0412528P.
 PR 23-SEP-2002; 2002US-0412731P.
 PR 30-SEP-2002; 2002US-0414801P.
 PR 30-SEP-2002; 2002US-0414839P.
 PR 30-SEP-2002; 2002US-0414840P.
 PR 30-SEP-2002; 2002US-0414954P.
 PR 09-OCT-2002; 2002US-0417186P.
 PR 09-OCT-2002; 2002US-0417406P.
 PR 23-OCT-2002; 2002US-0420639P.
 PR 28-OCT-2002; 2002US-0421156P.
 PR 31-OCT-2002; 2002US-0422690P.
 PR 01-NOV-2002; 2002US-0423130P.
 PR 05-NOV-2002; 2002US-00423798.
 PR 05-NOV-2002; 2002US-0423798P.
 PR 12-NOV-2002; 2002US-0425453P.
 XX
 PA (CURA-) CURAGEN CORP.

PI Alsbrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
 PI Catterton E, Crabtree-Bokor JR, Edinger SR, Ellerman K;
 PI Ettenberg S, Gangoli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
 PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
 PI Maciachlan T, Malyankar UM, Merick AJ, Millet I, Mishra VS;
 PI Padigaru M, Patturajan M, Pena CE, Peyman JA, Raha D, Rastelli L;
 PI Rieger DK, Rothenberg ME, Sciore P, Shency SG, Shimkets RA;
 PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
 PI Zhong H;

XX WPI; 2004-081935/08.
 DR P-PSDB; ADH71629.
 XX

PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
 PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
 PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

XX Example 21; SEQ ID NO 505; 1880pp; English.

XX The invention relates to a novel isolated polypeptide (NOVX). A
 CC polypeptide of the invention has cytostatic, immunomodulator,
 CC neuroprotective, anorectic, antidiabetic, antimicrobial, and
 CC anilipaeamic activity, and may have a use in gene therapy, and as a
 CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
 CC any of the 303 fully defined nucleotide sequences given in the
 CC specification. The polypeptide is useful in the manufacture of a
 CC medicament for treating a syndrome associated with a human disease. The
 CC polypeptide, polynucleotide and antibody are useful in diagnosing,
 CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
 CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
 CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
 CC further used as hybridisation probes, in chromosome mapping, tissue
 CC typing, preventive medicine, and pharmacogenomics. The present sequence
 CC encodes a NOVX polypeptide of the invention.

SQ Sequence 2881 BP; 526 A; 985 C; 868 G; 502 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 6.4e-53 Length: 2881

Score: 559.00 Matches: 104
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 12 Gaps: 0

US-10-624-932C-2_COPY_495_598 (1-104) x ADH71609 (1-2881)

Qy 1 ThrSerAsnMetThrTyrGlyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsn 20
 |||||
 Db 1569 ACCAGCAACATGACCTATGGACCTTCAACTTCCTCGGGGGCCGGCTGATCCCTAAT 1628
 |||||
 Qy 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrGluIle 40
 |||||
 Db 1629 ACAGGTATGACCTCTCTATCCCTCCAGATGCCATACCCGAGGGAAGATCTATGAGATC 1688
 |||||
 Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
 |||||
 Db 1689 TACCTCAGCTGCACAAGCCGGAAGACGTGAGGTTGCCCTAGCTGGCTGTGACAGCCCTG 1748
 |||||
 Qy 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
 |||||
 Db 1749 CTGAGTCCCATCGTGTAGCTGTGGACCCCTGGCGCTCCTGTCTACCCGGCCAGTCATCCTG 1808
 |||||
 Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTyrSerLeuArgLeuLysGln 100
 |||||
 Db 1809 GCTATGGACCACTGTGGGGAGCCCGCTGACAGCTGGAGCTGGCGCTCAAAAAGCAG 1868
 |||||
 Qy 101 SerCysGluGly 104
 |||||
 Db 1869 TCGTGGCAGGGC 1880

RESULT 14

ADH71629
 ID ADH71629 standard; DNA; 2881 BP.

XX AC ADH71629;

XX DT 25-MAR-2004 (first entry)

XX DE Human gene of the invention NOV21k SEQ ID NO:525.

XX ds; gene; human; cytostatic; immunomodulator; neuroprotective; neurotropic;
 KW anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;
 KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
 KW obesity; diabetes; infectious disease; metabolic syndrome X;
 KW dyslipidaemia.

XX OS Homo sapiens.

XX WO2003102155-A2.

XX PD 11-DEC-2003.

XX 03-JUN-2003; 2003WO-US017430.

XX 03-JUN-2002; 2002US-0385120P.

XX 04-JUN-2002; 2002US-0385784P.

XX 05-JUN-2002; 2002US-0386041P.

XX 05-JUN-2002; 2002US-0386047P.

XX 06-JUN-2002; 2002US-0386376P.

XX 06-JUN-2002; 2002US-0386453P.

XX 06-JUN-2002; 2002US-0386864P.

XX 07-JUN-2002; 2002US-0386796P.

XX 07-JUN-2002; 2002US-0386816P.

XX 07-JUN-2002; 2002US-0386931P.

XX 07-JUN-2002; 2002US-0386971P.

XX 07-JUN-2002; 2002US-0387262P.

XX 08-JUN-2002; 2002US-0296960P.

XX 10-JUN-2002; 2002US-0387400P.

XX 10-JUN-2002; 2002US-0387535P.

obesity; diabetes; infectious disease; metabolic syndrome X;

dyslipidaemia.

Homo sapiens.

WO2003102155-A2.

11-DEC-2003.

03-JUN-2003; 2003WO-US017430.

03-JUN-2002; 2002US-0385120P.

04-JUN-2002; 2002US-0385784P.

05-JUN-2002; 2002US-0386041P.

05-JUN-2002; 2002US-0386047P.

06-JUN-2002; 2002US-0386376P.

06-JUN-2002; 2002US-0386453P.

06-JUN-2002; 2002US-0386864P.

06-JUN-2002; 2002US-0387016P.

07-JUN-2002; 2002US-038796P.

07-JUN-2002; 2002US-0386816P.

07-JUN-2002; 2002US-0386931P.

07-JUN-2002; 2002US-0386942P.

07-JUN-2002; 2002US-0386971P.

07-JUN-2002; 2002US-0387262P.

08-JUN-2002; 2002US-0296960P.

10-JUN-2002; 2002US-0387400P.

10-JUN-2002; 2002US-0387535P.

11-JUN-2002; 2002US-0387610P.

11-JUN-2002; 2002US-0387625P.

11-JUN-2002; 2002US-0387634P.

11-JUN-2002; 2002US-0387668P.

11-JUN-2002; 2002US-0387696P.

11-JUN-2002; 2002US-0387702P.

11-JUN-2002; 2002US-0387836P.

11-JUN-2002; 2002US-0387859P.

12-JUN-2002; 2002US-0387933P.

12-JUN-2002; 2002US-0387934P.

12-JUN-2002; 2002US-0387960P.

12-JUN-2002; 2002US-0388022P.

12-JUN-2002; 2002US-0388096P.

13-JUN-2002; 2002US-0389123P.

14-JUN-2002; 2002US-0389112P.

14-JUN-2002; 2002US-0389120P.

14-JUN-2002; 2002US-0389144P.

14-JUN-2002; 2002US-0389146P.

KW

KW

XX

OS

XX

XX

FN

XX

XX

XX

PD

XX

PF

XX

XX

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

PR

```
Db 1689 TACCTCACGCTGCACAAAGCCGGAAGACGTGAGTTGCCCTAGCTGGCTGTGAGACCCCTG 1748
Qy 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
Db 1749 CTGAGTCCCATCGTTAGCTGTGACCCCTGGGTCCTGCTACCCGGCCAGTCAATCCG 1808
Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysLysGln 100
Db 1809 GCTATGGACCACTGTGGGGAGCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAG 1868
Qy 101 SerCysGluGly 104
Db 1869 TCGTGCAGGGC 1880
```

Search completed: September 9, 2005, 00:43:02
Job time : 545.856 secs

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 8, 2005, 23:51:22 ; Search time 165.773 Seconds
(without alignments)
1026.543 Million cell updates/sec

Title: US-10-624-932C-2_COPY_495_598

Perfect score: 559
Sequence: 1 TSNMTYGTFLGRLMPN.....CEPSPDSWSLRLKKQSCG 104

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh
-O=/cgn2_1/USPTO_spool_h/US10624932/runat_08092005_161706_15822/app_query.fasta_1.1386
-DB=Issued_Patents_NA -QWTF=fastcap -SUFFIX=rni -MINMATCH=0.1 -LOOPECL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10624932 @CGN 1.1 187 @runat_08092005_161706_15822 -NCPU=6 -ICPU=3
-NO_MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:
1: /cgn2_6/ptodata/1/ina/5A COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PTCUS COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	553	98.9	1787	2	US-08-808-982-2
2	553	98.9	1787	3	US-09-306-902A-2
3	553	98.9	3014	2	US-08-808-982-1
4	553	98.9	3014	3	US-09-306-902A-1
5	337	60.3	3008	4	US-09-949-016-4794
6	277	49.6	2831	2	US-08-808-982-3
7	277	49.6	2831	3	US-09-306-902A-3
8	243.5	43.6	1968	4	US-09-969-532-31
9	243.5	43.6	2001	4	US-09-969-532-29
10	243.5	43.6	2010	4	US-09-969-532-27
11	243.5	43.6	2043	4	US-09-969-532-25
12	243.5	43.6	2661	4	US-09-969-532-15

13	243.5	43.6	2694	4	US-09-969-532-13	Sequence 13, Appl
14	243.5	43.6	2703	4	US-09-969-532-11	Sequence 11, Appl
15	243.5	43.6	2736	4	US-09-969-532-9	Sequence 9, Appl
16	243.5	43.6	3411	4	US-09-969-532-33	Sequence 33, Appl
c 17	181	32.4	601	4	US-09-949-016-169999	Sequence 169999, A
18	181	32.4	114139	4	US-09-949-016-16536	Sequence 16536, A
19	163.5	29.2	7166	4	US-09-949-016-3599	Sequence 3599, Ap
20	163.5	29.2	7888	4	US-09-919-497-48	Sequence 48, Appl
c 21	163.5	29.2	8312	4	US-09-620-312D-1048	Sequence 1048, Ap
c 22	141	25.2	601	4	US-09-949-016-170000	Sequence 170000, A
c 23	140.5	25.1	771	1	US-08-253-155A-17	Sequence 17, Appl
24	139.5	25.0	777	4	US-09-270-767-14197	Sequence 14197, A
25	132.5	23.7	966	4	US-09-969-532-23	Sequence 23, Appl
26	132.5	23.7	999	4	US-09-969-532-21	Sequence 21, Appl
27	132.5	23.7	1008	4	US-09-969-532-19	Sequence 19, Appl
28	132.5	23.7	1041	4	US-09-969-532-17	Sequence 17, Appl
29	132.5	23.7	1659	4	US-09-969-532-7	Sequence 7, Appl
30	132.5	23.7	1692	4	US-09-969-532-5	Sequence 5, Appl
31	132.5	23.7	1701	4	US-09-969-532-3	Sequence 3, Appl
32	132.5	23.7	1734	4	US-09-969-532-1	Sequence 1, Appl
c 33	121.5	21.7	126254	4	US-09-949-016-15341	Sequence 15341, A
c 34	104	18.6	601	4	US-09-949-016-169988	Sequence 169988, A
35	80.5	14.4	744	4	US-09-270-767-10232	Sequence 10232, A
c 36	78.5	14.0	13795	4	US-09-949-016-15323	Sequence 15323, A
c 37	78	14.0	28438	4	US-09-820-790B-3	Sequence 3, Appl
38	76.5	13.7	1520	3	US-09-369-364A-3	Sequence 3, Appl
39	76	13.6	444	4	US-09-270-767-30319	Sequence 30319, A
c 40	76	13.6	137753	4	US-09-949-016-17404	Sequence 17404, A
c 41	75.5	13.5	42250	4	US-09-949-016-15426	Sequence 15426, A
c 42	75	13.4	21372	4	US-09-949-016-16941	Sequence 16941, A
43	74.5	13.3	601	4	US-09-949-016-148753	Sequence 148753, A
44	74.5	13.3	38519	4	US-09-952-060-29	Sequence 29, Appl
c 45	74	13.2	2031	2	US-08-448-561-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-808-982-2
; Sequence 2, Application US/08808982
; Patent No. 5919271
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; APPLICANT: Leonardo, E. David
; APPLICANT: Hink, Lindsey
; APPLICANT: Masu, Masayuki
; APPLICANT: Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,982
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 2:

```
;
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1787 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
US-08-808-982-2

Alignment Scores:
Pred. No.: 1.14e-61 Length: 1787
Score: 553.00 Matches: 103
Percent Similarity: 99.04% Conservativity: 0
Best Local Similarity: 99.04% Mismatches: 1
Query Match: 98.93% Indels: 0
DB: 2 Gaps: 0

US-10-624-932C-2_COPY_495_598 (1-104) x US-08-808-982-2 (1-1787)
Qy 1 ThrSerAsnMetThrTyTGlyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsn 20
Db 459 ACCAGCAACATGACCTATGGACCTTCAACTTCTCGGGGGCCGGCTGATGATCCCTAAT 518
Qy 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrGluIle 40
Db 519 ACAGGAATCAGCTCTCTCATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATC 578
Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 579 TACCTCAGCTGCAACACCGGAAGACGTGAGGTTGCCCTAGCTGGCTGTGCAGACCTG 638
Qy 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
Db 639 CTGAGTCCATCGTTAGCTGTGGACCCCTGCGCTCTGCTACCCGCCAGTATCTCTG 698
Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
Db 699 GCTATGGACCACTGTGGGAGCCAGCCCTGACAGCTGAGCCTGAGCCTGAGCCTGAGCCTG 758
Qy 101 SerCysGluGly 104
Db 759 TCGTGCAGGGA 770

RESULT 2
US-09-306-902A-2
; Sequence 2, Application US/09306902A
; Patent No. 6277585
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindsey
; Masu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/306,902A
; FILING DATE: 07-May-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627

;
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1787 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-306-902A-2

Alignment Scores:
Pred. No.: 1.14e-61 Length: 1787
Score: 553.00 Matches: 103
Percent Similarity: 99.04% Conservativity: 0
Best Local Similarity: 99.04% Mismatches: 1
Query Match: 98.93% Indels: 0
DB: 3 Gaps: 0

US-10-624-932C-2_COPY_495_598 (1-104) x US-09-306-902A-2 (1-1787)
Qy 1 ThrSerAsnMetThrTyTGlyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsn 20
Db 459 ACCAGCAACATGACCTATGGACCTTCAACTTCTCGGGGGCCGGCTGATGATCCCTAAT 518
Qy 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrGluIle 40
Db 519 ACAGGAATCAGCTCTCTCATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATC 578
Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 579 TACCTCAGCTGCAACACCGGAAGACGTGAGGTTGCCCTAGCTGGCTGTGCAGACCTG 638
Qy 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
Db 639 CTGAGTCCATCGTTAGCTGTGGACCCCTGCGCTCTGCTACCCGCCAGTATCTCTG 698
Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
Db 699 GCTATGGACCACTGTGGGAGCCAGCCCTGACAGCTGAGCCTGAGCCTGAGCCTGAGCCTG 758
Qy 101 SerCysGluGly 104
Db 759 TCGTGCAGGGA 770

RESULT 3
US-08-808-982-1
; Sequence 1, Application US/08808982
; Patent No. 593271
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; APPLICANT: Hink, Lindsey
; APPLICANT: Masu, Masayuki
; APPLICANT: Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
```

APPLICATION NUMBER: US/08/808,982

FILING DATE:

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: UC96-217

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 343-4341

TELEFAX: (415) 343-4342

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3014 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-808-982-1

Alignment Scores:

Pred. No.:	2,42e-61	Length:	3014
Score:	553.00	Matches:	102
Percent Similarity:	99.04%	Conservative:	1
Best Local Similarity:	98.08%	Mismatches:	1
Query Match:	98.93%	Indels:	0
DB:	2	Gaps:	0

US-10-624-932C-2_COPY_495_598 (1-104) x US-08-808-982-1 (1-3014)

Qy	1	ThrSerAsnMetThrTyrGlyThrPheAsnPhelLeuGlyArgLeuMetIleProAsn	20
Db	1483	ACCAACATGGCCCTACGGGACCTTCAACTTCTCGGGGGCGGCTGATGATCCCTAAT	1542
Qy	21	ThrGlyIleSerLeuLeuIleProAspAlaIleProArgGlyLysIleTyrGluIle	40
Db	1543	ACGGGATCAGCTCTCTATCCCGGATGCCATCCCGAGGAAAGATCTACGAGATC	1602
Qy	41	TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu	60
Db	1603	TACCTCACCTGCACAGCCAGAGACGTGAGTTGGCCCTAGCTGGCTGTGACAGCCTG	1662
Qy	61	LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu	80
Db	1663	CTGAGTCAGTCGTAGCTGTGGGCCCCCAGAGTCCTGCCTCACCGGCCAGTCATCCTT	1722
Qy	81	AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln	100
Db	1723	GCAATGGACCACTGTGGAGAGCCCGCCCTGACAGCTGGAGTCTGGGCTCATAAAGCAG	1782
Qy	101	SerCysGluGly	104
Db	1783	TCCTGCGAGGGC	1794

RESULT 4

US-306-902A-1

Sequence 1, Application US/09306902A

Patent No. 627585

GENERAL INFORMATION:

APPLICANT: Tessier-Lavigne, Marc

Leonardo, E. David

Hink, Lindsey

Masu, Masayuki

Kazuko, Keino-Masu

TITLE OF INVENTION: Netrin Receptors

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/306,902A

FILING DATE: 07-May-1999

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: UC96-217

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 343-4341

TELEFAX: (415) 343-4342

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3014 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-306-902A-1

Alignment Scores:

Pred. No.:	2,42e-61	Length:	3014
Score:	553.00	Matches:	102
Percent Similarity:	99.04%	Conservative:	1
Best Local Similarity:	98.08%	Mismatches:	1
Query Match:	98.93%	Indels:	0
DB:	3	Gaps:	0

US-10-624-932C-2_COPY_495_598 (1-104) x US-09-306-902A-1 (1-3014)

Qy	1	ThrSerAsnMetThrTyrGlyThrPheAsnPhelLeuGlyArgLeuMetIleProAsn	20
Db	1483	ACCAACATGGCCCTACGGGACCTTCAACTTCTCGGGGGCGGCTGATGATCCCTAAT	1542
Qy	21	ThrGlyIleSerLeuLeuIleProAspAlaIleProArgGlyLysIleTyrGluIle	40
Db	1543	ACGGGATCAGCTCTCTATCCCGGATGCCATCCCGAGGAAAGATCTACGAGATC	1602
Qy	41	TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu	60
Db	1603	TACCTCACCTGCACAGCCAGAGACGTGAGTTGGCCCTAGCTGGCTGTGACAGCCTG	1662
Qy	61	LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu	80
Db	1663	CTGAGTCAGTCGTAGCTGTGGGCCCCCAGAGTCCTGCCTCACCGGCCAGTCATCCTT	1722
Qy	81	AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln	100
Db	1723	GCAATGGACCACTGTGGAGAGCCCGCCCTGACAGCTGGAGTCTGGGCTCATAAAGCAG	1782
Qy	101	SerCysGluGly	104
Db	1783	TCCTGCGAGGGC	1794

RESULT 5

US-09-949-016-4794

Sequence 4794, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLO01307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768


```
;
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2831 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-306-902A-3

Alignment Scores:
Pred. No.: 1,45e-25 Length: 2831
Score: 277.00 Matches: 55
Percent Similarity: 69.23% Conservative: 17
Best Local Similarity: 52.88% Mismatches: 30
Query Match: 49.55% Indels: 2
DB: 3 Gaps: 2

US-10-624-932C-2_COPY_495_598 (1-104) x US-09-306-902A-3 (1-2831)
Qy 2 SerAsnMetThrTyTGlyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsnThr 21
Db 1618 AGCAGCAGTCGTCAGTGGCACCTTTGGTTGGCTGGGTGGGAGGCTGACCATTCCTCCGGCACA 1677
Qy 22 GlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyxGluIleTyx 41
Db 1678 GGGGTGACGCTGTTGGTACCAAAATGGAGCCATTCCCGAGGCGAAGTTCTATGACTTGTAT 1737
Qy 42 LeuThrLeuHisLysProGluAspValArgLeuProLeuAla---GlyCysGlnThrLeu 60
Db 1738 CTAGGTATCAACAGACTGAAAGCACC---CTCCCACTTTCGGAAGGTTCCAGACAGTA 1794
Qy 61 LeuSerProIleValSerCysGlyProGlyValLeuLeuThrArgProValIleLeu 80
Db 1795 TTGAGCCCTCGGTGACCTGCGGGGCCACCGGGCCCTCTCTGTGCGCCCTGTGTGCTCTC 1854
Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
Db 1855 ACTGTGCCCCACTGTGCTGAAGTCATTCCCGGAGACTGGATCTTCCAGCTCAAGACCCAG 1914
Qy 101 SerCysGluGly 104
Db 1915 GCCCATCAGGGC 1926

RESULT 8
US-09-969-532-31
; Sequence 31, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodir
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; PRIOR FILING DATE: 2001-10-02
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-31
```

```
Alignment Scores:
Pred. No.: 1,91e-21 Length: 1968
Score: 243.50 Matches: 47
Percent Similarity: 66.35% Conservative: 22
Best Local Similarity: 45.19% Mismatches: 34
Query Match: 43.56% Indels: 1
DB: 4 Gaps: 1

US-10-624-932C-2_COPY_495_598 (1-104) x US-09-969-532-31 (1-1968)
Qy 1 ThrSerAsnMetThrTyTGlyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsn 20
Db 724 ACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGCGCTTAGTATGCAAAAT 783
Qy 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyxGluIle 40
Db 784 ACAGGGTGAGCTTACTATACACACACGGTGCCATCCACAGAGGAGAATCTTGGGAGATT 843
Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 844 TATATGTCCATCAACCAAGGTGAACCC---AGCCTCCAGTCAGATGGCTCTGAGGTGCTC 900
Qy 61 LeuSerProIleValSerCysGlyProGlyValLeuLeuThrArgProValIleLeu 80
Db 901 CTGAGTCTCTGAAGTCACCTGTGGTCTCCAGACATGATCGTCACCACTCCCTTTCGATTG 960
Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
Db 961 ACCATCCCGCATGTGCAGATGTCAGTTCTGAGCATTCGAATATCCATTTAAAGAAGAGG 1020
Qy 101 SerCysGluGly 104
Db 1021 ACACAGCAGGGC 1032

RESULT 9
US-09-969-532-29
; Sequence 29, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; PRIOR FILING DATE: 2001-10-02
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 2001
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-29

Alignment Scores:
Pred. No.: 1,95e-21 Length: 2001
Score: 243.50 Matches: 47
Percent Similarity: 66.35% Conservative: 22
Best Local Similarity: 45.19% Mismatches: 34
Query Match: 43.56% Indels: 1
DB: 4 Gaps: 1

US-10-624-932C-2_COPY_495_598 (1-104) x US-09-969-532-29 (1-2001)
Qy 1 ThrSerAsnMetThrTyTGlyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsn 20
Db 757 ACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGCGCTTAGTATGCAAAAT 816
Qy 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyxGluIle 40
Db 817 ACAGGGTGAGCTTACTATACACACACGGTGCCATCCACAGAGGAGAATCTTGGGAGATT 876
```

```
Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
877 TATATGTCATCAACCAAGGTGAACCC---AGCTCCAGTCAGATGGCTCTGAGGTGCTC 933

Qy 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
934 CTGAGTCTGAAGTCACCTGTGGTCTCCAGACATGATCGTACCACCTCCCTTTGCATTG 993

Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
994 ACCATCCGGCACTGTCAGATGTCAGTTCTGAGCATTTGGAATATCCATTTAAAGAAGG 1053

Qy 101 SerCysGluGly 104
:::|||||:
Db 1054 ACACAGCAGGCGC 1065

RESULT 10
US-09-969-532-27
; Sequence 27, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-27

Alignment Scores:
Pred. No.: 1.96e-21 Length: 2010
Score: 243.50 Matches: 47
Percent Similarity: 66.35% Conservative: 22
Best Local Similarity: 45.19% Mismatches: 34
Query Match: 43.56% Indels: 1
Gaps: 4
Db: 1

US-10-624-932C-2_COPY_495_598 (1-104) x US-09-969-532-27 (1-2010)
Qy 1 ThrSerAsnMetThrTyrglyThrPheAsnPheLeuGlyArgLeuMetIleProAsn 20
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
766 ACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGCGCTTAGTAATGCCAAAT 825

Qy 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrGluIle 40
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
826 ACAGGGGTGAGCTTACTCATACCACACGGTGCCATCCAGACATGATCGTACCACCTCCCTTTGGGAGATT 885

Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
886 TATATGTCATCAACCAAGGTGAACCC---AGCTCCAGTCAGATGGCTCTGAGGTGCTC 942

Qy 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
943 CTGAGTCTGAAGTCACCTGTGGTCTCCAGACATGATCGTACCACCTCCCTTTGCATTG 1002

Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1003 ACCATCCGGCACTGTCAGATGTCAGTTCTGAGCATTTGGAATATCCATTTAAAGAAGG 1062

Qy 101 SerCysGluGly 104
:::|||||:
Db 1063 ACACAGCAGGCGC 1074

RESULT 11
US-09-969-532-25
```

```
; Sequence 25, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 2043
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-25

Alignment Scores:
Pred. No.: 2.01e-21 Length: 2043
Score: 243.50 Matches: 47
Percent Similarity: 66.35% Conservative: 22
Best Local Similarity: 45.19% Mismatches: 34
Query Match: 43.56% Indels: 1
Gaps: 4
Db: 1

US-10-624-932C-2_COPY_495_598 (1-104) x US-09-969-532-25 (1-2043)
Qy 1 ThrSerAsnMetThrTyrglyThrPheAsnPheLeuGlyArgLeuMetIleProAsn 20
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
799 ACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGCGCTTAGTAATGCCAAAT 858

Qy 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrGluIle 40
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
859 ACAGGGGTGAGCTTACTCATACCACACGGTGCCATCCAGACATGATCGTACCACCTCCCTTTGCATTG 918

Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
919 TATATGTCATCAACCAAGGTGAACCC---AGCTCCAGTCAGATGGCTCTGAGGTGCTC 975

Qy 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
976 CTGAGTCTGAAGTCACCTGTGGTCTCCAGACATGATCGTACCACCTCCCTTTGCATTG 1035

Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1036 ACCATCCGGCACTGTCAGATGTCAGTTCTGAGCATTTGGAATATCCATTTAAAGAAGG 1095

Qy 101 SerCysGluGly 104
:::|||||:
Db 1096 ACACAGCAGGCGC 1107

RESULT 12
US-09-969-532-15
; Sequence 15, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 2661
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-15
```

```
Alignment Scores:
Pred. No.: 2,95e-21 Length: 2661
Score: 243.50 Matches: 47
Percent Similarity: 66.35% Conservative: 22
Best Local Similarity: 45.19% Mismatches: 34
Query Match: 43.56% Indels: 1
DB: 4 Gaps: 1

US-10-624-932C-2_COPY_495_598 (1-104) x US-09-969-532-15 (1-2661)

Qy 1 ThrSerAsnMetThrTyGlyThrPheAsnPheLeuGlyArgLeuMetIleProAsn 20
Db 1417 ACAGAACTGAGGACAACTGGTCTCTTGGCCATTTAGGGGGCGCTTAGTAATGCCAAAT 1476

Qy 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrGlutIle 40
Db 1477 ACAGGGGTGAGCTTACTATACCACACCGTGCCATCCAGAGGAGAAATTCITGGGAGATT 1536

Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 1537 TATATGTCCATCAACCAAGGTGAACCC--AGCCTCCAGTCAGATGGCTCTGAGGTGCTC 1593

Qy 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
Db 1594 CTGAGTCTGAAGTCACCTGTGGTCTCCAGACATGATCGTCACCACTCCCTTTGCATTG 1653

Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTyrSerLeuArgLeuLysGln 100
Db 1654 ACCATCCCGCACTGTGCAGATGTCAGTTCTGAGCATTTGGAATATCCATTTAAAGAGAGG 1713

Qy 101 SerCysGluGly 104
Db 1714 ACACAGCAGGGC 1725

RESULT 13
US-09-969-532-13
; Sequence 13, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodi
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969.532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 2694
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-13

Alignment Scores:
Pred. No.: 3e-21 Length: 2694
Score: 243.50 Matches: 47
Percent Similarity: 66.35% Conservative: 22
Best Local Similarity: 45.19% Mismatches: 34
Query Match: 43.56% Indels: 1
DB: 4 Gaps: 1

US-10-624-932C-2_COPY_495_598 (1-104) x US-09-969-532-13 (1-2694)

Qy 1 ThrSerAsnMetThrTyGlyThrPheAsnPheLeuGlyArgLeuMetIleProAsn 20
Db 1450 ACAGAACTGAGGACAACTGGTCTCTTGGCCATTTAGGGGGCGCTTAGTAATGCCAAAT 1509

Qy 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrGlutIle 40
Db 1510 ACAGGGGTGAGCTTACTATACCACACCGTGCCATCCAGAGGAGAAATTCITGGGAGATT 1569
```

```
Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 1570 TATATGTCCATCAACCAAGGTGAACCC--AGCCTCCAGTCAGATGGCTCTGAGGTGCTC 1626

Qy 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
Db 1627 CTGAGTCTGAAGTCACCTGTGGTCTCCAGACATGATCGTCACCACTCCCTTTGCATTG 1686

Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTyrSerLeuArgLeuLysGln 100
Db 1687 ACCATCCCGCACTGTGCAGATGTCAGTTCTGAGCATTTGGAATATCCATTTAAAGAGAGG 1746

Qy 101 SerCysGluGly 104
Db 1747 ACACAGCAGGGC 1758

RESULT 14
US-09-969-532-11
; Sequence 11, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodi
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969.532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 2703
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-11

Alignment Scores:
Pred. No.: 3.01e-21 Length: 2703
Score: 243.50 Matches: 47
Percent Similarity: 66.35% Conservative: 22
Best Local Similarity: 45.19% Mismatches: 34
Query Match: 43.56% Indels: 1
DB: 4 Gaps: 1

US-10-624-932C-2_COPY_495_598 (1-104) x US-09-969-532-11 (1-2703)

Qy 1 ThrSerAsnMetThrTyGlyThrPheAsnPheLeuGlyArgLeuMetIleProAsn 20
Db 1459 ACAGAACTGAGGACAACTGGTCTCTTGGCCATTTAGGGGGCGCTTAGTAATGCCAAAT 1518

Qy 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrGlutIle 40
Db 1519 ACAGGGGTGAGCTTACTATACCACACCGTGCCATCCAGAGGAGAAATTCITGGGAGATT 1578

Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 1579 TATATGTCCATCAACCAAGGTGAACCC--AGCCTCCAGTCAGATGGCTCTGAGGTGCTC 1635

Qy 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
Db 1636 CTGAGTCTGAAGTCACCTGTGGTCTCCAGACATGATCGTCACCACTCCCTTTGCATTG 1695

Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTyrSerLeuArgLeuLysGln 100
Db 1696 ACCATCCCGCACTGTGCAGATGTCAGTTCTGAGCATTTGGAATATCCATTTAAAGAGAGG 1755

Qy 101 SerCysGluGly 104
Db 1756 ACACAGCAGGGC 1767

RESULT 15
```

```
US-09-969-532-9
; Sequence 9, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2736
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-9

Alignment Scores:
Pred. No.:      3.07e-21      Length:      2736
Score:          243.50      Matches:      47
Percent Similarity: 66.35%      Conservative: 22
Best Local Similarity: 45.19%      Mismatches: 34
Query Match:      43.56%      Indels:      1
DB:               4          Gaps:      1

US-10-624-932C-2_COPY_495_598 (1-104) x US-09-969-532-9 (1-2736)

Qy      1 ThrSerAsnMetThrTyrGlyThrPheAsnPheLeuGlyArgLeuMetIleProAsn 20
Db      1492 ACAGAACTGAGGACAACTGGTCTTTGGCCATTAGGGGGCCCTTAGTAATGCCAAT 1551

Qy      21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrGluIle 40
Db      1552 ACAGGGGTGAGCTTACTCATACCACACGGTGCCATCCAGAGGAGAAATCTTGGGAGATT 1611

Qy      41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db      1612 TATATGTCCATCAACCAAGGTGAACCC---AGCCTCCAGTCAGATGGCTCTGAGGTGCTC 1668

Qy      61 LeuSerProIleValSerCysGlyProGlyValLeuLeuThrArgProValIleLeu 80
Db      1669 CTGAGTCTCTGAGTCACCTGTGGTCTCTCCAGACATGTCACCACTCCCTTTGCATTG 1728

Qy      81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
Db      1729 ACCATCCGCACTGTGCAGATGTCAGTTCTGAGCATTGGAATATCCATTAAAGAAGAGG 1788

Qy      101 SerCysGluGly 104
Db      1789 ACACAGCAGGGC 1800

Search completed: September 9, 2005, 09:51:53
Job time : 172.773 secs
```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 9, 2005, 04:41:16 ; Search time 1037.83 Seconds
(without alignments)
658.098 Million cell updates/sec

Title: US-10-624-932c-2_COPY_495_598

Perfect score: 559

Sequence: 1 TSNMTYGTNFGLRLMPN.....CGEFPSPDWSLRLKKQSCG 104

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 7351250 seqs, 3283620254 residues

Total number of hits satisfying chosen parameters: 14702500

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool_h/US10624932/rnat_08092005_161709_15882/app_query.fasta_1.1386
-DB=Published Applications_NA -QPM=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blom62
-TRANS=human40.cdi -LIST=45 -DOCALLGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10624932 @cgn1.1.989 @rnat_08092005_161709_15882
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*
- 20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
- 21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
- 22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
- 24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	559	100.0	2752	10	US-09-918-779-1	Sequence 1, Appli
2	559	100.0	2752	18	US-10-624-932-1	Sequence 1, Appli
3	559	100.0	2881	10	US-09-970-944-1	Sequence 1, Appli
4	559	100.0	3561	20	US-10-643-795A-77	Sequence 77, Appl
5	559	100.0	3561	21	US-10-948-518-77	Sequence 13, Appl
6	559	100.0	3580	17	US-10-311-623-13	Sequence 2, Appli
7	553	98.9	1787	10	US-09-933-261-2	Sequence 2, Appli
8	553	98.9	1787	14	US-10-256-702-2	Sequence 15, Appl
9	553	98.9	2697	16	US-10-240-154-15	Sequence 1, Appli
10	553	98.9	3014	10	US-09-933-261-1	Sequence 1, Appli
11	553	98.9	3014	14	US-10-256-702-1	Sequence 1, Appli
12	503	90.0	1321	18	US-10-296-115-365	Sequence 365, App
C 13	393.5	70.4	9582	9	US-09-764-861-62	Sequence 62, Appl
C 14	393.5	70.4	9582	10	US-09-764-861-62	Sequence 62, Appl
C 15	393.5	70.4	9582	14	US-10-115-928-62	Sequence 62, Appl
C 16	393.5	70.4	18772	9	US-09-764-861-63	Sequence 63, Appl
C 17	393.5	70.4	18772	10	US-09-764-861-63	Sequence 63, Appl
C 18	393.5	70.4	18772	14	US-10-115-928-63	Sequence 63, Appl
19	287	51.3	1026	9	US-09-764-870-171	Sequence 171, App
20	287	51.3	1026	14	US-10-125-540-171	Sequence 171, App
21	287	51.3	2406	17	US-10-108-260A-239	Sequence 239, App
22	287	51.3	2449	20	US-10-723-860-5786	Sequence 5786, Ap
23	287	51.3	2860	17	US-10-087-684-1	Sequence 1, Appli
24	287	51.3	2860	17	US-10-087-684-3	Sequence 3, Appli
25	287	51.3	2860	17	US-10-218-779-1	Sequence 1, Appli
26	287	51.3	2860	17	US-10-218-779-3	Sequence 3, Appli
27	287	51.3	2895	18	US-10-037-417-37	Sequence 37, Appl
28	287	51.3	2995	11	US-09-972-211-55	Sequence 55, Appl
29	287	51.3	2995	18	US-10-096-625-55	Sequence 55, Appl
30	287	51.3	3485	9	US-09-816-828-18	Sequence 18, Appl
31	287	51.3	3501	17	US-10-295-027-1123	Sequence 1123, Ap
32	287	51.3	3884	14	US-10-028-072-145	Sequence 145, App
33	287	51.3	3884	14	US-10-140-808-145	Sequence 145, App
34	287	51.3	3884	14	US-10-121-049-145	Sequence 145, App
35	287	51.3	3884	14	US-10-123-904-145	Sequence 145, App
36	287	51.3	3884	14	US-10-140-470-145	Sequence 145, App
37	287	51.3	3884	14	US-10-175-746-145	Sequence 145, App
38	287	51.3	3884	14	US-10-176-918-145	Sequence 145, App
39	287	51.3	3884	14	US-10-176-921-145	Sequence 145, App
40	287	51.3	3884	14	US-10-137-865-145	Sequence 145, App
41	287	51.3	3884	14	US-10-140-474-145	Sequence 145, App
42	287	51.3	3884	14	US-10-142-431-145	Sequence 145, App
43	287	51.3	3884	14	US-10-143-114-145	Sequence 145, App
44	287	51.3	3884	14	US-10-142-419-145	Sequence 145, App
45	287	51.3	3884	14	US-10-123-262-145	Sequence 145, App

ALIGNMENTS

RESULT 1

US-09-918-779-1
; Sequence 1, Application US/09918779
; Publication No. US20030064369A1
; GENERAL INFORMATION:
; APPLICANT: Taupier, Raymond
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Rastelli, Luca
; APPLICANT: Spaderna, Steven
; APPLICANT: Shimkets, Richard
; APPLICANT: Zerkhusen, Bryan
; APPLICANT: Spytek, Kimberly
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Gusev, Vladimir
; APPLICANT: Grosse, William

APPLICANT: Alsobrook, John
APPLICANT: Lepley, Denise
APPLICANT: Burgess, Catherine
APPLICANT: Gerlach, Valerie
APPLICANT: Ellerman, Karen
APPLICANT: MacDougall, John
APPLICANT: Stone, David
APPLICANT: Smithson, Glenda
TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-074 US
CURRENT APPLICATION NUMBER: US/09/918,779
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/221,409
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/222,840
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: 60/223,752
PRIOR FILING DATE: 2000-08-08
PRIOR APPLICATION NUMBER: 60/223,762
PRIOR FILING DATE: 2000-08-08
PRIOR APPLICATION NUMBER: 60/223,770
PRIOR FILING DATE: 2000-08-08
PRIOR APPLICATION NUMBER: 60/223,769
PRIOR FILING DATE: 2000-08-08
PRIOR APPLICATION NUMBER: 60/225,146
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/225,392
PRIOR FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: 60/225,697
PRIOR FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: 60/263,662
PRIOR FILING DATE: 2001-02-01
PRIOR APPLICATION NUMBER: 60/281,645
PRIOR FILING DATE: 2001-04-05
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 2752
TYPE: DNA
ORGANISM: Homo sapiens
US-09-918-779-1

Alignment Scores:
Pred. No.: 2,05e-66 Length: 2752
Score: 559.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-624-932c-2_copy_495_598 (1-104) x US-09-918-779-1 (1-2752)

Qy 1 ThrSerAsnMetThrTyrGlyThrPheAsnPheLeuGlyArgLeuMetIleProAsn 20
Db 1528 ACCGACACATGACTATGGACCTTCACTTCTCGGGGCGCGCTGATGATCCCTAAT 1587
Qy 21 ThrGlyLeuSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrGluIle 40
Db 1588 ACAGGTATACGCTCTCATCCCCCAGATGCCATACCCGAGGAGAGATCTATGAGATC 1647
Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGluThrIleu 60
Db 1648 TACCTACGCTGCACAAAGCCGAGAGAGCTGAGGTGGCCCTAGCTGGCTGCAGACCCCTG 1707
Qy 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
Db 1708 CTGAGTCCCATCTGTAGCTGTGGACCCCTCGGCTGCTGCTCACCGGCCAGTCTATCTCTG 1767
Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
Db 1768 GCTATGGACCACTGTGGGGAGCCAGCCCTGACAGCTGAGCCTCGCCTCAAAAAGCAG 1827

Qy 101 SerCysGluGly 104
Db 1828 TCGTGCAGGGC 1839
RESULT 2
US-10-624-932-1
Sequence 1, Application US/10624932
Publication No. US20040096877A1
GENERAL INFORMATION:
APPLICANT: Taupier, Raymond
APPLICANT: Padigar, Muralidhara
APPLICANT: Rastelli, Luca
APPLICANT: Spaderna, Steven
APPLICANT: Shimkets, Richard
APPLICANT: Zerhusen, Bryan
APPLICANT: Spytek, Kimberly
APPLICANT: Shenoy, Suresh
APPLICANT: Li, Li
APPLICANT: Gusev, Vladimir
APPLICANT: Grosse, William
APPLICANT: Alsobrook, John
APPLICANT: Lepley, Denise
APPLICANT: Burgess, Catherine
APPLICANT: Gerlach, Valerie
APPLICANT: Ellerman, Karen
APPLICANT: MacDougall, John
APPLICANT: Stone, David
APPLICANT: Smithson, Glenda
TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-074 US
CURRENT APPLICATION NUMBER: US/10/624,932
CURRENT FILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: 09/918,779
PRIOR FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: 60/221,409
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/222,840
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: 60/223,752
PRIOR FILING DATE: 2000-08-08
PRIOR APPLICATION NUMBER: 60/223,762
PRIOR FILING DATE: 2000-08-08
PRIOR APPLICATION NUMBER: 60/223,770
PRIOR FILING DATE: 2000-08-08
PRIOR APPLICATION NUMBER: 60/223,769
PRIOR FILING DATE: 2000-08-08
PRIOR APPLICATION NUMBER: 60/225,146
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/225,392
PRIOR FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: 60/225,470
PRIOR FILING DATE: 2000-08-15
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 2752
TYPE: DNA
ORGANISM: Homo sapiens
US-10-624-932-1

Alignment Scores:
Pred. No.: 2,05e-66 Length: 2752
Score: 559.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-10-624-932c-2_COPY_495_598 (1-104) x US-10-624-932-1 (1-2752)

Qy 1 ThrSerAsnMetThrTyrGlyThrPheAsnPheLeuGlyArgLeuMetIleProAsn 20

```
Db 1528 ACCAGCAACATGACCTATGTGGACCTTCAACTTCTCGGGGGCCGGCTCATATCCCTAAT 1587
Qy 21 ThrGlyIleSerLeuLeuIleProAspAlaIleProArgGlyLysIleTyrGluIle 40
Db 1588 ACAGGTATCAGCTCTCTATCCCCCAGATGCCATACCCGAGGGAAGATCTATGAGATC 1647
Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 1648 TACCTCAGCTGCAACAGCCGAGACGTCGTAGGTTGCCCTAGCTGGCTGTGAGACCCCTG 1707
Qy 61 LeuSerProIleValSerCysGlyProGlyValLeuLeuThrArgProValIleLeu 80
Db 1708 CTGAGTCCCATCGTTAGCTGTGGACCCCTGGCGTCTGCTACCCGCGCCAGTCATCCTG 1767
Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
Db 1768 GCTATGGACCACTGTGGGAGCCAGCCCTGCACGCTGGAGCTGGCGCTCAAAAAGCAG 1827
Qy 101 SerCysGluGly 104
Db 1828 TCGTGGAGGGC 1839

RESULT 3
US-09-970-944-1
; Sequence 1, Application US/09970944
; Publication No. US20030204052A1
; GENERAL INFORMATION:
; APPLICANT: Herrman, John L
; APPLICANT: Rastelli, Luca
; APPLICANT: Shimkets, Richard A
; TITLE OF INVENTION: No. US20030204052A1el Proteins and Nucleic Acids Encoding Same an
; TITLE OF INVENTION: Antibodies Directed Against these Proteins
; FILE REFERENCE: 21402-138
; CURRENT APPLICATION NUMBER: US/09/970,944
; PRIOR FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 60/237,862
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2881
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-970-944-1

Alignment Scores:
Pred. No.: 2,186-66 Length: 2881
Score: 559.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-624-932C-2_COPY_495_598 (1-104) x US-09-970-944-1 (1-2881)
Qy 1 ThrSerAsnMetThrTyrGlyThrPheAsnPheLeuGlyArgLeuMetIleProAsn 20
Db 1569 ACCAGCAACATGACCTATGTGGACCTTCAACTTCTCGGGGGCCGGCTCATATCCCTAAT 1628
Qy 21 ThrGlyIleSerLeuLeuIleProAspAlaIleProArgGlyLysIleTyrGluIle 40
Db 1629 ACAGGTATCAGCTCTCTATCCCCCAGATGCCATACCCGAGGGAAGATCTATGAGATC 1688
Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 1689 TACCTCAGCTGCAACAGCCGAGACGTCGTAGGTTGCCCTAGCTGGCTGTGAGACCCCTG 1748
Qy 61 LeuSerProIleValSerCysGlyProGlyValLeuLeuThrArgProValIleLeu 80
Db 1749 CTGAGTCCCATCGTTAGCTGTGGACCCCTGGCGTCTGCTACCCGCGCCAGTCATCCTG 1808
Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
```

```
Db 1809 GCTATGGACCACTGTGGGGAGCCCGAGCCCTGCAGCTGGAGCTGCCTCAAAAAGCAG 1868
Qy 101 SerCysGluGly 104
Db 1869 TCGTGGAGGGC 1880

RESULT 4
US-10-643-795A-77
; Sequence 77, Application US/10643795A
; Publication No. US20040241703A1
; GENERAL INFORMATION:
; APPLICANT: FREDERIC J. DESAUVAGE
; APPLICANT: GRETCHEN FRANTZ
; APPLICANT: KENNETH J. HILLAN
; APPLICANT: PAUL POLAKIS
; APPLICANT: ANDREW POLSON
; APPLICANT: VICTORIA SMITH
; APPLICANT: SUSAN D. SPENCER
; APPLICANT: THOMAS D. WU
; APPLICANT: ZEMIN ZHANG
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5026R1-US
; CURRENT APPLICATION NUMBER: US/10/643,795A
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405,645
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/413,192
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: US 60/419,008
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/426,847
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/484,959
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 158
; SEQ ID NO 77
; LENGTH: 3561
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-643-795A-77

Alignment Scores:
Pred. No.: 2,866-66 Length: 3561
Score: 559.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 20 Gaps: 0

US-10-624-932C-2_COPY_495_598 (1-104) x US-10-643-795A-77 (1-3561)
Qy 1 ThrSerAsnMetThrTyrGlyThrPheAsnPheLeuGlyArgLeuMetIleProAsn 20
Db 1318 ACCAGCAACATGACCTATGTGGACCTTCAACTTCTCGGGGGCCGGCTCATATCCCTAAT 1377
Qy 21 ThrGlyIleSerLeuLeuIleProAspAlaIleProArgGlyLysIleTyrGluIle 40
Db 1378 ACAGGAATCAGCTCTCTATCCCTCCAGATGCCATACCCGAGGGAAGATCTATGAGATC 1437
Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 1438 TACCTCAGCTGCAACAGCCGAGACGTCGTAGGTTGCCCTAGCTGGCTGTGAGACCCCTG 1497
Qy 61 LeuSerProIleValSerCysGlyProGlyValLeuLeuThrArgProValIleLeu 80
Db 1498 CTGAGTCCCATCGTTAGCTGTGGACCCCTGGCGTCTGCTACCCGCGCCAGTCATCCTG 1557
Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
```

Db 1558 GCTATGGACCACTGTGGGGAGCCAGCCCTGACAGCTGGAGCCTCAAAAAGCAG 1617
Qy 101 SerCysGluGly 104
Db 1618 TCGTGGCAGGGC 1629
RESULT 5
US-10-948-518-77
; Sequence 77, Application US/10948518
; Publication No. US20050064492A1
; GENERAL INFORMATION:
; APPLICANT: FREDERIC J. DESAUVAGE
; APPLICANT: GRETCHEN FRANTZ
; APPLICANT: KENNETH J. HILLAN
; APPLICANT: PAUL POLAKIS
; APPLICANT: ANDREW POLSON
; APPLICANT: VICTORIA SMITH
; APPLICANT: SUSAN D. SPENCER
; APPLICANT: THOMAS D. WU
; APPLICANT: ZEMIN ZHANG
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITL OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5026R1-US
; CURRENT APPLICATION NUMBER: US/10/948,518
; CURRENT FILING DATE: 2004-09-22
; PRIOR APPLICATION NUMBER: US/10/643,795
; PRIOR FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405,645
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/413,192
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: US 60/419,008
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/426,847
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/484,959
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 158
; SEQ ID NO 77
; LENGTH: 3561
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-948-518-77
Alignment Scores:
Pred. No.: 2,86e-66 Length: 3561
Score: 559.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0
US-10-624-932C-2_COPY_495_598 (1-104) x US-10-948-518-77 (1-3561)
Qy 1 ThrSerAsnMetThrTyrglyThrPheAsnPheLeuGlyArgLeuMetIleProAsn 20
Db 1318 ACCAGCAACATGACCTATGGAGCCTTCAACTTCTCGGGGGCCGGCTGATGATCCCTAAT 1377
Qy 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrgluile 40
Db 1378 ACAGGAATCAGCTCTCTCATCCCCCAGATGCCATACCCGAGGGAAGATCTATGAGATC 1437
Qy 41 TyrlleuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrleu 60
Db 1438 TACCTCAGCTGCACAAGCCGGAAGACGTGAGGTGGCCCTAGCTGGCTGTGCAGACCTG 1497
Qy 61 LeuSerProIleValSerCysGlyProGlyValleuLeuThrArgProValIleleu 80
Db 1498 CTGAGTCCCATCGTAGCTGTGGACCCCTCGCTGCTACCCGGCCAGTCATCCTG 1557
Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100

Db 1558 GCTATGGACCACTGTGGGGAGCCAGCCCTGACAGCTGGAGCCTCAAAAAGCAG 1617
Qy 101 SerCysGluGly 104
Db 1618 TCGTGGCAGGGC 1629
RESULT 6
US-10-311-623-13
; Sequence 13, Application US/10311623
; Publication No. US20040023244A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; GRIFFIN, Jennifer A.
; APPLICANT: KALLICK, Deborah A.; TRIBOULEV, Catherine M.
; APPLICANT: YUE, Henry; NGUYEN, Danniell B.
; APPLICANT: TANG, Y. Tom; LAU, Preeti G.
; APPLICANT: POLICKY, Jennifer L.; AZIMZAI, Yalda
; APPLICANT: LU, Dyung Aina M.; GRAUL, Richard C.
; APPLICANT: YAO, Monique G.; BURFORD, Neil
; APPLICANT: HAPALIA, April J. A.; BAUGHN, Mariah R.
; APPLICANT: BANDMAN, Olga; ARVIZU, Chandra S.
; APPLICANT: YANG, Junming; XU, Yuming
; APPLICANT: GANDHI, Ameena R.; WARREN, Bridget A.
; APPLICANT: DING, Li; SANJANWALA, Madhusudan M.
; APPLICANT: DUGGAN, Brendan M.; LU, Yan
; TITLE OF INVENTION: RECEPTORS
; FILE REFERENCE: PE-0793 USN
; CURRENT APPLICATION NUMBER: US/10/311,623
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 01/19942
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/214,027
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: US 60/228,045
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/255,104
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PERL Program
; SEQ ID NO 13
; LENGTH: 3580
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040023244A1 6052371CB1
US-10-311-623-13
Alignment Scores:
Pred. No.: 2,88e-66 Length: 3580
Score: 559.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0
US-10-624-932C-2_COPY_495_598 (1-104) x US-10-311-623-13 (1-3580)
Qy 1 ThrSerAsnMetThrTyrglyThrPheAsnPheLeuGlyArgLeuMetIleProAsn 20
Db 1318 ACCAGCAACATGACCTATGGAGCCTTCAACTTCTCGGGGGCCGGCTGATGATCCCTAAT 1377
Qy 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrgluile 40
Db 1378 ACAGGAATCAGCTCTCTCATCCCCCAGATGCCATACCCGAGGGAAGATCTATGAGATC 1437
Qy 41 TyrlleuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrleu 60
Db 1438 TACCTCAGCTGCACAAGCCGGAAGACGTGAGGTGGCCCTAGCTGGCTGTGCAGACCTG 1497
Qy 61 LeuSerProIleValSerCysGlyProGlyValleuLeuThrArgProValIleleu 80
Db 1498 CTGAGTCCCATCGTAGCTGTGGACCCCTCGCTGCTACCCGGCCAGTCATCCTG 1557

```

Qy      81  AlawetAspHisCysGlyGluProSerProAspSerTrpSerIleuArgLeuLysLysGln 100
      |||
      |||
      |||
Db      1558  GCTATGACCACTGTGTGGGAGCCCGACGCTGGAGCTGGAGCTGCGCCTCAAAAGCAG 1617
      |||
      |||
      |||
Qy      101  SerCysGluGly 104
      |||
      |||
      |||
Db      1618  TCGTGGCGGGC 1629
      |||
      |||
      |||

RESULT 7
US-09-933-261-2
; Sequence 2, Application US/09933261
; Publication No. US20030040046A1
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
;             Leonardo, E. David
;             Hink, Lindsey
;             Masu, Masayuki
;             Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/933,261
; FILING DATE: 20-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/808,982
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1787 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-933-261-2

Alignment Scores:
Pred. No.:      7.93e-66      Length:      1787
Score:          553.00      Matches:      103
Percent Similarity: 99.04%      Conservative: 0
Best Local Similarity: 99.04%      Mismatches: 1
Query Match:      98.93%      Indels:      0
DB:              10      Gaps:      0

US-10-624-932C-2_COPY_495_598 (1-104) x US-09-933-261-2 (1-1787)

Qy      1  Thr-SerAsnMetThrTyrGlyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsn 20
      |||
      |||
      |||
Db      459  ACCAGCAGCATGACCTATGGAGCTTCACTTCTCGGGGGCGGCGGTGATGATCCCTAAT 518
      |||
      |||
      |||
Qy      21  ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrGluIle 40
      |||
      |||
      |||

```

Db	519	ACAGGAATCAGCTCTTCATATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATC	578
Qy	41	TyrLeuThrLrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu	60
Db	579	TACCTCAGCTGCACAAGCGCGGAAGACGTGAGGTGGCCCTAGCTGGCTGTGCAGACCCCTG	638
Qy	61	LeuSerProIleValSerCysGlyProProClyValLeuLeuLeuThrArgProValIleLeu	80
Db	639	CTGAGTCCCCATCGTTAGCTGTGGACCCCTCGCGCTCTGCCTACCCCGGCCAGTCAATCCCTG	698
Qy	81	AlaMetAspHisCysGlyGluProSerProAspSerTtpSerLeuArgLeuLysLysGln	100
Db	699	GCTATGACCACTGTGTGGAGCCCGACCCCTGACAGCTGGAGCCTGGCCCTCAAAAAGCAG	758
Qy	101	SerCysGluGly 104	
Db	759	TCGTGCGAGGGA 770	
RESULT 8			
US-10-256-702-2			
: Sequence 2, Application US/10256702			
: Publication No. US20030059859A1			
: GENERAL INFORMATION:			
: APPLICANT: Tessier-Lavigne, Marc			
: Leonardo, E. David			
: Hink, Lindsey			
: Masu, Masayuki			
: Kazuko, Keino-Masu			
: TITLE OF INVENTION: Netrin Receptors			
: NUMBER OF SEQUENCES: 8			
: CORRESPONDENCE ADDRESS:			
: ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP			
: STREET: 268 BUSH STREET, SUITE 3200			
: CITY: SAN FRANCISCO			
: STATE: CALIFORNIA			
: COUNTRY: USA			
: ZIP: 94104			
: COMPUTER READABLE FORM:			
: MEDIUM TYPE: Floppy disk			
: COMPUTER: IBM PC compatible			
: OPERATING SYSTEM: PC-DOS/MS-DOS			
: SOFTWARE: PatentIn Release #1.0, Version #1.30			
: CURRENT APPLICATION DATA:			
: APPLICATION NUMBER: US/10/256.702			
: FILING DATE: 27-Sep-2002			
: CLASSIFICATION: <Unknown>			
: PRIOR APPLICATION DATA:			
: APPLICATION NUMBER: US/09/933.261			
: FILING DATE: 20-Aug-2001			
: APPLICATION NUMBER: 08/808.982			
: FILING DATE: <Unknown>			
: ATTORNEY/AGENT INFORMATION:			
: NAME: OSMAN, RICHARD A			
: REGISTRATION NUMBER: 36,627			
: REFERENCE/DOCKET NUMBER: UC96-217			
: TELECOMMUNICATION INFORMATION:			
: TELEPHONE: (415) 343-4341			
: TELEFAX: (415) 343-4342			
: INFORMATION FOR SEQ ID NO: 2:			
: SEQUENCE CHARACTERISTICS:			
: LENGTH: 1787 base pairs			
: TYPE: nucleic acid			
: STRANDEDNESS: double			
: TOPOLOGY: linear			
: MOLECULE TYPE: cDNA			
: SEQUENCE DESCRIPTION: SEQ ID NO: 2:			
US-10-256-702-2			
Alignment Scores:			
Pred. No.:		7.93e-66	Length: 1787
Score:		553.00	Matches: 103
Percent Similarity:		99.04%	Conservative: 0
Best Local Similarity:		99.04%	Mismatches: 1

```
Query Match: 98.93% Indels: 0
DB: 14 Gaps: 0

US-10-624-932C-2_COPY_495_598 (1-104) x US-10-256-702-2 (1-1787)

Qy 1 ThrSerAenMetThrTyrGlyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsn 20
Db 459 ACCAGCAACATGACTATGGACCTTCACTTCTCGGGGCGCGCTGATGATCCCTAAT 518
Qy 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrGluIle 40
Db 519 ACAGGAATCAGCTCCTCATCCGCCAGATGCCATACCCCGAGGGAAGATCTATGAGATC 578
Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 579 TACCTCAGCTGCAAGCCGAGAGAGCTGAGGTGGCCCTAGCTGGCTGTCAGACCCCTG 638
Qy 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
Db 639 CTGAGTCCCATCGTTAGCTGTGGACCCCTGGCGTCTGCTCACCCGCGCAGTCATCTG 698
Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
Db 699 GCTATGGACCACTGTGGGAGCCAGCCCTGACAGCTGGAGCTGGCCCTCAAAAAGCAG 758
Qy 101 SerCysGluGly 104
Db 759 TCGTGGCGAGGGA 770

RESULT 9
US-10-154-15
; Sequence 15, Application US/10240154
; Publication No. US20030175741A1
; GENERAL INFORMATION:
; APPLICANT: Cochran et al.
; TITLE OF INVENTION: SCHIZOPHRENIA RELATED GENES
; FILE REFERENCE: CRFW-P01-006
; CURRENT APPLICATION NUMBER: US/10/240.154
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: PCT/GB01/01486
; PRIOR FILING DATE: 2001-04-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 2697
; TYPE: DNA
; ORGANISM: Rattus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2697)
US-10-240-154-15
Alignment Scores:
Pred. No.: 1.35e-65 Length: 2697
Score: 553.00 Matches: 102
Percent Similarity: 99.04% Conservative: 1
Best Local Similarity: 98.08% Mismatches: 1
Query Match: 98.93% Indels: 0
DB: 16 Gaps: 0

US-10-624-932C-2_COPY_495_598 (1-104) x US-10-240-154-15 (1-2697)

Qy 1 ThrSerAenMetThrTyrGlyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsn 20
Db 1483 ACCAGCAACATGCGCTACGGACCTTCACTTCTCGGGGCGCGCTGATGATCCCTAAT 1542
Qy 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrGluIle 40
Db 1543 ACGGGGATCAGCTCCTCATACCCCGGATGCCATCCCGAGGGAAGATCTACGAGATC 1602
Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 1603 TACCTCAGCTGCAAGCCGAGAGAGCTGAGGTGGCCCTAGCTGGCTGTCAGACCCCTG 1662

Qy 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
Db 1663 CTGAGTCCCATCGTTAGCTGTGGGCGCCCGCAGGAGTCTGTGCTCACCCGCGCAGTCATCTT 1722
Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
Db 1723 GCATGAGCACCTGTGAGAGAGCCGCTGACAGCTGGAGTCTGGCGCTCAAAAAGCAG 1782
Qy 101 SerCysGluGly 104
Db 1783 TCCTGCGAGGCG 1794

RESULT 10
US-09-933-261-1
; Sequence 1, Application US/09933261
; Publication No. US20030040046A1
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindsay
; Masu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/933.261
; FILING DATE: 20-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/808,982
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3014 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-933-261-1
Alignment Scores:
Pred. No.: 1.56e-65 Length: 3014
Score: 553.00 Matches: 102
Percent Similarity: 99.04% Conservative: 1
Best Local Similarity: 98.08% Mismatches: 1
Query Match: 98.93% Indels: 0
DB: 10 Gaps: 0

US-10-624-932C-2_COPY_495_598 (1-104) x US-09-933-261-1 (1-3014)

Qy 1 ThrSerAenMetThrTyrGlyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsn 20
Db 1783 TCCTGCGAGGCG 1794
```

Db 1483 ACCAGCAATGCGCTACGGGACCTTCAACTTCTCGGGGGCCGCTGATGATCCCTAAT 1542
Qy 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrGluIle 40
Db 1543 ACGGGGATCAGCTCTCTATACCCCGGATGCCATCCCGGAGGAAAGATCTACGAGATC 1602
Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 1603 TACCTCACACTGCACAGCCAGACGTCGAGTTGCCCTAGCTGGCTGTACAGACCCGTG 1662
Qy 61 LeuSerProIleValSerCysGlyProProGlyValLeuThrArgProValIleLeu 80
Db 1663 CTGAGTCAGTCGTTAGCTGTGGGCCCCCAGAGTCTGCTCACC CGGCGCAGTCATCCTT 1722
Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
Db 1723 GCAATGGACCACTGTGGAGAGCCAGCCCTGCACAGCTGGAGTCTCGGCTCAAAAAGCAG 1782
Qy 101 SerCysGluGly 104
Db 1783 TCCTGCGAGGCG 1794

RESULT 11

US-10-256-702-1
; Sequence 1, Application US/10256702
; Publication No. US20030059859A1
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindsey
; Masu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10256,702
; FILING DATE: 27-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/933,261
; FILING DATE: 20-Aug-2001
; APPLICATION NUMBER: 08/808,982
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3014 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-256-702-1

Alignment Scores:

Pred. No.: 1,56e-65 Length: 3014
Score: 553.00 Matches: 102
Percent Similarity: 99.04% Conservative: 1
Best Local Similarity: 98.08% Mismatches: 1
Query Match: 98.93% Indels: 0
DB: 14 Gaps: 0
US-10-624-932C-2_COPY_495_598 (1-104) x US-10-256-702-1 (1-3014)
Qy 1 ThrSerAsnMetThrTyrGlyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsn 20
Db 1483 ACCAGCAATGCGCTACGGGACCTTCAACTTCTCGGGGGCCGCTGATGATCCCTAAT 1542
Qy 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrGluIle 40
Db 1543 ACGGGGATCAGCTCTCTATACCCCGGATGCCATCCCGGAGGAAAGATCTACGAGATC 1602
Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 1603 TACCTCACACTGCACAGCCAGACGTCGAGTTGCCCTAGCTGGCTGTACAGACCCGTG 1662
Qy 61 LeuSerProIleValSerCysGlyProProGlyValLeuThrArgProValIleLeu 80
Db 1663 CTGAGTCAGTCGTTAGCTGTGGGCCCCCAGAGTCTGCTCACC CGGCGCAGTCATCCTT 1722
Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
Db 1723 GCAATGGACCACTGTGGAGAGCCAGCCCTGCACAGCTGGAGTCTCGGCTCAAAAAGCAG 1782
Qy 101 SerCysGluGly 104
Db 1783 TCCTGCGAGGCG 1794
RESULT 12
US-10-296-115-365
; Sequence 365, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296,115
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 365
; LENGTH: 1321
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-296-115-365
Alignment Scores:
Pred. No.: 4,5e-59 Length: 1321
Score: 503.00 Matches: 103
Percent Similarity: 95.37% Conservative: 0
Best Local Similarity: 95.37% Mismatches: 1
Query Match: 89.98% Indels: 4
DB: 18 Gaps: 0
US-10-624-932C-2_COPY_495_598 (1-104) x US-10-296-115-365 (1-1321)
Qy 1 ThrSerAsnMetThrTyrGlyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsn 20
Db 94 ACCAGCAATGCGCTACGGGACCTTCAACTTCTCGGGGGCCGCTGATGATCCCTAAT 153
Qy 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrGluIle 40
Db 154 ACAGGAATCAGCTCTCTATACCCCGCAGATGCCATACCCCGAGGAAAGATCTATGAGATC 213
Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60

```
|||||
Db 214 TACCTCAGCTGCACAGCGGAGAGAGCTGAGGTTGCCCTAGCTGTCAGACCTGTG 273
|||
Qy 61 LeuSerProIleValSerCysGlyProPro-GlyValLeuLeuThrArgProValIleLe 80
|||
Db 274 CTGAGTCCCATCGTTAGCTGTGGACCCCTCGGCGTCTCTGCTTACCGCGCAGTCACTCT 333
|||
Qy 80 u-AlaMetAspHisCys-GlyGluProSerProAspSerTrp-SerLeuArgLeuLeuLy 99
|||
Db 334 GGGGTATGGACCACTGTGGGGAGCCAGCCCTCACAGCTGGGAGCCTGCCTCAAAA 393
|||
Qy 99 sGlnSerCysGluGly 104
|||
Db 394 GCAGTCTGTCGAGSGC 409
|||
RESULT 13
US-09-764-861-62/c
; Sequence 62, Application US/09764861
; Publication No. US20020086811A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT204
; CURRENT APPLICATION NUMBER: US/09/764,861
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
; LENGTH: 9582
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-861-62
Alignment Scores:
Pred. No.: 8.61e-43 Length: 9582
Score: 393.50 Matches: 83
Percent Similarity: 49.40% Conservative: 0
Best Local Similarity: 49.40% Mismatches: 0
Query Match: 70.39% Indels: 85
DB: 9 Gaps: 1
US-10-624-932C-2_COPY_495_598 (1-104) x US-09-764-861-62 (1-9582)
Qy 22 GlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyGluIleTy 41
Db 3709 GGAATCAGCTCTCTCATCCCCCAGATGCCATACCCCGAGGAGAGATCTATGAGATCTAC 3650
Qy 42 LeuThrLeuHisLysProGluAspVal----- 50
Db 3649 CTCACGCTGCACAGCGGAGAGACGTGAGGTGTGGCCGCGGCGCTGTTCGGGGGTGG 3590
Qy 50 ----- 50
Db 3589 GAGGACCTGCTGCTGCTTCCGTTCCAGGAAGCCCTGCCCCAGCTGTTGTGCC 3530
Qy 50 ----- 50
Db 3529 TGGCCCGAGCGCGGGGAGAAAGAGCTGTGCCTAAGCCCCACGTTGCTTCGACGCCAAG 3470
Qy 50 ----- 50
Db 3469 CCCCTGGCCCCCTGGATGCTGCTGCCCTTGGCTAGCCCTCAGAGCCAGGATGG 3410
Qy 51 -----ArgLeuProLeuAlaGly 56
Db 3409 GCCACTGACACCTTTCCCTCCCAACCCATATTTCCCACTTGGAGTTGCCCTAGCTGCG 3350
Qy 57 CysGlnThrLeuLeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArg 76
Db 3349 TGTACAGCCCTGCTGAGTCCCATCTGAGTGTGAGACCCCTCGGCTCTCTCACCCGG 3290
Qy 77 ProValIleLeuAlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArg 96
Db 3289 CCAGTCACTCTGGCTATGGACCACTGTGGGGAGCCAGCCCTGACAGCTGGAGCTGCGC 3230
Qy 97 LeuLysLysGlnSerCysGluGly 104
Db 3229 CTCAAAAGCAGTCTGTCGAGGGC 3206
|||
RESULT 15
```

```
|||||
Db 3289 CCAGTCACTCTGGCTATGGACCACTGTGGGGAGCCAGCCCTGACAGCTGGAGCTGCGC 3230
|||
Qy 97 LeuLysLysGlnSerCysGluGly 104
|||
Db 3229 CTCAAAAGCAGTCTGTCGAGGGC 3206
|||
RESULT 14
US-09-764-861-62/c
; Sequence 62, Application US/09764861
; Publication No. US20030171252A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT204
; CURRENT APPLICATION NUMBER: US/09/764,861
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
; LENGTH: 9582
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-861-62
Alignment Scores:
Pred. No.: 8.61e-43 Length: 9582
Score: 393.50 Matches: 83
Percent Similarity: 49.40% Conservative: 0
Best Local Similarity: 49.40% Mismatches: 0
Query Match: 70.39% Indels: 85
DB: 10 Gaps: 1
US-10-624-932C-2_COPY_495_598 (1-104) x US-09-764-861-62 (1-9582)
Qy 22 GlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyGluIleTy 41
Db 3709 GGAATCAGCTCTCTCATCCCCCAGATGCCATACCCCGAGGAGAGATCTATGAGATCTAC 3650
Qy 42 LeuThrLeuHisLysProGluAspVal----- 50
Db 3649 CTCACGCTGCACAGCGGAGAGACGTGAGGTGTGGCCGCGGCGCTGTTCGGGGGTGG 3590
Qy 50 ----- 50
Db 3589 GAGGACCTGCTGCTGCTGCTTCCGTTCCAGGAAGCCCTGCCCCAGCTGTTGTGCC 3530
Qy 50 ----- 50
Db 3529 TGGCCCGAGCGCGGGGAGAAAGAGCTGTGCCTAAGCCCCACGTTGCTTCGACGCCAAG 3470
Qy 50 ----- 50
Db 3469 CCCCTGGCCCCCTGGATGCTGCTGCCCTTGGCTAGCCCTCAGAGCCAGGATGG 3410
Qy 51 -----ArgLeuProLeuAlaGly 56
Db 3409 GCCACTGACACCTTTCCCTCCCAACCCATATTTCCCACTTGGAGTTGCCCTAGCTGCG 3350
Qy 57 CysGlnThrLeuLeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArg 76
Db 3349 TGTACAGCCCTGCTGAGTCCCATCTGAGTGTGAGACCCCTCGGCTCTCTCACCCGG 3290
Qy 77 ProValIleLeuAlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArg 96
Db 3289 CCAGTCACTCTGGCTATGGACCACTGTGGGGAGCCAGCCCTGACAGCTGGAGCTGCGC 3230
Qy 97 LeuLysLysGlnSerCysGluGly 104
Db 3229 CTCAAAAGCAGTCTGTCGAGGGC 3206
|||
RESULT 15
```


US-10-115-928-62/c
; Sequence 62, Application US/10115928
; Publication No. US20030092615A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT204CI
; CURRENT APPLICATION NUMBER: US/10/115,928
; CURRENT FILING DATE: 2002-04-05
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
; LENGTH: 9582
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-115-928-62

Alignment Scores:
Pred. No.: 8,61e-43 Length: 9582
Score: 393.50 Matches: 83
Percent Similarity: 49.40% Conservative: 0
Best Local Similarity: 49.40% Mismatches: 0
Query Match: 70.39% Indels: 85
DB: 14 Gaps: 1

US-10-624-932C-2_COPY_495_598 (1-104) x US-10-115-928-62 (1-9582)

Qy	22	GlyLeuSerLeuLeuLeuProProAlaIleProArgGlyLysIleTyrCluileTyr	41
Db	3709	GGAATCAGCCCTCTCATCCCCCAGATACCCCGAGGAGATCTATGAGATCTAC	3650
Qy	42	LeuThrLeuHisLysProGluAspVal	50
Db	3649	CTCAGCTGCACAAACCGAGACCTGAGTGTGCGCGGGCCCTGTTCGGGGGTGG	3590
Qy	50	-----	50
Db	3589	GAGGACCTGCTGCTGCTTGGTCCCGAGGAGCCCTGCCCCACCACTGTTGTGCC	3530
Qy	50	-----	50
Db	3529	TGGCCCGAGCGCGCGGGGAAAGAGCTGTGCTAAGCCCCACAGTGTCTGAGCCCAAG	3470
Qy	50	-----	50
Db	3469	CCCCCTGGCCCTGGGATGCTGCTGCCCTGGCCCTAGCCCTCAGGACCCAGGATGG	3410
Qy	51	-----ArgLeuProLeuAlaGly	56
Db	3409	GCCACTGACACCTTTCCCTCCGCCACCCATATTTCCCCACTTGAGGTTGCCCTAGCTGGC	3350
Qy	57	CysGlnThrLeuLeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArg	76
Db	3349	TGTACAGCCCTGCTGAGTCCCATCTAGCTGTGAGCCCTTGGCGTCTGCTACCCGG	3290
Qy	77	ProValIleLeuAlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArg	96
Db	3289	CCAGTCATCTGCTATGACCACTGTGGGAGCCAGCCCTGACAGCTGGAGCTGGCC	3230
Qy	97	LeuLysLysGlnSerCysGluGly	104
Db	3229	CTCAAAAAGCAGTCGTGCGAGGGC	3206

Search completed: September 9, 2005, 18:52:38
Job time : 1049.83 secs

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 8, 2005, 22:38:37 ; Search time 3422.83 Seconds
(without alignments)
1156.553 Million cell updates/sec

Title: US-10-624-932C-2_COPY_495_598

Perfect score: 559

Sequence: 1 TSNMTYGTFTNPLGRLMPN.....CCEPSPDSWSRLKKQSCG 104

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters: -DEV=xlh
-MODEL=frame+ p2n.model
-O=/cgn2.1/USPTO spool h/US10624932/runat_08092005_161706_15792/app_query.fasta_1.1386
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCLALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10624932 @CGN 1 1 8180 @runat_08092005_161706_15792 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_ges1:*
9: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	559	100.0	788	1	AI951556
2	548	98.0	678	6	CAV49784
3	515	92.1	399	7	H43716
4	502	89.8	756	5	BU612387
5	464	83.0	859	2	BF311896
6	460	82.3	382	7	R89529
7	397.5	71.1	934	2	BF311804
8	374	66.9	604	2	BE314370
9	354.5	63.4	815	7	CK140529

10	348	62.3	506	7	CF173478
11	348	62.3	2791	9	AY406493
12	348	62.3	3790	3	AK031655
13	337	60.3	329	1	AL119797
14	337	60.3	2802	9	AY406491
15	324	58.0	2802	9	AY406492
16	315	56.4	323	5	BQ339379
17	309	55.3	842	5	BX744794
18	303	54.2	731	1	AJ729964
19	302	54.0	874	5	BQ689148
20	302	54.0	889	5	BQ691915
21	295	52.8	1147	5	BU840446
22	287	51.3	432	5	BQ339228
23	287	51.3	481	2	BF775467
24	287	51.3	537	2	BF073665
25	287	51.3	745	7	CK835492
26	287	51.3	770	1	AU127790
27	287	51.3	986	5	BQ709159
28	287	51.3	2532	9	AY411747
29	281	50.3	798	6	CB592227
30	277	49.6	810	6	CA511645
31	274	49.0	673	5	BU611727
32	274	49.0	816	7	CN527193
33	274	49.0	2532	9	AY411749
34	274	49.0	3866	3	AK018177
35	269	48.1	348	4	BF950493
36	268	47.9	524	2	AW654577
37	252	45.1	352	7	CN219416
38	221	39.5	2532	9	AY411748
39	220	39.4	343	4	BF946952
40	212	37.9	860	2	BF312306
41	207	37.0	939	4	BG331653
42	195.5	35.0	990	5	BQ707104
43	193	34.5	735	7	CN441440
44	192	34.3	464	2	AW629051
45	192	34.3	537	5	EX094642

ALIGNMENTS

RESULT 1

AI951556

LOCUS

DEFINITION

AI951556

wv36f04.x1 NCI CGAP Ov18 Homo sapiens cDNA clone IMAGE:2531647 3',

similar to TR:O08721 O08721 TRANSMEMBRANE RECEPTOR UNC5H1. ;, mRNA

sequence.

AI951556

AI951556.1 GI:5743866

EST.

EST.

Homo sapiens

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 788)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: M. Bento

Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The

I.M.A.G.E. Consortium DNA Sequencing by: Washington University

Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 1125 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 446.

Location/Qualifiers

1. .788

FEATURES

source

```
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2531647"
/tissue_type="fibrotheoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NCI_CGAP_Ov18"
/notes="Organ: ovary; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; let strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTCGGAGCGCGCGACATTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."
```

ORIGIN

```
Alignment Scores:
Pred. No.:      2.57e-50      Length:      788
Score:          559.00      Matches:    104
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:     100.00%      Indels:    0
DB:              1          Gaps:      0
```

US-10-624-932C-2_COPY_495_598 (1-104) x AT951556 (1-788)

```
Qy 1 ThrSerAsnMetThrTyrGlyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsn 20
Db 60 ACCAGCAATGACCTCTCATCCCCCAGATGCATACCCGAGGGAAGATCTATGAGATC 179
Qy 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrGluIle 40
Db 120 ACAGGAATCAGCCTCTCATCCCCCAGATGCATACCCGAGGGAAGATCTATGAGATC 179
Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 180 TACCTTCACGCTGCACAAACCGGAGACGTGAGTTGGCCCTAGCTGGCTGTGCAGACCTG 239
Qy 61 LeuSerProIleValSerCysGlyProGlyValLeuLeuThrArgProValIleLeu 80
Db 240 CTGAGTCCCATCGTTAGCTGTGGACCCCTCGCGTTCTGCTACCCGCGCATCTCTG 299
Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
Db 300 GCTATGAGCACTGTGGGAGCCAGCCCTGACAGCTGGAGCTGCGCTCAAAAAGCAG 359
Qy 101 SerCysGluGly 104
Db 360 TCGTGGAGGGG 371
```

```
RESULT 2
CA749784
LOCUS
DEFINITION
UI-M-FD0-cdg-c-11-0-UI-r1 NIH_BMAP_F00 Mus musculus cDNA clone
IMAGE:6828324 5', mRNA sequence.
CA749784
VERSION
CA749784.1 GI:25572600
EST.
SOURCE
Mus musculus (house mouse)
```

ORGANISM

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 678)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cga9bs-romail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
```

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

Seq primer: pYX-5.
Location/Qualifiers

FEATURES
source

```
1..678
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:6828324"
/tissue_type="whole brain"
/dev_stage="embryo 12.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_F00"
/notes="Organ: brain; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; the library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is TGAGAGAGCC. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
```

ORIGIN

```
Alignment Scores:
Pred. No.:      3.34e-49      Length:      678
Score:          548.00      Matches:    102
Percent Similarity: 98.08%      Conservative: 0
Best Local Similarity: 98.08%      Mismatches: 2
Query Match:     98.03%      Indels:    0
DB:              6          Gaps:      0
```

US-10-624-932C-2_COPY_495_598 (1-104) x CA749784 (1-678)

```
Qy 1 ThrSerAsnMetThrTyrGlyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsn 20
Db 226 ACCAGCAATGACCTCTCATCCCCCAGATGCATACCCGAGGGAAGATCTATGAGATC 285
Qy 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrGluIle 40
Db 286 ACAGGAATCAGCCTCTCATCCCCCAGATGCATACCCGAGGGAAGATCTATGAGATC 345
Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 346 TACCTTCACCTGTGCACAAACCGGAGACGTGAGTTGGCCCTAGCTGGCTGTGCAGACCTG 405
Qy 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
Db 406 CTGAGTCTCTATCGTTAGCTGTGGCCCGCAGGAGTCTCTGCTACCCGCGCATCTCTCT 465
Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
Db 466 GCCATGAGCACTGTGGGAGCCAGCCAGTCCCGACAGCTGGAGCCTGCGCCTCAAAAAGCAG 525
Qy 101 SerCysGluGly 104
Db 526 TCGTGTGAGGG 537
```

RESULT 3

```
H43716
LOCUS
DEFINITION
yo80g05.s1 Soares adult brain N2b4HB55y Homo sapiens cDNA clone
399 bp mRNA linear EST 31-JUL-1995
```

IMAGE:184280 3', mRNA sequence.	Db	44	ACGAGCAACATGACCTATGGGACCTTCAACTTCTCGGGGGCCGGCTGATGATCCCTAAT	103
CESSION	Qy	21	ThrGlylleSerLeuLeuileProProAspAlalleProArgGlylyseleYrGlulle	40
VERSION	Db	104	ACAGGAATCAGCCTCTCATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATC	163
WORDS	Qy	41	TyrLeuThrLeuHisLysProGluAspValargLeuProLeuAlaGlyCysGlnThrLeu	60
ORGANISM	Db	164	TACCTCAGCAGTGCACAGCCGAGACGCTGAGGTGTGCCCTAGCTGGCTGTGAGACCCCTG	223
REFERENCE	Qy	61	LeuSerProilleValSerCysGlyProPro-GlyValLeuLeuThrArgProValillele	80
AUTHORS	Db	224	CTGAGTCCCATCGTTAGCTGTGGACCCCTCTGGGCGCTCTCTCACCGGCCAGTCATCCT	283
TITLE	Qy	80	u-AlaMetAspHisCysGlyGluProSerProAspSerTrp-SerLeuArgLeuLys	99
JOURNAL	Db	284	GGGCTATGGACACACTGTGGGGAGCCAGCCCTGACAGCTGGGAGCTCGCCCTCAAAAG	343
COMMENT	Qy	100	GlnSerCysGluGly	104
	Db	344	CAGTCGTCGGAGGCGN	358
	RESULT 4			
	BU612387			
	LOCUS			
	DEFINITION			
	ACCESSION			
	VERSION			
	KEYWORDS			
	SOURCE			
	ORGANISM			
	REFERENCE			
	AUTHORS			
	TITLE			
	COMMENT			

normalization to a Cot = 53. Library constructed by Bento Soares and M. Fatima Bonaldo. The adult brain RNA was provided by Dr. Donald H. Gilden. Tissue was acquired 17-18 hours after death which occurred in consequence of a ruptured aortic aneurysm. RNA was prepared from a pool of tissues representing the following areas of the brain: frontal, parietal, temporal and occipital cortex from the left and right hemispheres, subcortical white matter, basal ganglia, thalamus, cerebellum, midbrain, pons and medulla."

ALIGNMENT

Alignment Scores:			
Seq. No.:	6,67e-46	Length:	399
Score:	515.00	Matches:	103
Percent Similarity:	96.26%	Conservative:	0
Local Similarity:	96.26%	Mismatches:	1
Indels:	92.13%	Indels:	3
Match:	7	Gaps:	0

1 ThrSerAsnMetThrTyrGlyThrPheAnPheLeuGlyVGLYargLeuMetIleProAsn 20

(BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Alignment Scores:
 Pred. No.: 3,78e-44 Length: 756
 Score: 502.00 Matches: 94
 Percent Similarity: 97.92% Conservative: 0
 Best Local Similarity: 97.92% Mismatches: 2
 Query Match: 89.80% Indels: 0
 DB: 5 Gaps: 0

US-10-624-932C-2_COPY_495_598 (1-104) x BU612387 (1-756)

Qy 1 ThrSerAnMetThrTyTGlyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsn 20
 Db 467 ACCAGCAATGGCGCTATGGACCTTCAACTTCCTCGGGGGCGGCTGATGATCCCTAAC 526
 Qy 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyGluIle 40
 Db 527 ACAGGAATCAGCTCTCTCATCCCGCGACGCCATCCCCCGAGGAAGATCTACGAGATC 586
 Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrIleu 60
 Db 587 TACCTCACTGCAACAGCAAGACGTGAGGTGCCCCCTAGCTGGCTGTGACACCCCTG 646
 Qy 61 LeuSerProfileValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
 Db 647 CTGAGTCTATCGTTAGCTGTGGGCCCCCAGGAGTCTCTGCTCACCGGCCAGTCTCTT 706
 Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArg 96
 Db 707 GCCATGGACCACTCGGGGAGCCCGAGTCNCACAGCTGGAGCCTGCGC 754

RESULT 5
 BF3111896
 LOCUS BF3111896 859 bp mRNA linear EST 21-NOV-2000
 DEFINITION 601897733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126760 5', mRNA sequence.

ACCESSION BF3111896

VERSION BF3111896

KEYWORDS EST

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC <http://mhc.nci.nih.gov/>

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: L10M1017 row: b column: 09

High quality sequence stop: 684.

Location/Qualifiers

FEATURES

source

1..859 /organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4126760"

/tissue_type="neuroblastoma"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_19"

/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:

EcoRI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
 Pred. No.: 5,93e-40 Length: 859
 Score: 464.00 Matches: 95
 Percent Similarity: 92.38% Conservative: 2
 Best Local Similarity: 90.48% Mismatches: 7
 Query Match: 83.01% Indels: 2
 DB: 2 Gaps: 0

US-10-624-932C-2_COPY_495_598 (1-104) x BF311896 (1-859)

Qy 1 ThrSerAnMetThrTyTGlyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsn 20
 Db 412 ACCAGCAATGACCTATGGACCTTCACTTCCTCGGGGGCGGCTGATGATCCCTAAT 471
 Qy 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyGluIle 40
 Db 472 ACAGGAATCAGCTCTCTCATCCCGCGACGCCATCCCCGAGGAAGATCTATGAGATC 531
 Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrIleu 60
 Db 532 TACCTCACTGCAACAGCAAGACGTGAGGTGCCCCCTAGCTGGCTGTGACACCCCTG 591
 Qy 61 LeuSerProfileValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
 Db 592 CTGAGTCCCATCGTTAGCTGTGGACCCCTCGGCTGCTGCTCACCGGCCAGTCTCTG 651
 Qy 81 AlaMet-AspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGly 100
 Db 652 GCTATGGGACCACTGTGCGGGAGCCAGCTGACAGCTTGGAGCCTGGC-CTCAAAAAGCA 710
 Qy 100 nSerCysGluGly 104
 Db 711 GCGGTGCTAAGGG 723

RESULT 6

R89529

LOCUS

DEFINITION

Ym97d12.s1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone

IMAGE:166871 3', mRNA sequence.

R89529

ACCESSION

VERSION

R89529.1 GI:954356

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1995)

Contact: Wilton RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Insert Size: 1642

High quality sequence stops: 298

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Possible reversed clone: polyT not found

Insert Length: 1642 Std Error: 0.00

Seq primer: Promega -21m13
High quality sequence stop: 298.

FEATURES

Location/Qualifiers
1..382
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:587566"
/db_xref="taxon:9606"
/clone="IMAGE:166871"
/sex="Male"
/dev_stage="55-year old"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares adult brain N2B4HB55Y"
/note="Organ: brain; Vector: p7T3D (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAGTGGAGCGCGCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified p7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 53. Library constructed by Bento Soares and M. Fatima Bonaldo. The adult brain RNA was provided by Dr. Donald H. Gilden. Tissue was acquired 17-18 hours after death which occurred in consequence of a ruptured aortic aneurysm. RNA was prepared from a pool of tissues representing the following areas of the brain: frontal, parietal, temporal and occipital cortex from the left and right hemispheres, subcortical white matter, basal ganglia, thalamus, cerebellum, midbrain, pons and medulla."

ORIGIN

Alignment Scores:
Pred. No.: 5,958-40 Length: 382
Score: 460.00 Matches: 92
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 82.29% Indels: 3
DB: 7 Gaps: 0

US-10-624-932c-2_COPY_495_598 (1-104) x R89529 (1-382)

Qy 1 ThrSerAsnMetThrTyrGlyThrPheAsnPhLeuGlyGlyArgLeuMetileProAsn 20
Db 98 ACCAGCAACATGACCTATGGGACCTTCACTTCTCGGGGGCGGCTGATGATCCCTAAT 157
Qy 21 ThrGlyIleSerLeuLeuLeuProProAspAlaIleProArgGlyIleTyrGluile 40
Db 158 ACAGGAATCAGCTCTCTATCCCGCCAGATGCCATACCCCGAGGGAAGATCTATGAGATC 217
Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 218 TACCTCAGCTGCACACGCGGAGACGTGAGTTGCCCTAGCTGGCTGTCAGACCCCTG 277
Qy 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValileLe 80
Db 278 CTGAGTCCCATCGTTAGCTGTGGACCCCTCGGGCGCTCTGCTTACCGGCCAGTCATCCT 337
Qy 80 u-AlaMetAspHisCys-GlyGluProSerProAspSerTtp 93
Db 338 GGGGTATGAGCACTGTGGGGAGCCAGCCCTGACAGCTGG 379

RESULT 7
BF311804
LOCUS BF311804 934 bp mRNA linear EST 21-NOV-2000
DEFINITION 601897316F1 NTH_MGC_19 Homo sapiens cDNA clone IMAGE:4126706 5', mRNA sequence.
ACCESSION BF311804
VERSION BF311804.1 GI:11259566
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
1. (bases 1 to 934)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCW1016 row: p column: 03
High quality sequence stop: 707.

FEATURES

Location/Qualifiers
1..934
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4126706"
/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_19"
/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
Pred. No.: 1,1e-32 Length: 934
Score: 397.50 Matches: 89
Percent Similarity: 85.71% Conservative: 1
Best Local Similarity: 84.76% Mismatches: 14
Query Match: 71.11% Indels: 4
DB: 2 Gaps: 1

US-10-624-932c-2_COPY_495_598 (1-104) x BF311804 (1-934)

Qy 1 ThrSerAsnMetThrTyrGlyThrPheAsnPhLeuGlyGlyArgLeuMetileProAsn 20
Db 414 ACCAGCAACATGACCTATGGGACCTTCACTTCTCGGGGGCGGCTGATGATCCCTAAT 473
Qy 21 ThrGlyIleSerLeuLeuLeuProProAspAlaIleProArgGlyIleTyrGluile 40
Db 474 ACAGGAATCAG-CTCCTCATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATC 532
Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 533 TACCTCAGCTGCACACGCGGAGACGTGAGTTGCCCTA-GCTGGCTGTGACACCCCTG 591
Qy 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValileLeu 80
Db 592 CTGAGTCCCATCGTTAGCTGTGGACCCCTCGGGCGCTCTGCTTACCGGCCAGTCATCCT 651
Qy 81 Ala---MetAspHisCysGlyGluProSerProAspSerTtpSerLeuArgLeuLys 99
Db 652 GGCTAATGGACCCACTGTGGGGAAGC-CAGCCTGACAGCTTGAGCCTGGGCTCAAAAAGG 710
Qy 100 GlnSerCysGluGly 104
Db 711 AGTCGGTCGAGGGC 725

RESULT 8

BE314370
LOCUS BE314370 604 bp mRNA linear EST 26-OCT-2000
DEFINITION 601147261F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3162710 5',

```

mRNA sequence.
ACCESSION BE314370
VERSION BE314370.1 GI:9135413
KEYWORDS EST.
SOURCE EST.
ORGANISM Homo sapiens (human)
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: L10M122 row: i column: 15
High quality sequence stop: 601.
FEATURES
Location/Qualifiers
source
1. .604
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3162710"
/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 19"
/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dr priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
ORIGIN
Alignment Scores:
Pred. No.: 2.29e-30 Length: 604
Score: 374.00 Matches: 70
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 66.91% Indels: 0
DB: 2 Gaps: 0
US-10-624-932C-2_COPY_495_598 (1-104) x BE314370 (1-604)
Qy 1 ThrSerAsnMetThrTyrGlyThrPheAsnPheLeuGlyArgLeuMetIleProAsn 20
Db 395 ACCAGCAACATGACCATATGGACCTTCAACTTCTCGGGGCGCGCTGATGATCCCTAAT 454
Qy 21 ThrGlyIleSerLeuLeuLeuProAspAlaIleProArgGlyLeuIleTyrGluIle 40
Db 455 ACAGGAATCAGCCTCTCATCCCCCAGATGCCATACCAGGAGGAGATCTATGAGATC 514
Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 515 TACCTCAGCTGCACACCGAGAGCTGAGGTTCCTAGCTGCTGCTGCTGCTGCTGCTG 574
Qy 61 LeuSerProIleValSerCysGlyProPro 70
Db 575 CTGAGTCCCATCGTTAGCTGTGGACCCCGC 604
RESULT 9
CK140529 815 bp mRNA linear EST 03-DEC-2003
LOCUS AGENCOURT_16886288 NCI_CGAP_ZEMB3 Danio rerio cDNA clone
IMAGE:7058133 5', mRNA sequence.
ACCESSION CK140529
mRNA sequence.
CK140529.1 GI:38651455
EST.
SOURCE EST.
ORGANISM Danio rerio (zebrafish)
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
JOURNAL Cypriniformes; Cyprinidae; Danio.
COMMENT 1 (bases 1 to 815)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics / NIH
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Chi-Bin Chien
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L10M14841 row: f column: 19
High quality sequence start: 5
High quality sequence stop: 746.
FEATURES
Location/Qualifiers
source
1. .815
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:7058133"
/tissue_type="embryo"
/lab_host="NCI CGAP ZEMB3"
/clone_lib="NCI CGAP ZEMB3"
/note="Vector: pCMV-SPORT6.1; Site 1: EcoRV; Site 2: NotI;
Cloned unidirectionally. Primer: Oligo dt. Average insert
size 2.1 kb. Constructed by J. Wang (Research Genetics,
Invitrogen Corp) from tissue donated by L. Zon (Harvard
University). Note: this is a NCI_CGAP Library."
ORIGIN
Alignment Scores:
Pred. No.: 4.34e-28 Length: 815
Score: 354.50 Matches: 67
Percent Similarity: 85.71% Conservative: 11
Best Local Similarity: 73.63% Mismatches: 12
Query Match: 63.42% Indels: 2
DB: 7 Gaps: 1
US-10-624-932C-2_COPY_495_598 (1-104) x CK140529 (1-815)
Qy 3 AsnMetThrTyrGlyThrPheAsnPheLeuGlyArgLeuMetIleProAsnThrGly 22
Db 527 AACACCTCGTACGACACTTCAACTTCTCGGGCGGAGCTGAGCTGCCACACGGA 586
Qy 23 IleSerLeuLeuLeuProAspAlaIleProArgGlyLeuIleTyrGluIleTyrLeu 42
Db 587 ATCAGCTGTCTATCCCGCAGAGCCATTCCTCCAGAGGAGAGATTACGAGATTACCTC 646
Qy 43 ThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSer 62
Db 647 ACTATTGAGAGAGAGAGACATGAGGCTCGCGCTGGCGGGCTGTCAGAGCTGCTGAGC 706
Qy 63 ProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeuAlaMet 82
Db 707 CCCGTGTGAGCTGCGGACCGCCGCGCTCATGTCTCANC CGCGCTCATCTCTG---CAT 763
Qy 83 AspHisCysGlyGluProSerProAspSerTrp 93
Db 764 GGACACTGCTCAGATGCTGCTGCTG-GAGAACTGG 795
RESULT 10

```


CF173478
 LOCUS B0924C04-5 NIA Mouse Unfertilized Egg cDNA Library (Long 1) Mus EST 25-JUL-2003
 DEFINITION musculus cDNA clone NIA:B0924C04 IMAGE:30474555 5', mRNA sequence.
 ACCESSION CF173478
 VERSION CF173478.1 GI:33283027
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 506)
 Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.
 Construction of long-transcript enriched cDNA libraries from
 submicrogram amounts of total RNAs by a universal PCR amplification
 method
 Genome Res. 11 (9), 1553-1558 (2001)
 2142908
 1154199
 Contact: Dawood B. Dudekula
 Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
 Email: cdna@igsun.grc.nia.nih.gov
 Plate: B0924 row: C column: 04
 Seq primer: M13 Reverse
 High quality sequence stop: 506
 POLYA=No.

FEATURES

source
 1..506
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="niaEST:B0924C04-5"
 /db_xref="taxon:10090"
 /clone="NIA:B0924C04 IMAGE:30474555"
 /dev_stage="Unfertilized Egg"
 /lab_host="DH10B"
 /clone_lib="NIA Mouse Unfertilized Egg cDNA Library (Long 1)"
 /note="Vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI; Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (<http://igsun.grc.nia.nih.gov/cDNA>). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). PMID: 11544199). Total RNAs were extracted from a pool of 1488 unfertilized eggs. Double-stranded cDNAs were synthesized with an Oligo(dT) primer (Invitrogen):
 5'-pGACTAGTTCTAGATCGGAGCGCGCCCTTTTTTTTTTTT-3',
 treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Piao."

ORIGIN

Alignment Scores:
 Pred. No.: 1.23e-27 Length: 506
 Score: 348.00 Matches: 58
 Percent Similarity: 81.82% Conservative: 23
 Best Local Similarity: 58.59% Mismatches: 18
 Query Match: 62.25% Indels: 0
 Gaps: 0

US-10-624-932C-2_COPY_495_598 (1-104) x CF173478 (1-506)
 QY 6 TyrGlyThrPheAspPheLeuGlyArgLeuMetIleProAsnThrGlyIleSerLeu 25
 ::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
 Db 186 TTTGGTACTTCAACTCTCTTGGGGGTCACTCATCATCTCTTAATTCAGGAGTAGCTTG 245
 ::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
 QY 26 LeuIleProProAspAlaIleProArgGlyIleTyrGluIleTyrLeuThrLeuHis 45
 ::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
 Db 246 CTGATTCCCGCTGGGGCCATTCTCAGGGAGAGTCTATGAATGTATGTGACTGTACAC 305
 ::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
 QY 46 LysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleVal 65
 ::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
 Db 306 AGGAAGAAATATAGAGCCCCCCCCAGAGCTCTCAGACCCCTACTTACCCCTGTGGTG 365
 ::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
 QY 66 SerCysGlyProProGlyValLeuThrArgProValIleLeuAlaMetAspHisCys 85
 ::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
 Db 366 AGCTGTGGGCTCTCTGGAGCTCTGTGACCCGCCCTGTCTCATCTCTGCATCACTGT 425
 ::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
 QY 86 GlyGluProSerProAspSerTyrSerLeuArgLeuLysGlnSerCysGluGly 104
 ::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
 Db 426 CGAGACCCAGCAGCAGGAGTCTGGAAGATCCAGCTCAAAAACCGAGCAGTGCAGGA 482
 ::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||

RESULT 11

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

gene

ORIGIN

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

US-10-624-932C-2_COPY_495_598 (1-104) x AY406493 (1-2791)

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

US-10-624-932C-2_COPY_495_598 (1-104) x AY406493 (1-2791)

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

US-10-624-932C-2_COPY_495_598 (1-104) x AY406493 (1-2791)

Qy 6 TyrGlyThrPheAsnPhLeuGlyGlyArgLeuMetIleProAenThrGlyIleSerLeu 25
 Db 1592 TTTGGTACCTTCAACTCTCTTTGGGGGTCCACCTCATCTATCTCTAAATTCAGGAGTAAAGCTTG 1651

Qy 26 LeuIleProProAspAlaIleProArgGlyLysIleTyrGluIleTyrLeuThrLeuHis 45
 Db 1652 CTGATTCCTCCGTGGGCCATTCCTCAGGGGAGAGTCTATGAATATGATGACATGTACAC 1711

Qy 46 LysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleVal 65
 Db 1712 AGGAAGAAATATGAGGCCCCCATGGAAGACTCTCAGACCTTACTTACCCCTGTGGTG 1771

Qy 66 SerCysGlyProProGlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCys 85
 Db 1772 AGCTGTGGGCTCTCGGAGCTCTGCTGACCGCCCTGTCATCTCCTCATCTGCATCACTGT 1831

Qy 86 GlyGluProSerProAspSerTrpSerLeuArgLeuLysLysGlnSerCysGluGly 104
 Db 1832 GCAGACCCAGCAGGAGCTGGAGATCCAGCTCAAAACACGAGGAGTGCAGGGA 1888

RESULT 12
 LOCUS AK031655
 DEFINITION Mus musculus 13 days embryo male testis cDNA, RIKEN full-length enriched library, clone:6030473H24 product:unc5 homolog (C. elegans) 3, full insert sequence.

ACCESSION AK031655
 VERSION AK031655.1 GI:26327502
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1
 AUTHORS Carninci, P. and Hayashizaki, Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636

REFERENCE 2
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 20499374
 PUBMED 11042159

REFERENCE 3
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsuoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 TITLE RIKEN integrated sequence analysis, (RISA) system--384-format sequencing pipeline with 384 multipipillary sequencer
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE 20530913
 PUBMED 11076861

REFERENCE 4
 AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
 TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6
 AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,

Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuura, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

DIRECT SUBMISSION
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.jp/
 URL: http://fantom.gsc.riken.jp/
 Location/Qualifiers
 1. 3790
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="FANTOM_DB:6030473H24"
 /db_xref="taxon:10090"
 /clone="6030473H24"
 /sex="male"
 /tissue_type="testis"
 /clone_lib="RIKEN full-length enriched mouse cDNA library"
 /dev_stage="13 days embryo"
 118. 2970
 /note="unnamed protein product; putative unc5 homolog (C. elegans) 3 (MGD|GI:1095412, GB|NM_009472, evidence: BLASTN, 99%, match=464)"
 /codon_start=1
 /protein_id="BAC27495.1"
 /translation="MRKGLRATAARCGLIGYLLQMLVLPALALLSASGTGSAQQDDEFFHELPTFPDPPEPLPHFLIPEEAYIVKNFPVNLCKASPATQIYFCNSEWVHQKDHWDRVDETSGLIIVREYSIISROQVEELPGEDYWCQCVAMWSAGTQKSKAVVRIAYLRKTFEQEPLGKEVSLQEVLQCRPEGI PVAEVELKNEDIIDPAEDRNFYI TIDHNLIIKQARLSDTANYTCVAKNIIVAKSKSTATIVYVNGWSTWTSVCNSRCGRGQKTRCTCTPAPLNGAGFCGQGVQSKIACTTICPDGRTWSWKSCTCGTECTHWRRECTAPAPKNGKDCDGLVLOSKNCTDGLCMQGIYPISTHRPONEYGFSSAPDSDLLVAVGVGIVAVTVCIAITVVVALFVYRNHRDFSDIIDSALNGQFPVNIKAA ROLLVAPPOLTSAAAMRGVVALHDVSDKIPMTNSPILDPFLNPKIKVNSSCAVTPODLAEFFSKLSPQMTQSLILEALNLKNQSLAROTDPSCTAFGTNSLGGHLIIPN SGVSLIIPACALPQGRYVEMYVTHKENRPMEDSQTLITPVS CGPGCALTRPV ILTLHHCADPSTEDWKIQLKNQAVQGVQWEDVVVGVGENFTTPCIIQDLAEACHLTEN LSTYALVGQSTTKAAAKRLKLAIFGLPCSSLSYIRVCLDDTQDALKVQLERQM GGQLEEPKALRFKSGIHNRLSHIDIAHLSKLSKLAKYQEI PFYHWSGSQRLHC TPTLERLSLNTVELVCKLCVROGEQIIFQLNCTVSEETPIDLPLDPASTITVT GPASFTPLPIROKLCSSLDAPOTRGHDWRMLAKHLNLYNFATKSSPTGVILDL WEANQFPDGNLSMLA VLEEMGRHETVTVLAABEQY"

ORIGIN
 Alignment Scores:
 Pred. No.: 1,46e-26 Length: 3790
 Score: 348.00 Matches: 58
 Percent Similarity: 81.82% Conservative: 23
 Best Local Similarity: 58.59% Mismatches: 18
 Query Match: 62.25% Indels: 0
 DB: 3 Gaps: 0

US-10-624-932C-2_COPY_495_598 (1-104) x AK031655 (1-3790)

```

QY      6 TyrGlyThrPheAsnPheLeuGlyArgLeuMetIleProAsnThrGlyIleSerLeu 25
      ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1771 TTTGGTACCTTCAACTCTCTTGGGGTCACTCATCATCTTCTTAATTCAGAGTACGTTG 1830

QY      26 LeuIleProProAspAlaIleProArgGlyIleTyrGluIleTyrLeuThrLeuHis 45
      ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1831 CTGATTCCCGCTGGGGCCATTCTCAGGGGAGAGTCTATGAAATGTATGTGACTGTAC 1890

QY      46 LysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleVal 65
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1891 AGAAGAAGAAATATGAGCCCCCTCAGGAAGACTCTCAGACCTACTTACCCCTGTGGG 1950

QY      66 SerCysGlyProProGlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCys 85
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1951 AGCTGTGGGCTCTGTGAGCTCTGTGACCCCGCCCTGTCTCATCTCTGCATCATGT 2010

QY      86 GlyGluProSerProAspSerTrpSerLeuArgLeuLysGlnSerCysGluGly 104
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      2011 GCAGACCCCGAGCAGGAGTCCAGAGATCCAGCTCAAAACCCAGGAGTGCAGGGA 2067

```

RESULT 13

AL119797
 LOCUS
 DEFINITION DKFZp761G1524 r1 761 (synonym: hamy2) Homo sapiens cDNA clone
 DKFZp761G1524 5', mRNA sequence.

ACCESSION AL119797

VERSION AL119797.1 GI:5925696

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 329)
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Bloeker,H., Boecher,M., Brandt,P., Mewes,H.W., Gassenhuber,J. and Wiemann,S.

TITLE EST (Bloeker, et al.)

JOURNAL Unpublished (1999)

COMMENT Contact: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany

This is the 5' sequence of the clone insert

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the German Genome Project.

No si sequence available.

This clone (DKFZp761G1524) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

source
 Location/Qualifiers
 1..329
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DKFZp761G1524"
 /tissue_type="amygdala"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="761 (synonym: hamy2)"
 /note="Vector: pSport1; Site_1: NotI; Site_2: SalI"

ORIGIN

Alignment Scores:
 Pred. No.: 1.13e-26 Length: 329
 Score: 337.00 Matches: 55
 Percent Similarity: 79.80% Conservative: 24
 Best Local Similarity: 55.56% Mismatches: 20
 Query Match: 60.29% Indels: 0
 Gaps: 0

US-10-624-932C-2_COPY_495_598 (1-104) x AL119797 (1-329)

```

QY      6 TyrGlyThrPheAsnPheLeuGlyArgLeuMetIleProAsnThrGlyIleSerLeu 25
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      21 TTTGACAGTTCACCTCGCTGGAGGTCACTTATTTGTTCCCAATTCAGAGTACGTTG 80

QY      26 LeuIleProProAspAlaIleProArgGlyIleTyrGluIleTyrLeuThrLeuHis 45
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      81 CTGATTCCCGCTGGGGCCATTCCCCAAGGGAGAGTCTACGAAATGTATGTGACTGTAC 140

QY      46 LysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleVal 65
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      141 AGGAAGAAACTATGAGGCCCATGATGATGACTCTCAGACACTTTTGACCCCTGTGGG 200

QY      66 SerCysGlyProProGlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCys 85
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      201 AGCTGTGGGCCCCCAGGAGCTCTGCTACCCGCCCGCTCGTCTCATGTGATGATG 260

QY      86 GlyGluProSerProAspSerTrpSerLeuArgLeuLysGlnSerCysGluGly 104
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      261 GCAGACCCCAATACCGAGGAGTGGGAAATACTGCTCAAGAACCCAGGAGCAGGGA 317

```

RESULT 14

AY406491

LOCUS

DEFINITION Homo sapiens UNC5C gene, VIRTUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.

ACCESSION AY406491

VERSION AY406491.1 GI:39762465

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 2802)

AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,

Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,

Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,

Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous

gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 2802)

AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,

Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,

Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,

Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,

Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering

them based on alignment.

FEATURES

Location/Qualifiers
 1..2802
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 <1..>2802
 /gene="UNC5C"
 /locus_tag="HCW2575"

ORIGIN

Alignment Scores:
 Pred. No.: 1.58e-25 Length: 2802
 Score: 337.00 Matches: 55
 Percent Similarity: 79.80% Conservative: 24
 Best Local Similarity: 55.56% Mismatches: 20
 Query Match: 60.29% Indels: 0
 Gaps: 0

US-10-624-932C-2_COPY_495_598 (1-104) x AY406491 (1-2802)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 8, 2005, 23:47:02 ; Search time 3365.92 Seconds
(without alignments)
1166.064 Million cell updates/sec

Title: US-10-624-932C-2_COPY_817_897

Perfect score: 423
Sequence: 1 QK1TSSLDPPCRGDMRTL.....AAVAGLGQPDAGLFTVSEAE 81

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters: -MODEL=frame+ p2n.model -DEV=xlh
-O=/cgn2_1/USPTO spool_h/US10624932/runat_08092005_161705_15773/app_query.fasta_1.1386
-DB=GenEmbl -QFMT=fastap -SURFIX=rg -MINMATCH=0.1 -LOOPCL=0 -DOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10624932@cgn 1 1 7509 @runat_08092005_161705_15773 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- GenEmbl.*
- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	423	100.0	2688	9 BC009333	BC009333 Homo sapi
2	423	100.0	2697	6 AX451652	AX451652 Sequence
3	423	100.0	2752	6 AX449572	AX449572 Sequence
4	423	100.0	2784	6 CQ730306	CQ730306 Sequence

5	423	100.0	2881	6 AX527916	AX527916 Sequence
6	423	100.0	3580	6 AX367094	AX367094 Sequence
7	423	100.0	9700	6 AX054976	AX054976 Sequence
8	410	96.9	2697	6 AX268596	AX268596 Sequence
9	410	96.9	2697	10 RN087305	U87305 Rattus norv
10	410	96.9	3014	6 BD057524	BD057524 Netrin re
11	410	96.9	3844	10 BC058084	BC058084 Mus muscu
12	410	96.9	3992	10 MMU487852	AJ487852 Mus muscu
13	410	96.9	4294	10 AK122575	AK122575 Mus muscu
14	376	88.9	1787	6 BD057525	BD057525 Netrin re
C 15	359.5	85.0	171419	2 AC135142	AC135142 Rattus no
C 16	359.5	85.0	231407	2 AC139592	AC139592 Rattus no
C 17	357.5	84.5	6495	9 AB075856	AB075856 Homo sapi
C 18	357.5	84.5	6522	6 BD186447	BD186447 Novel gen
C 19	357.5	84.5	121282	9 AC027318	AC027318 Homo sapi
C 20	357.5	84.5	166534	2 AC034209	AC034209 Homo sapi
C 21	352.5	83.3	242128	2 AC123700	AC123700 Mus muscu
C 22	351.5	83.1	168168	2 AC012283	AC012283 Homo sapi
C 23	305	72.1	276	6 AX451658	AX451658 Sequence
C 24	304	71.9	341	6 CQ460895	CQ460895 Sequence
C 25	222	52.5	1575	6 AX054890	AX054890 Sequence
C 26	221	52.2	1393	6 AX054886	AX054886 Sequence
C 27	221	52.2	1438	6 AX054888	AX054888 Sequence
C 28	221	52.2	2013	6 CQ729046	CQ729046 Sequence
C 29	221	52.2	2612	6 CQ881064	CQ881064 Sequence
C 30	221	52.2	2780	6 CQ881054	CQ881054 Sequence
C 31	221	52.2	2986	6 CQ881052	CQ881052 Sequence
C 32	221	52.2	3646	6 CQ881060	CQ881060 Sequence
C 33	221	52.2	3646	9 AF055634	AF055634 Homo sapi
C 34	221	52.2	9299	10 MMU72634	U72634 Mus musculu
C 35	221	52.2	9328	10 AB118026	AB118026 Rattus no
C 36	217	51.3	2962	5 AY187310	AY187310 Gallus ga
C 37	201	47.5	3672	10 BC048162	BC048162 Mus muscu
C 38	201	47.5	3672	10 BC057560	BC057560 Mus muscu
C 39	201	47.5	3788	10 MMU487853	AJ487853 Mus muscu
C 40	199	47.0	2832	5 AX099459	AX099459 Xenopus l
C 41	198	46.8	2831	6 BD057526	BD057526 Netrin re
C 42	198	46.8	2838	10 RN087306	U87306 Rattus norv
C 43	191	45.2	1948	6 BD159676	BD159676 Primer fo
C 44	191	45.2	1948	6 AX882354	AX882354 Sequence
C 45	191	45.2	1948	9 AK022859	AK022859 Homo sapi

ALIGNMENTS

RESULT 1	BC009333	Homo sapiens unc-5 homolog A (C. elegans), partial cds.	2688 bp	mrna	linear	PRI_25-MAR-2004
LOCUS	BC009333	IMAGE:4126760, partial cds.				
DEFINITION	BC009333	BC009333.2 GI:40226527				
ACCESSION	BC009333					
VERSION	BC009333					
KEYWORDS	BC009333					
SOURCE	BC009333					
ORGANISM	BC009333					
REFERENCE	BC009333					
AUTHORS	BC009333					

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2688)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toehiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krayninski,M.I., Skalska,U., Smailus,D.E., Scherch,A., Schein,J.E., Jones,S.J., and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 2688)
Strausberg,R.
Direct Submission
Submitted (12-JUN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
On Dec 19, 2003 this sequence version replaced gi:14424611.
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Sequencing Center (NISC), Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@hgri.nih.gov
Ahter,N., Ayle,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brookes,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Madduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IPAL Plate: 26 Row: 9 Column: 22.

FEATURES

source
1..2688
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4126760"
/tissue_type="Brain, neuroblastoma"
/clone_lib="NIH_MGC_19"
/lab_host="DH10B-R"
/note="Vector: pOTB7"
<1..2688
/gene="UNC5A"
/note="synonym: UNC5H1"
/db_xref="LocusID:90249"
/db_xref="MIM:607869"
<1..1627
/gene="UNC5A"
/codon_start=2
/product="UNC5A protein"
/protein_id="AAH09333.2"
/db_xref="GI:40226528"
/db_xref="LocusID:90249"
/db_xref="MIM:607869"
/translation="DVALYVGLIAVAVCLVLLVLLVLCYCKEGLDSDVADSSILTSGFQVSIKPSKADNPILLTITQDLSITTTTYQSLCPQDQSPKPFOLTNGHLLSPLGGHRTLHSSPTSEAEFVRLSTQNYFRLPRGTSNMTYGTNFGLGLRMIPTNGI SLLIPDIPKGIYIYLTLLHKPEDVRLPAGCQTLLSPVSCGPGVLLTRPVILA MDHCEPSPDSWSLRLKQSCGSEWEDVHLGEEAPSHLYYCQLEASACVYFTBQLR FALVGEALSVAARLLKLLLPAPVACTSLKNVSLKLLVYOEIPFYHWNQYQLHCTFT LIQPRVLHFDKSHYLNLSIHDPVSLWKLIVSYOEIPFYHWNQYQLHCTFT LERVSPSTDCLAKLWNQVGDGQSFISNFIKTRFAELLALSEAGVPALVGPS APKPPLLRQKLIISLDPCRGADMRITLAKLHLDLSLFFASKPSFTAMLLNWEA RHPFNGLQSLAAVAGLQDPDAGLFTVSEAC"
413..724
/gene="UNC5A"

misc_feature

/note="ZUS; Region: Domain present in ZO-1 and Unc5-like netrin receptors"
/db_xref="CDD:smart00218"
1343..1594
/gene="UNC5A"
/note="DEATH; Region: DEATH domain, found in proteins involved in cell death (apoptosis). Alpha-helical domain present in a variety of proteins with apoptotic functions. Some (but not all) of these domains form homotypic and heterotypic dimers"
/db_xref="CDD:smart00005"
ORIGIN
Alignment Scores:
Pred. No.: 1.39e-41 Length: 2688
Score: 423.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-10-624-932c-2_COPY_817_897 (1-81) x BC009333 (1-2688)
Qy 1 GlnLysllelleSerSerLeuAspProProCyArgArgGlyAlaAspTrpArgThrLeu 20
|||||
Db 1379 CAGAAGATAATTTCCAGCTGGACCCACCTGTAGGCGGGTGCAGCTGGCGACTCTG 1438
Qy 21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40
|||||
Db 1439 GCCCAGAAATCCACCTGGACGACATCTCAGCTTCTTTGGCTCCAGCCCGCCCA 1498
Qy 41 AlaMetlleLeuAnLeuTtpGluAlaArgHisPheProAnGlyAnLeuSerGlnLeu 60
|||||
Db 1499 GCCATGATCTCAACCTGTGGAGCGCGGCACCTTCCCACGCGCACCTCAGCAGCTG 1558
Qy 61 AlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla 80
|||||
Db 1559 GCTCAGCAGTGGCTGGACTGGGCGCAGCCAGCAGCTGGCTTTCACAGTGTGAGGCT 1618
Qy 81 Glu 81
|||
Db 1619 GAG 1621
RESULT 2
AX451652
LOCUS AX451652 2697 bp DNA linear PAT 03-JUL-2002
DEFINITION Sequence 1 from Patent WO0233080.
ACCESSION AX451652
VERSION AX451652.1 GI:21698587
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Koehler,R.H.
TITLE Regulation of human netrin binding membrane receptor unc5h-1
JOURNAL Patent: WO 0233080-A 1 25-APR-2002;
Bayer Aktiengesellschaft (DE)
FEATURES
source
1..2697
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 1.39e-41 Length: 2697
Score: 423.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
misc_feature
/note="ZUS; Region: Domain present in ZO-1 and Unc5-like netrin receptors"
/db_xref="CDD:smart00218"
1343..1594
/gene="UNC5A"
/note="DEATH; Region: DEATH domain, found in proteins involved in cell death (apoptosis). Alpha-helical domain present in a variety of proteins with apoptotic functions. Some (but not all) of these domains form homotypic and heterotypic dimers"
/db_xref="CDD:smart00005"

US-10-624-932C-2_COPY_817_897 (1-81) x AX451652 (1-2697)

QY 1 GlnLysIleSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeu 20
|||||
Db 2449 CAGAAGATAATTTCCAGCTGGACCCACCTGTAGCGGGTGGCGACTGGCGGACTCTG 2508

QY 21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPheAlaSerLysProSerProThr 40
|||||
Db 2509 GCCCAGAAATCCACCTGGACAGCATCTCAGCTTTTGGCTCCAGGCCAGCCGCCACA 2568

QY 41 AlaMetIleLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
|||||
Db 2569 GCCATGATCTCAACCTGTGGGAGCGGGCAGCTTCCCAACGGCAACCTCAGCCAGCTG 2628

QY 61 AlaAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla 80
|||||
Db 2629 GCTGACGAGTGGCTGGACTGGGCCAGCAGACGCTGGCTTTTACAGTGTGCGAGGCT 2689

QY 81 Glu 81
|||||
Db 2689 GAG 2691

RESULT 3
LOCUS AX449572 2752 bp DNA linear PAT 03-JUL-2002
DEFINITION Sequence 1 from Patent WO210216.
ACCESSION AX449572
VERSION AX449572.1 GI:21698195

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Padigaru, M., Mezes, P., Mishra, V., Burgess, C., Casman, S.,
Grosse, W. M., Alsobrook, J. P., Lepley, D. M., Gerlach, V. L.,
Macdougall, J. R. and Smithson, G.
TITLE Proteins and nucleic acids encoding same
JOURNAL Patent: WO 0210216-A 1 07-FEB-2002;
Curagen Corporation (US)

FEATURES
source
1..2752
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores:
Pred. No.: 1.42e-41 Length: 2752
Score: 423.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x AX449572 (1-2752)

QY 1 GlnLysIleSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeu 20
|||||
Db 2494 CAGAAGATAATTTCCAGCTGGACCCACCTGTAGCGGGTGGCGACTGGCGGACTCTG 2553

QY 21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPheAlaSerLysProSerProThr 40
|||||
Db 2554 GCCCAGAAATCCACCTGGACAGCATCTCAGCTTTTGGCTCCAGGCCAGCCGCCACA 2613

QY 41 AlaMetIleLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
|||||
Db 2614 GCCATGATCTCAACCTGTGGGAGCGGGCAGCTTCCCAACGGCAACCTCAGCCAGCTG 2673

QY 61 AlaAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla 80
|||||
Db 2674 GCTGACGAGTGGCTGGACTGGGCCAGCAGACGCTGGCTTTTACAGTGTGCGAGGCT 2733

QY 81 Glu 81
|||||
Db 2734 GAG 2736

RESULT 4
LOCUS CQ730306 2784 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 16240 from Patent WO02068579.
ACCESSION CQ730306
VERSION CQ730306.1 GI:42303801

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Venter, C. J., Adams, M. C., Li, P. W. and Myers, E. W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof

JOURNAL Patent: WO 02068579-A 16240 06-SEP-2002;

FEATURES
source
Location/Qualifiers
1..2784
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores:
Pred. No.: 1.44e-41 Length: 2784
Score: 423.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x CQ730306 (1-2784)

QY 1 GlnLysIleSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeu 20
|||||
Db 2536 CAGAAGATAATTTCCAGCTGGACCCACCTGTAGCGGGTGGCGACTGGCGGACTCTG 2595

QY 21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPheAlaSerLysProSerProThr 40
|||||
Db 2596 GCCCAGAAATCCACCTGGACAGCATCTCAGCTTTTGGCTCCAGGCCAGCCGCCACA 2655

QY 41 AlaMetIleLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
|||||
Db 2656 GCCATGATCTCAACCTGTGGGAGCGGGCAGCTTCCCAACGGCAACCTCAGCCAGCTG 2715

QY 61 AlaAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla 80
|||||
Db 2716 GCTGACGAGTGGCTGGACTGGGCCAGCAGCTGGCTTTTACAGTGTGCGAGGCT 2775

QY 81 Glu 81
|||||
Db 2776 GAG 2778

RESULT 5
LOCUS AX527916 2881 bp DNA linear PAT 21-NOV-2002
DEFINITION Sequence 1 from Patent WO0229038.
ACCESSION AX527916
VERSION AX527916.1 GI:25172359

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Herrmann, J. L., Rastelli, L. and Shimkets, R. A.

TITLE Novel proteins and nucleic acids encoding same and antibodies directed against these proteins
JOURNAL Patent: WO 0229038-A 1 11-APR-2002; Curagen Corporation (US)
FEATURES
source 1..2881
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 1.5e-41 Length: 2881
Score: 423.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-624-932C-2_COPY_817_897 (1-81) x AX527916 (1-2881)
Qy 1 GlnlysllelleSerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrleu 20
Db 2538 CAGAAGATAATTTCCAGCCTGGACCCACCTGTAGCGGGTGGCGACTCTG 2597
Qy 21 AlaGlnlysllelleSerSerHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40
Db 2598 GCCCAGAAACTCCACCTGGACGAGCATCTCAGCTTCTTTGGCTTCCAGCCCGCCACCA 2657
Qy 41 AlaMetlleleuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnleu 60
Db 2658 GCCATGATCTCTCACTGTGGAGCGGGGCACTTCCCAACGGCACTCAGCCAGCTG 2717
Qy 61 AlaAlaAlaValAlaGlyLeuGlnProAspAlaGlyLeuPheThrValSerGluAla 80
Db 2718 GCTGCAGCAGTGGCTGGAGTGGCGCAGCCAGACGCTGGCCTCTTCACAGTGTGCGAGGCT 2777
Qy 81 Glu 81
Db 2778 GAG 2780
RESULT 6
AX367094 AX367094 3580 bp DNA linear PAT 16-FEB-2002
LOCUS Sequence 13 from Patent WO0198354.
DEFINITION AX367094
ACCESSION AX367094
VERSION AX367094.1 GI:19855296
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Griffin,J.A., Kallick,D.A., Tribouley,C.M., Yue,H., Nguyen,D.B., Tang,Y.T., Lal,P., Policky,J.L., Azimzai,Y., Lu,D.A., Graul,R., Yao,M.G., Burford,N., Hafalia,A.J., Baughn,M.R., Bandman,O., Patterson,C., Yang,J., Xu,Y., Warren,B.A., Ding,L. and Sanjanwalla,M.S.
TITLE Receptors
JOURNAL Patent: WO 0198354-A 13 27-DEC-2001; Incyte Genomics, Inc. (US)
FEATURES
source 1..3580
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Incyte ID No: 6052371CB1"
ORIGIN
Alignment Scores:
Pred. No.: 1.92e-41 Length: 3580
Score: 423.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-624-932C-2_COPY_817_897 (1-81) x AX367094 (1-3580)
Qy 1 GlnlysllelleSerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrleu 20
Db 2284 CAGAAGATAATTTCCAGCCTGGACCCACCTGTAGCGGGTGGCGACTCTG 2343
Qy 21 AlaGlnlysllelleSerSerHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40
Db 2344 GCCCAGAAACTCCACCTGGACGAGCATCTCAGCTTCTTTGGCTTCCAGCCCGCCACCA 2403
Qy 41 AlaMetlleleuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnleu 60
Db 2404 GCCATGATCTCTCACTGTGGAGCGGGGCACTTCCCAACGGCACTCAGCCAGCTG 2463
Qy 61 AlaAlaAlaValAlaGlyLeuGlnProAspAlaGlyLeuPheThrValSerGluAla 80
Db 2464 GCTGCAGCAGTGGCTGGAGTGGCGCAGCCAGACGCTGGCCTCTTCACAGTGTGCGAGGCT 2523
Qy 81 Glu 81
Db 2524 GAG 2526
RESULT 7
AX054976 AX054976 9700 bp DNA linear PAT 13-JAN-2001
LOCUS Sequence 91 from Patent WO0073328.
DEFINITION AX054976
ACCESSION AX054976
VERSION AX054976.1 GI:12228344
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS van Criekeing, W., Roelens, I., Bogaert, T. and Verwaerde, P.
TITLE Unc-5 constructs and screening methods
JOURNAL Patent: WO 0073328-A 91 07-DEC-2000; Devgen NV (BE)
FEATURES
source 1..9700
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="plasmid pGC1037"
ORIGIN
Alignment Scores:
Pred. No.: 6.03e-41 Length: 9700
Score: 423.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-624-932C-2_COPY_817_897 (1-81) x AX054976 (1-9700)
Qy 1 GlnlysllelleSerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrleu 20
Db 1064 CAGAAGATAATTTCCAGCCTGGACCCACCTGTAGCGGGTGGCGACTCTG 1123
Qy 21 AlaGlnlysllelleSerSerHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40
Db 1124 GCCCAGAAACTCCACCTGGACGAGCATCTCAGCTTCTTTGGCTTCCAGCCCGCCACCA 1183
Qy 41 AlaMetlleleuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnleu 60
Db 1184 GCCATGATCTCTCACTGTGGAGCGGGGCACTTCCCAACGGCACTCAGCCAGCTG 1243
Qy 61 AlaAlaAlaValAlaGlyLeuGlnProAspAlaGlyLeuPheThrValSerGluAla 80

Db 1244 GCTGCAGCAGTGGCTGGACTGGCCAGCAGACGCTGGCCTCTTACAGTGTGCGAGGCT 1303

Qy 81 Glu 81
|||

Db 1304 GAG 1306

RESULT 8
AX268596
LOCUS AX268596
DEFINITION Sequence 15 from Patent WO0175440.
ACCESSION AX268596
VERSION AX268596.1 GI:16541710
KEYWORDS
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1
AUTHORS Cochran,S.W., Paterson,G.Y., Ohashi,Y.W., Morris,B.Y. and Pratt,J.Y.
TITLE Schizophrenia related genes
JOURNAL Patent: WO 0175440-A 15 11-OCT-2001;
WELFIDE CORPORATION (JP)
FEATURES
source
1. .2697
/organism="Rattus sp."
/mol_type="unassigned DNA"
/db_xref="taxon:10118"

ORIGIN
Alignment Scores:
Pred. No.: 5.46e-40 Length: 2697
Score: 410.00 Matches: 78
Percent Similarity: 97.53% Conservative: 1
Best Local Similarity: 96.30% Mismatches: 2
Query Match: 96.93% Indels: 0
DB: 6 Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x AX268596 (1-2697)

Qy 1 GlnlysllelleSerSerLeuAspProProCysArgArgGlyAlaAspTrrArgThrLeu 20
|||:::|||||

Db 2449 CAAAAGATCATCGCAGCTCGACCCACCTTCGAGCGGGCGCGACTGGAGAACTCTA 2508

Qy 21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPheAlaSerLysProSerProThr 40
|||||

Db 2509 GCCCAGAACTTCACCTGGACAGCCATCTTAGCTTCTTGGCTCCAAAGCCCGCCCTACA 2568

Qy 41 AlaMetIleLeuAsnLeuTrrpGluAlaAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
|||||

Db 2569 GCCATGATCTCAACCTATGGAGGACCGGCACCTTCCCAAGCGCAACTCGGCCAGCTG 2628

Qy 61 AlaAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla 80
|||||

Db 2629 GCAGCAGTGTGGCGGAGCTGGCCCAACAGATGCTGGCCTCTTCACGGTGTGCGAGGCC 2688

Qy 81 Glu 81
|||

Db 2689 GAG 2691

RESULT 9
RNU87305
LOCUS RNU87305
DEFINITION Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds.
ACCESSION U87305
VERSION U87305.1 GI:2055391
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 2697)
AUTHORS Leonardo,B.D., Hinck,L., Masu,M., Keino-Masu,K., Ackerman,S.I. and Tessier-Lavigne,M.
TITLE Vertebrate homologues of C. elegans UNC-5 are candidate netrin receptors
JOURNAL Nature 386 (6627), 833-838 (1997)
MEDLINE 97271897
PUBMED 9126742

REFERENCE 2 (bases 1 to 2697)
AUTHORS Leonardo,B.D., Hinck,L., Masu,M., Keino-Masu,K. and Tessier-Lavigne,M.
TITLE Direct Submission
JOURNAL Submitted (28-JAN-1997) Anatomy, UCSF, 513 Parnassus, San Francisco, CA 94143-0452, USA

FEATURES
source
1. .2697
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/tissue_type="brain and ventral spinal cord"
/dev_stage="18 day embryo and 13 day embryo"

CDS
1. .2697
/codon_start=1
/product="transmembrane receptor UNC5H1"
/protein_id="AAB57678.1"
/db_xref="GI:2055392"
/translation="MAVRPGLWPVLGIVLAALRGSGAQQSATVANPVGANPDLLP
HFLVPEBDVYIVKNKPVLLVCKAVPATQIFPKCNQWVRQVDHVIERTSDSSGLPTM
EVRINVSROQVEKVFGLVEEYWCQVAMSSGCTTKSQAYIRIAYLRKNPEOEPLAKEV
SLEQIVLPCRPPEGIPPAEVEWLRNEDLVDPDLPNVIITREHSLVVRQARLADTAN
YTCVAKNIVARRSTSAAVIYVNGSWSTWTSVCSASCRGWQKRSCNTNPAPLN
GGAFCEGQVQKTACATLCPVDGSSWSKWSACGLDCTHWRSECDSPAPRNGEEC
RGADSLRNTCTDLCLHTASCPEDVALYIGLVAVAVCLFLLLALGLYICRKEGLDS
DVADSLITSGFQPVSIKSKADNPILLTIQDLSLTSTTTTQVGLSCSDQDGPSPKFLQ
SNCHLSPLAGSRHTLHSSPTSEADPVSLSTQNVPSLRCTSNMAYGTFTFLGG
RLMIPNTGISLLIIPDPAIPRGIYEIYTLHKPEDVPLPACQTLSPVSVSCGPPGV
LLTRPVILAMDHCQEPSPSWSLRKKQSCGSEWEDVHLHLESGSHLYYQCLEAGAC
YVFTQELGRFALVGEALSVAATRLRLFPVACTSLEYINRIVYCLRDTHDALKEVV
QYKQLGGLQIQRVLFKDSYHNLRSLHDVPSLSKSLYSQIPIPFYIWNGT
QOYLHCTFTLIERINASTLDLACKVWQVEGDGQSFNFINFTKDTREAEILLALESEG
GVPAIVGPSAFKIPILIRQKIIASIDPPCSRGADWRTLAQKLHLDLSLHSLFFASKPSPT
AMILNLWEARHPFNGNLGQLAAAVAGLQPDAGLFTVSEABC"

ORIGIN
Alignment Scores:
Pred. No.: 5.46e-40 Length: 2697
Score: 410.00 Matches: 78
Percent Similarity: 97.53% Conservative: 1
Best Local Similarity: 96.30% Mismatches: 2
Query Match: 96.93% Indels: 0
DB: 10 Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x RNU87305 (1-2697)

Qy 1 GlnlysllelleSerSerLeuAspProProCysArgArgGlyAlaAspTrrArgThrLeu 20
|||||

Db 2449 CAAAAGATCATCGCAGCTCGACCCACCTTCGAGCGGGCGCGACTGGAGAACTCTA 2508

Qy 21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPheAlaSerLysProSerProThr 40
|||||

Db 2509 GCCCAGAACTTCACCTATGGAGGACCGGCACCTTCCCAAGCGCAACTCGGCCAGCTG 2628

Qy 61 AlaAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla 80
|||||

Db 2629 GCAGCAGTGTGGCGGAGCTGGCCCAACAGATGCTGGCCTCTTCACGGTGTGCGAGGCC 2688

Qy 81 Glu 81
|||

Db 2689 GAG 2691

```

RESULT 10
BD057524
LOCUS      BD057524
DEFINITION Netrin receptors.
ACCESSION  BD057524
VERSION    BD057524.1 GI:22603130
KEYWORDS   JP 2001505062-A/1.
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1 (bases 1 to 3014)
AUTHORS    Lavigne,M.T., Leonardo,D.E., Hinck,L., Masu,M. and Masu,K.K.
TITLE      Netrin receptors
JOURNAL    Patent: JP 2001505062-A 1 17-APR-2001;
            THE REGENTS OF THE UNIV OF CALIFORNIA
COMMENT    PN JP 2001505062-A/1
            PD 17-APR-2001
            PF 19-FEB-1998 JP 1998536840
            PR 19-FEB-1997 US 08/808982
            PI MARC TESSIER LAVIGNE,DAVID E LEONARDO,LINDSAY HINCK,MASAYUKI
            PI MASU,
            PC C07K1/00,C07K14/00,C07K17/00,C07H21/02,C07H21/04,G01N33/53 CC
            Strandedness: Double;
            CC Topology: Linear;
            FH Key Location/Qualifiers.
FEATURES             Location/Qualifiers
     source           1..3014
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN
Alignment Scores:
Pred. No.:          6.2e-40          Length:          3014
Score:              410.00           Matches:          78
Percent Similarity: 97.53%           Conservative:     1
Best Local Similarity: 96.30%         Mismatches:      2
Query Match:        96.93%           Indels:          0
DB:                 6                Gaps:           0

US-10-624-932C-2_COPY_817_897 (1-81) x BD057524 (1-3014)
Qy      1 GlnylslelleSerSerLeuAspProProCysArgArgGlyAlaAspTrrArgThrleu 20
        |||||
Db      2449 CAAAGATCATCGCAGCTGTGGACCCACCTGCGAGCGGGCGCGGCTGGAGAACTCTA 2508
        |||||
Qy      21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40
        |||||
Db      2509 GCCCAGAAACTTCACCTGGACAGGCATCTTAGCTTCTTGGCTCCAGCCCGCCCTACA 2568
        |||||
Qy      41 AlaMetlleLeuAsnLeuTrrGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
        |||||
Db      2569 GCCATGATCTCTCAACCTATGGAGGACGCGGACCTTCCCAACGGCAACCTCGGCAGCTG 2628
        |||||
Qy      61 AlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla 80
        |||||
Db      2629 GCACGAGCTGTGGCGGAGCTGGCGGCAACCAAGATGCTGGCCTCTTTCACGGTGTGGAGGCC 2688
        |||||
Qy      81 Glu 81
        |||
Db      2689 GAG 2691

RESULT 11
BC058084
LOCUS      BC058084
DEFINITION Mus musculus unc-5 homolog A (C. elegans), mRNA (cDNA clone
ACCESSION  MGC:66671 IMAGE:6813463), complete cds.
VERSION    BC058084.1 GI:34784158
KEYWORDS   MGC.
SOURCE     Mus musculus (house mouse)

```

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 3844)

REFERENCE
AUTHORS

Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Haiehl,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.I., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalios,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932
2 (bases 1 to 3844)
Strausberg,R.
Direct Submission
Submitted (08-SEP-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-rc@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Lilisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smalios, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAC Plate: 126 Row: b Column: 11
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 23346570.

FEATURES
source

1..3844
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="MGC:66671 IMAGE:6813463"
/tissue_type="Brain, mouse, 13.5, 14.5, 16.5, 17.5 dpc"
/clone_lib="NIH BMAP_FWO"
/lab_host="DH10B"
/note="Vector: pYX-ASC"
1..3844
/gene="Unc5a"
/db_xref="LocusID:107448"
/db_xref="MGI:894682"
252..2780

gene

CDS

/gene="Unc5a"
/codon_start=1
/product="Unc5a protein"
/protein_id="AAH58084.1"
/db_xref="GI:34784159"
/db_xref="locusID:107448"
/db_xref="MGI:894682"
/translation="MAVRPGLWPALLGIVLTAWLRGSGAQOSATVANVPGANPDLLP
HFLVPEDEVIVKPKVLLVCKAVPATQIFKCNQGEWVRQDVHIERSTGSSGLPTM
EVRINVSQVQKVEGLSEYKQCWAMSSGTTKQKAYIRIAYLRKNFEOBPLAKEV
SLEQGIIVLPCRPPEGI PAEVEWLENEIDLVDPSLDPNVITREHSLVRQARLADTN
YTCVAKNIVARRRSAAVIVYVDSWSPWSKACGLDCTHWRSECDPARNNGE
ECRGADLTCTSLDCLHTSSGPEDEVYIGLVAVAVCLILLLVLYCRKKEGL
DSVDVADSIITSGFQVSKSKADNPHTLIQPDLSITTTTQGSGLCPROQDGPSPKF
QLSNGHLSPLGSGRHTLHSSPTSEADPFVSLSTQNYFRSLPGTSMNAYGTFFNL
GGRMLIPVLTSLIPDAIPRGKIYEIYLTHKPEDVRLPLAGCOTLLSLVYCOLEAG
GVLITRPVILAMDHCQSPDSWLSRLKQSCGSEWEDVLHGRESPLHYLVCLEAG
ACVYPTGOLGRFALVGEALSVAAKRLILLFPAPVACTSLEWNRVYCLHTHDAKE
VYQELKGGQLIQPRVILHFDKSYHNRLSLHDPVSSLWKSLLVSTQEPFFTHWN
GTQYLLCTFLTERVNASTDLACKVWVQVEGDSQFNINFTKDTFAEMLALESE
EGVPAIVGSPAFKIPFLIRQKIITSLDPPCSRGADWRTLAQKHLDSLHLSFFASKPS
PTAMILNWEARHFPNGNLGQLAAAVAGLQPDAGLFTVSEAC"
714. .926
/gene="Unc5a"
/note="Ig; Region: Immunoglobulin"
/db_xref="CDD:smart00409"
984. .1130
/gene="Unc5a"
/note="nspl; Region: Thrombospondin type 1 repeats"
/db_xref="CDD:smart00209"
1566. .1877
/gene="Unc5a"
/note="ZU5; Region: Domain present in ZO-1 and Unc5-like
netrin receptors"
/db_xref="CDD:smart00218"
2496. .2684
/gene="Unc5a"
/note="DEATH; Region: DEATH domain, found in proteins
involved in cell death (apoptosis). Alpha-helical domain
present in a variety of proteins with apoptotic functions.
Some (but not all) of these domains form homotypic and
heterotypic dimers"
/db_xref="CDD:smart00005"
ORIGIN
Alignment Scores:
Pred. No.: 8, 19e-40 Length: 3844
Score: 410.00 Matches: 78
Percent Similarity: 97.53% Conservative: 1
Best Local Similarity: 96.30% Mismatches: 2
Query Match: 96.93% Indels: 0
DB: 10 Gaps: 0
US-10-624-932C-2_COPY_817_897 (1-81) x BC058084 (1-3844)
Qy 1 GlnlylIleSerSerLeuAspProProCyArGArgGlyAlaAspTrpArgThrLeu 20
Db 2532 CAAGAATCATTTACAGCGCTGGACCCACCTGCGAGCGGGCGCGACTGGCGAACTCTA 2591
Qy 21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPheAlaSerLysProSerProThr 40
Db 2592 GCGGAGAACTTACCTGAGCGGCGGCGACTTCCCGACCGGCAACTCGGCCAGCTG 2651
Qy 41 AlaMetIleLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
Db 2652 GCCATGATCTCTCAACTATGGAGGCGGCGGCACTTCCCGACCGGCAACTCGGCCAGCTG 2711
Qy 61 AlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla 80
Db 2712 GCGGAGCTGTGGCGGACTGGCGCAGCAGATGCTGCGCTCTTCACTGTGTCAGAGGCC 2771
Qy 81 Glu 81
|||

Db 2772 GAG 2774
RESULT 12
MMU487852 3992 bp mRNA linear ROD 24-SEP-2002
LOCUS
DEFINITION Mus musculus mRNA for netrin receptor Unc5h1 (Unc5h1 gene).
ACCESSION AJ487852
VERSION AJ487852.1 GI:22035783
KEYWORDS netrin receptor Unc5h1; Unc5h1 gene.
SOURCE Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1
Engelkamp,D.
AUTHORS
TITLE Cloning of three mouse Unc5 genes and their expression patterns at
mid-gestation
JOURNAL Mech. Dev. 118 (1-2), 191-197 (2002)
MEDLINE 22359710
PUBMED 12351186
REFERENCE 2 (bases 1 to 3992)
AUTHORS Engelkamp,D.
TITLE Direct Submision
JOURNAL Submitted (15-MAY-2002) Neuroanatomy, Max Planck Institute for
Brain Research, Deutschordenstrasse 46, Frankfurt 60528, GERMANY
FEATURES
Location/Qualifiers
1..3992
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
1..3992
/gene="Unc5h1"
232..2928
/gene="Unc5h1"
/codon_start=1
/product="netrin receptor Unc5h1"
/protein_id="CAD32250.1"
/db_xref="GI:22035784"
/db_xref="GOA:Q8K1S4"
/db_xref="UniProt/TrEMBL:Q8K1S4"
/translation="MAVRPGLWPALLGIVLTAWLRGSGAQOSATVANVPGANPDLLP
HFLVPEDEVIVKPKVLLVCKAVPATQIFKCNQGEWVRQDVHIERSTGSSGLPTM
EVRINVSQVQKVEGLSEYKQCWAMSSGTTKQKAYIRIAYLRKNFEOBPLAKEV
SLEQGIIVLPCRPPEGI PAEVEWLENEIDLVDPSLDPNVITREHSLVRQARLADTN
YTCVAKNIVARRRSAAVIVYVDSWSPWSKACGLDCTHWRSECDPARNNGE
ECRGADLTCTSLDCLHTSSGPEDEVYIGLVAVAVCLILLLVLYCRKKEGLDS
VDVADSIITSGFQVSKSKADNPHTLIQPDLSITTTTQGSGLCPROQDGPSPKFQ
SNGHLSPLGSGRHTLHSSPTSEADPFVSLSTQNYFRSLPGTSMNAYGTFFNL
LMTPTNGISLLIPDAIPRGKIYEIYLTHKPEDVRLPLAGCOTLLSLVYCOLEAG
LLTRPVILAMDHCQSPDSWLSRLKQSCGSEWEDVLHGRESPLHYLVCLEAGAC
VYPTGOLGRFALVGEALSVAAKRLILLFPAPVACTSLEWNRVYCLHTHDAKEV
OLEKQSGQLIQPRVILHFDKSYHNRLSLHDPVSSLWKSLLVSTQEPFFTHWNGT
QOYLHCTFLTERVNASTDLACKVWVQVEGDSQFNINFTKDTFAEMLALESE
GVPAIVGSPAFKIPFLIRQKIITSLDPPCSRGADWRTLAQKHLDSLHLSFFASKPSPT
AMILNWEARHFPNGNLGQLAAAVAGLQPDAGLFTVSEAC"
ORIGIN
Alignment Scores:
Pred. No.: 8, 55e-40 Length: 3992
Score: 410.00 Matches: 78
Percent Similarity: 97.53% Conservative: 1
Best Local Similarity: 96.30% Mismatches: 2
Query Match: 96.93% Indels: 0
DB: 10 Gaps: 0
US-10-624-932C-2_COPY_817_897 (1-81) x MMU487852 (1-3992)
Qy 1 GlnlylIleSerSerLeuAspProProCyArGArgGlyAlaAspTrpArgThrLeu 20
Db 2680 CAAGAATCATTTACAGCGCTGGACCCACCTGCGAGCGGGCGCGACTGGCGAACTCTA 2739
Qy 21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPheAlaSerLysProSerProThr 40

```

|||||
Db 2740 GCCCAGAAATTCACCTGGACGACATCTTAGCTCTTTCCTCCAGCCGAGCCCTTACA 2799
|||||
Qy 41 AlaMetIleLeuAenLeuTTPGluAlaArgHisPheProAenGlyAenLeuSerGlnLeu 60
|||||
Db 2800 GCCATGATCTCTCAACCTATGGAGCGCGGACATTCGCCAACGCAACCTCGGCAGCTG 2859
|||||
Qy 61 AlalaValAlaGlyLeuGlnProAspIlaGlyLeuPheThrValSerGluAla 80
|||||
Db 2860 GCCCAGCTGTGGCGGAGTGGCGCAGCCAGATGCTGGCTCTTTCACCGTGTCCAGAGGCC 2919
|||||
Qy 81 Glu 81
|||||
Db 2920 GAG 2922

RESULT 13
AKI22575 4294 bp mRNA linear ROD 15-MAR-2003
DEFINITION Mus musculus mRNA for mKIAA1976 protein.
ACCESSION AKI22575
VERSION AKI22575.1 GI:28972881
SOURCE Fli CDNA.
ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 Okazaki,N., Kikuno,R., Ohara,R., Inamoto,S., Aizawa,H., Yuasa,S.,
Nakajima,D., Nagase,T., Ohara,O. and Koga,H.
Prediction of the coding sequences of mouse homologues of KIAA
gene: II. The complete nucleotide sequences of 400 mouse
KIAA-homologous cDNAs identified by screening of terminal sequences
of cDNA clones randomly sampled from size-fractionated libraries
DNA Res. 10, 35-48 (2003)
2 (bases 1 to 4294)
Okazaki,N., Kikuno,R., Nagase,T., Ohara,O. and Koga,H.
Direct Submission
Submitted (07-FEB-2003) Hisashi Koga, Kazusa DNA Research
Institute, Laboratory for Genome Informatics; 2-6-7
Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan
(E-mail:mouse@kazusa.or.jp, Tel:81-438-52-3919, Fax:81-438-52-3918)
The CREATE program supported by Japan science and technology
corporation; cDNA full insert sequencing: Kazusa DNA Research
Institute; cDNA library construction, clone selection and 5'- &
3'-end one pass sequencing.
FEATURES
source
location/Qualifiers
1..4294
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="mbh03993"
/tissue_type="brain"
/dev_stages="adult"
/note="vector:modified pBC SK+"
1..4294
/gene="mKIAA1976"
<2263..3249
/gene="mKIAA1976"
/note="CDS is predicted by in silico analysis. Start codon
is not identified."
/codon_start=1
/evidence=not experimental
/product="mKIAA1976 protein"
/protein_id="BAC65857.1"
/db_xref="GI:28972882"
/translation="SLYPAIKTKTLTSLAASSGPEVALYIGLVAVAVCLILLLVLL
LIYCRKKGDSVDADSSILTSFGPVSIKPSKADNPHLLTIPDLSITTTTYQGSIC
PROGSPKFOLEKQGLQJQEPVLHFQDSYHNRLSIHDVPSLWKSLLVSYOE
IPFYHNGTQOVLHCTFTFLRVNASTDLACKVMVQVGEDGGSFNINNTKIDTRF
AEMLALESGVPALVGPFAFKIEFLIRKQIITSIDPFCRCAGDWRTIAQKLDSLH
SFFASKSPSTAMILNLEARHFPNGNLGQLAAAVAGLQPDAGLFTVSEAC"

Alignment Scores:
Pred. No.: 9.3e-40 Length: 4294
Score: 410.00 Matches: 78
Percent Similarity: 97.53% Conservative: 1
Best Local Similarity: 96.30% Mismatches: 2
Query Match: 96.93% Indels: 0
Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x AKI22575 (1-4294)
Qy 1 GlnlyIleleSerSerLeuAspProProCyArgArgGlyAlaAspTTPArgThrLeu 20
Db 3001 CAAAAGATCATTTACCACTGGACCCACCTTCGACGCGGGCGCTGACTGGCGAACTCTA 3060
Qy 21 AlaGlnlyLeuHisLeuAspSerHisLeuSerPhePheAlaSerIlyProSerProThr 40
Db 3061 GCCCAGAAATTCACCTGGACGACATCTTAGCTCTTTCCTCCAGCCGAGCCCTTACA 3120
Qy 41 AlaMetIleLeuAenLeuTTPGluAlaArgHisPheProAenGlyAenLeuSerGlnLeu 60
Db 3121 GCCATGATCTCTCAACCTATGGAGCGCGGACATTCGCCAACGCAACCTCGGCAGCTG 3180
Qy 61 AlalaValAlaGlyLeuGlnProAspIlaGlyLeuPheThrValSerGluAla 80
Db 3181 GCCCAGCTGTGGCGGAGTGGCGCAGCCAGATGCTGGCTCTTTCACCGTGTCCAGAGGCC 3240
Qy 81 Glu 81
Db 3241 GAG 3243

RESULT 14
BD057525 1787 bp DNA linear PAT 27-AUG-2002
LOCUS Netrin receptors.
DEFINITION BD057525
ACCESSION BD057525.1 GI:22603131
VERSION JP 2001505062-A/2.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 1787)
AUTHORS Lavigne,M.T., Leonardo,D.E., Hinck,L., Masu,M. and Masu,K.K.
TITLE Netrin receptors
JOURNAL Patent: JP 2001505062-A 2 17-APR-2001;
THE REGENTS OF THE UNIV OF CALIFORNIA
COMMENT PN JP 2001505062-A/2
PD 17-APR-2001
PF 19-FEB-1998 JP 1998536840
PR 19-FEB-1997 US 08/808982
PI MARC TESSIER LAVIGNE,DAVID E LEONARDO,LINDSAY HINCK,MASAYUKI
PI MASU
PI KAZUKO KEINO MASU
PC C07K1/00,C07K14/00,C07K17/00,C07H21/02,C07H21/04,G01N33/53 CC
Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers.
FEATURES
source
location/Qualifiers
1..1787
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Alignment Scores:
Pred. No.: 5.02e-36 Length: 1787
Score: 376.00 Matches: 77
Percent Similarity: 92.77% Conservative: 0
Best Local Similarity: 92.77% Mismatches: 4
Query Match: 88.89% Indels: 2
Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x BD057525 (1-1787)

```

QY 1 GlnLysIleSerSerLeuAspProProCyArgArgGlyAlaAspTrpArgThrLeu 20
 Db 1420 CAGAAGATAATTTCCAGCCTGGACCCACCCCTGTAGCGGGGTGCCACTGGCGGACTCTG 1479
 QY 21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPhePheAlaSerIysProSerProThr 40
 Db 1480 GCCCAGAAACTCACCCTGGACAGCCATCTCAGCTTCTTTGGCTTCCAAAGCCGACCCACCA 1539
 QY 41 AlaMetIleLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
 Db 1540 GCCATGATCTCAACCTGTGGAGGGCGGCACCTTCCCAACGGCACTCAGCCAGCTG 1599
 QY 61 AlaAlaValAlaGlyLeuGlnProAspAlaGlyLeu-PheThrVal-SerGluA 80
 Db 1600 GTTCGACGAGTGGCTGGGACTGGCCAGCAGCAGCGGTGGCTTCTTTTTCACAGTGTTCGGAGG 1659
 QY 80 laglu 81
 Db 1660 CTGAG 1664
 RESULT 15
 AC135142/c
 LOCUS
 DEFINITION Rattus norvegicus clone CH230-169P5, *** SEQUENCING IN PROGRESS
 AC135142
 AC135142.2 GI:25007239
 HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
 KEYWORDS Rattus norvegicus (Norway rat)
 SOURCE Rattus norvegicus
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE
 AUTHORS 1 (bases 1 to 171419)
 Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Eacotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, W., Foster, P., Frazer, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, S., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hognes, M., Hollins, B., Howells, S., Huliy, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuewa, L., Loulsegged, H., Lozado, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindarne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mathew, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Parks, K., Nwankwelu, O., Okwuonu, G., Olampunsgoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfankoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, P., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shateman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D.,

Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Umani, K., Valas, R., Vera, V., Villanueva, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Wilson, R., Wiczyski, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, S., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
 Direct Submission
 Unpublished
 2 (bases 1 to 171419)
 Rat Genome Sequencing Consortium.
 Submitted (08-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 171419)
 Rat Genome Sequencing Consortium.
 Direct Submission
 Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 On Nov 15, 2002 this sequence version replaced gi:23578050.
 The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
 ----- Genome Center of Medicine
 Center: Baylor College of Medicine
 Web site: http://www.hgsc.bcm.tmc.edu/
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: KCMS
 Center clone name: CH230-169P5
 ----- Summary Statistics
 Assembly program: Phrap; version 0.990329
 Consensus quality: 127081 bases at least Q40
 Consensus quality: 131254 bases at least Q30
 Consensus quality: 133849 bases at least Q20
 Estimated insert size: 128800; sum-of-contigs estimation
 Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

 * NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
 * 1 18754: contig of 18754 bp in length
 * 18755 18854: gap of unknown length
 * 18855 147860: contig of 129006 bp in length
 * 147861 147960: gap of unknown length
 * 147961 159835: contig of 11875 bp in length
 * 159836 159935: gap of unknown length
 * 159936 161085: contig of 1150 bp in length
 * 161086 161185: gap of unknown length
 * 161186 162489: contig of 1304 bp in length
 * 162490 162589: gap of unknown length

* 162590 164048: contig of 1459 bp in length
* 164049 164148: gap of unknown length
* 164149 165318: contig of 1170 bp in length
* 165319 165418: gap of unknown length
* 165419 167567: contig of 2149 bp in length
* 167568 167667: gap of unknown length
* 167668 171419: contig of 3752 bp in length.

FEATURES

source
1..171419
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-169P5"

ORIGIN

Alignment Scores:

Pred. No.: 9.82e-32 Length: 171419
Score: 359.50 Matches: 78
Percent Similarity: 61.24% Conservative: 1
Best Local Similarity: 60.47% Mismatches: 2
Query Match: 84.93% Indels: 48
DB: 2 Gaps: 1

US-10-624-932C-2_COPY_817_897 (1-81) x AC135142 (1-171419)

Qy 1 GlnLysIleIleSerSerLeuAspProCysArgAtgGlyAlaAspTirArgThrLeu 20
Db 19498 CAAAGATCATCGCCAGTCTGGACCCACCTCTGCAGCCGGCGCGGACTGGAGAACTCTA 19439
Qy 21 AlaGlnLysLeuHisLeuAsp----- 27
Db 19438 GCCCAGAAACTTCACCTGGACAGGTGGGTGGCGCTAGGCAGGGGACGCTGGCTGAGCAA 19379
Qy 27 ----- 27
Db 19378 GTGAGGCAGCCGGAGGTTTACAGTCTCTGGCCCCAACCGCTAGGGTATCTGAGGGCAG 19319
Qy 28 -----SerHisLeuSerPhePh 33
Db 19318 CCTGGAGTGGAGCCAGGCTGTGACAGACTGTGTCTTTTCTCCAGCCATCTTAGCTTCTT 19259
Qy 33 eAlaSerLysProSerProThrAlaMetIleLeuAsnLeuTirpGluAlaArgHisPhePr 53
Db 19258 TGCCTCCAAAGCCAGCCCTACAGCCATGATCTCAACCTATGGAGGGCAGCGCACTTCCC 19199
Qy 53 oAsnGlyAsnLeuSerGlnLeuAlaAlaValAlaGlyLeuGlyGlnProAspAlaGl 73
Db 19198 CAACGGCAACCTCGGCCAGCTGGCAGCAGCTGTGGCCGAGCTGGGCCCAACCAAGATGCTGG 19139
Qy 73 yLeuPheThrValSerGluAlaGlu 81
Db 19138 CCTCTTCACGGTGTGGAGGGCCGAG 19114

Search completed: September 9, 2005, 09:42:59
Job time : 3399.92 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 8, 2005, 20:54:46 ; Search time 418.907 Seconds
(without alignments)
1144.643 Million cell updates/sec

Title: US-10-624-932C-2_COPY_817_897

Perfect score: 423
Sequence: 1 QK1SSLDPPCRRGADWRTL.....AAVAGLGQPDAGLFTVSRAE 81

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters: -DEV=xlh
-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO spool_h/US10624932/runat_08092005_161705_15766/app_query.fasta_1.1386
-DB=N_Geneseq -QFMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10624932 @CGN 1.1.1052 @runat_08092005_161705_15766 -NCPU=6 -ICPU=3
-NO_MMAP -LARGQUERY -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_16Dec04:*
1: Geneseq1980a:*
2: Geneseq1990a:*
3: Geneseq2000a:*
4: Geneseq2001a:*
5: Geneseq2001bs:*
6: Geneseq2002a:*
7: Geneseq2002bs:*
8: Geneseq2003a:*
9: Geneseq2003bs:*
10: Geneseq2003cs:*
11: Geneseq2003ds:*
12: Geneseq2004a:*
13: Geneseq2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	423	100.0	2463	12 ADH71623	Adh71623 Human gen
2	423	100.0	2575	12 ADH71621	Adh71621 Human gen
3	423	100.0	2635	11 ADN95100	Adn95100 Human LEC
4	423	100.0	2697	6 ABK52891	Abk52891 Human net
5	423	100.0	2752	6 ABK37922	Abk37922 cDNA enco

6	423	100.0	2752	12 ADH71617	Adh71617 Human gen
7	423	100.0	2880	12 ADH71633	Adh71633 Human gen
8	423	100.0	2881	6 ABK49422	Abk49422 DNA enco
9	423	100.0	2881	10 ADG42568	Adg42568 Novel hum
10	423	100.0	2881	12 ADH71635	Adh71635 Human gen
11	423	100.0	2881	12 ADH71637	Adh71637 Human gen
12	423	100.0	2881	12 ADH71641	Adh71641 Human gen
13	423	100.0	2881	12 ADH71609	Adh71609 Human gen
14	423	100.0	2881	12 ADH71629	Adh71629 Human gen
15	423	100.0	2881	12 ADH71631	Adh71631 Human gen
16	423	100.0	2881	12 ADH71645	Adh71645 Human gen
17	423	100.0	2881	12 ADH71627	Adh71627 Human gen
18	423	100.0	2881	12 ADH71639	Adh71639 Human gen
19	423	100.0	2881	12 ADH71643	Adh71643 Human gen
20	423	100.0	2881	12 ADH71625	Adh71625 Human gen
21	423	100.0	2881	12 ADH71647	Adh71647 Human gen
22	423	100.0	2907	4 AAK52261	Aak52261 Human pol
23	423	100.0	3561	12 ADL06497	Adl06497 Human tum
24	423	100.0	3580	6 ABK15169	Abk15169 Human R&P
25	423	100.0	3700	4 AAC90958	Aac90958 Plaemid p
26	410	96.9	2697	6 AAS16843	Aas16843 Rat netri
27	410	96.9	3014	2 AAV52940	Av52940 Rat UNC-5
28	409	96.7	2881	12 ADH71649	Adh71649 Human gen
29	393	92.9	1269	4 AAS34792	Aas34792 cDNA enco
30	393	92.9	1269	10 ADC45950	Adc45950 Human neo
31	376	88.9	1787	2 AAV52941	Aav52941 Human UNC
32	368	87.0	1321	4 AAH99530	Aah99530 Human pro
33	364	86.1	574	4 AAD16536	Aad16536 Human nov
34	364	86.1	574	4 AAS34948	Aas34948 cDNA enco
35	364	86.1	574	6 ABS64126	Ab64126 Human apo
36	364	86.1	574	10 ADC46106	Adc46106 Human neo
37	364	86.1	574	10 AAD60435	Aad60435 Human sec
38	357.5	84.5	6522	8 AAL51204	Aal51204 Human gen
39	357.5	84.5	9582	4 AAD16560	Aad16560 Human nov
40	357.5	84.5	9582	6 ABS64150	Ab64150 Human apo
41	357.5	84.5	9582	10 AAD60459	Aad60459 Human sec
42	351.5	83.1	18772	4 AAD16561	Aad16561 Human nov
43	351.5	83.1	18772	6 ABS64151	Ab64151 Human apo
44	351.5	83.1	18772	10 AAD60460	Aad60460 Human sec
45	305	72.1	276	6 ABK52895	Abk52895 Human net

ALIGNMENTS

RESULT 1
ADH71623
ID ADH71623 standard; DNA; 2463 BP.
XX
AC ADH71623;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human gene of the invention NOV21h SEQ ID NO:519.
XX
KW ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX
OS Homo sapiens.
XX
PN WO2003102155-A2.
XX
PD 11-DEC-2003.
XX
PF 03-JUN-2003; 2003WO-US017430.
XX
PR 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 05-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.

PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 06-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-0386796P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386916P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388036P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 15-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
XX PA (CURA-) CURAGEN CORP.

XX PI Alsbrook JP, Alvarez E, Anderson DM, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigaru M, Patturajan M, Pena CE, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CM, Voss EZ, Zhong M;
XX PI Zhong H;
XX WPI: 2004-081935/08.
DR P-PSDB; ADH71624.
XX
PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
PS Example 21; SEQ ID NO 519; 1880pp; English.
XX
CC The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaeamic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.
XX
SQ Sequence 2463 BP; 470 A; 828 C; 721 G; 444 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.03e-43 Length: 2463
Score: 423.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12

US-10-624-932C-2_COPY_817_897 (1-81) x ADH71623 (1-2463)

Qy 1 GlnLysIleIleSerSerLeuAspProCysArgArgGlyAlaAspTrpArgThrLeu 20
Db 2212 CAGAAGATAATTTCCAGCTGGACCCACCTGTAGGGGGTGGCGACTGGCGACTCTG 2271

Qy 21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40
Db 2272 GCCCAGAAACTCCACCTGGACGCCATCTCAGCTTCCTTGGCTCCAGCCAGCCCCACA 2331

Qy 41 AlaMetIleLeuAenLeuTrpGluAlaArgHisPheProAnGlyAenLeuSerGlnLeu 60
Db 2332 GCCATGATCTCTCAACCTGTGGAGCGCGGCACATTCCCAACGCGCAACTCAGCGACTG 2391

Qy 61 AlaAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla 80
Db 2392 GCTGACGAGTGGCTGGACTGGGCGACGACGCTGGCTTCTTTCACAGTGTGCGAGGCT 2451

Qy 81 Glu 81
Db 2452 GAG 2454

RESULT 2
ADH71621
ID ADH71621 standard; DNA; 2575 BP.
XX
AC ADH71621;

XX 25-MAR-2004 (first entry)
DT Human gene of the invention NOV21g SEQ ID NO:517.
DE ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
XX anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;
KW cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
XX dyslipidaemia.
OS Homo sapiens.
XX WO2003102155-A2.
PN 11-DEC-2003.
XX 03-JUN-2003; 2003WO-US017430.
XX 03-JUN-2003; 2002US-0385120P.
PR 04-JUN-2003; 2002US-0385784P.
PR 05-JUN-2003; 2002US-0386041P.
PR 05-JUN-2003; 2002US-0386047P.
PR 06-JUN-2003; 2002US-0386376P.
PR 06-JUN-2003; 2002US-0386453P.
PR 06-JUN-2003; 2002US-0386864P.
PR 06-JUN-2003; 2002US-0387016P.
PR 07-JUN-2003; 2002US-0386796P.
PR 07-JUN-2003; 2002US-0386816P.
PR 07-JUN-2003; 2002US-0386931P.
PR 07-JUN-2003; 2002US-0386942P.
PR 07-JUN-2003; 2002US-0386971P.
PR 07-JUN-2003; 2002US-0387262P.
PR 08-JUN-2003; 2002US-0296960P.
PR 10-JUN-2003; 2002US-0387400P.
PR 10-JUN-2003; 2002US-0387535P.
PR 11-JUN-2003; 2002US-0387610P.
PR 11-JUN-2003; 2002US-0387625P.
PR 11-JUN-2003; 2002US-0387634P.
PR 11-JUN-2003; 2002US-0387668P.
PR 11-JUN-2003; 2002US-0387696P.
PR 11-JUN-2003; 2002US-0387702P.
PR 11-JUN-2003; 2002US-0387836P.
PR 11-JUN-2003; 2002US-0387859P.
PR 12-JUN-2003; 2002US-0387933P.
PR 12-JUN-2003; 2002US-0387934P.
PR 12-JUN-2003; 2002US-0387960P.
PR 12-JUN-2003; 2002US-0388022P.
PR 12-JUN-2003; 2002US-0388096P.
PR 13-JUN-2003; 2002US-0389123P.
PR 14-JUN-2003; 2002US-0389118P.
PR 14-JUN-2003; 2002US-0389120P.
PR 14-JUN-2003; 2002US-0389144P.
PR 14-JUN-2003; 2002US-0389146P.
PR 17-JUN-2003; 2002US-0389729P.
PR 17-JUN-2003; 2002US-0389742P.
PR 18-JUN-2003; 2002US-0389884P.
PR 19-JUN-2003; 2002US-0390066P.
PR 19-JUN-2003; 2002US-0390209P.
PR 21-JUN-2003; 2002US-0390763P.
PR 17-JUL-2003; 2002US-0396706P.
PR 06-AUG-2003; 2002US-0401628P.
PR 09-AUG-2003; 2002US-0402156P.
PR 09-AUG-2003; 2002US-0402256P.
PR 09-AUG-2003; 2002US-0402389P.
PR 12-AUG-2003; 2002US-0402786P.
PR 12-AUG-2003; 2002US-0402816P.
PR 12-AUG-2003; 2002US-0402821P.
PR 12-AUG-2003; 2002US-0402832P.
PR 13-AUG-2003; 2002US-0403448P.
PR 13-AUG-2003; 2002US-0403459P.
PR 13-AUG-2003; 2002US-0403531P.
PR 13-AUG-2003; 2002US-0403532P.

PR 13-AUG-2003; 2002US-0403563P.
PR 13-AUG-2003; 2002US-0406317P.
PR 15-AUG-2003; 2002US-0403617P.
PR 26-AUG-2003; 2002US-0406182P.
PR 26-AUG-2003; 2002US-0406355P.
PR 27-AUG-2003; 2002US-0406240P.
PR 12-SEP-2003; 2002US-0410084P.
PR 20-SEP-2003; 2002US-0412528P.
PR 23-SEP-2003; 2002US-0412731P.
PR 30-SEP-2003; 2002US-0414801P.
PR 30-SEP-2003; 2002US-0414839P.
PR 30-SEP-2003; 2002US-0414840P.
PR 30-SEP-2003; 2002US-0414954P.
PR 09-OCT-2003; 2002US-0417186P.
PR 09-OCT-2003; 2002US-0417406P.
PR 23-OCT-2003; 2002US-0420639P.
PR 28-OCT-2003; 2002US-0421156P.
PR 31-OCT-2003; 2002US-0422690P.
PR 01-NOV-2003; 2002US-0423130P.
PR 05-NOV-2003; 2002US-00423798.
PR 05-NOV-2003; 2002US-0423798P.
PR 12-NOV-2003; 2002US-0425453P.
XX (CURA-) CURAGEN CORP.
XX Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VV, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigaru M, Patturajan M, Pena CEA, Feyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shinkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
XX Zhong H;
XX WPI: 2004-081935/08.
DR P-PSDB; ADH71622.
XX New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
XX obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
PS Example 21; SEQ ID NO 517; 1880pp; English.
XX The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.
XX SQ Sequence 2575 BP; 490 A; 873 C; 754 G; 458 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1.09e-43 Length: 2575
Score: 423.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0
US-10-624-932C-2_COPY_817_897 (1-81) x ADH71621 (1-2575)
QY 1 GlnLysIleIleSerSerLeuAspProCysArgGlyAlaAspTrpArgThrLeu 20

|||||
 2356 CAGAGATAATTTCCAGGCTGGACCCACCTGTAGCGGGGTGCGACTGCGGACTCTG 2315
 Qy 21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40
 Db 2316 GCCCAGAACTCCACCTGACAGGACATCTCAGCTCTTTTGGCTCCAGGCCAGCCACACA 2375
 Qy 41 AlaMetIleLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
 Db 2376 GCCATGATCTCTCAACCTGTGGAGGCGCGGACATTCCTCCCAACGGCACTCAGCCAGCTG 2435
 Qy 61 AlaAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla 80
 Db 2436 CCTGCAGCAGTGGCTGGAGCTGGCCAGCCAGACGCTGCCTCTTCACAGTGTGGAGGCT 2495
 Qy 81 Glu 81
 Db 2496 GAG 2498
 RESULT 3
 ADN95100
 ID ADN95100 standard; DNA; 2635 BP.
 XX
 AC ADN95100;
 XX
 DT 01-JUL-2004 (first entry)
 DE Human LEC gene sequence SeqID22.
 XX
 KW growth; differentiation; blood endothelial cell; BEC;
 KW lymphatic endothelial cell; LEC; hereditary lymphoedema; VEGFR-3;
 KW lymphatic growth agent; VEGF-C; VEGF-D; angiogenic; cytotatic;
 KW vasotrophic; antiinflammatory; gene therapy; endothelial cell disorder;
 KW inflammatory disease; cancer metastasis; lymphatic system; gene; ds;
 KW human.
 XX
 OS Homo sapiens.
 XX
 FN WO2003080640-A1.
 XX
 PD 02-OCT-2003.
 XX
 PF 07-MAR-2003; 2003WO-US006900.
 XX
 PR 07-MAR-2002; 2002US-0363019P.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 PA (LICN) LICENTIA LTD.
 XX
 PI Alitalo K, Makinen T, Petrova T, Saharinen P, Saharinen J;
 XX
 DR WPI; 2003-876899/81.
 DR P-PSDB; ADN95115.
 XX
 PS Claim 23; SEQ ID NO 22; 176pp; English.
 XX
 CC This invention relates to a method of differentially modulating the
 CC growth or differentiation of blood endothelial cells (BEC) or lymphatic
 CC endothelial cells (LEC) comprises contacting endothelial cells with a
 CC composition comprising an agent that differentially modulates blood or
 CC lymphatic endothelial cells. Treating hereditary lymphoedema comprises
 CC identifying a human subject with lymphoedema and with a mutation in at
 CC least one allele of a gene encoding a LEC protein, where the mutation
 CC correlates with lymphoedema in human subjects, and with the proviso that
 CC the LEC protein is not VEGFR-3; and administering to the subject a
 CC composition comprising a lymphatic growth agent selected from VEGF-C or
 CC VEGF-D polypeptides and polynucleotides. The invention may be useful for
 CC the development of compounds with an angiogenic, cytotatic,
 CC vasotrophic or antiinflammatory activity or for gene therapy. The method
 CC is useful in modulating the growth or differentiation of blood
 CC endothelial cells or lymphatic endothelial cells, in treating hereditary
 CC lymphoedema, in screening for an endothelial cell disorder or
 CC predisposition to the disorder or in monitoring the efficacy or toxicity

CC of a drug on endothelial cells. The agent is useful in manufacturing a
 CC medicament for the differential modulation of blood vessel endothelial
 CC cell or lymphatic vessel endothelial cell growth or differentiation. The
 CC lymphatic growth agent may also be used in manufacturing a medicament for
 CC the treatment of hereditary lymphoedema resulting from a mutation in a
 CC LEC gene or of other diseases involving the lymphatic vessels, such as
 CC various inflammatory diseases and cancer metastasis via the lymphatic
 CC system. The present sequence is that of a human LEC/BEC differentially
 CC expressed gene which is related to the method of the invention. Note: The
 CC specification data for this patent did not form part of the printed
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 2635 BP; 483 A; 935 C; 722 G; 495 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1.13e-43 Length: 2635
 Score: 423.00 Matches: 81
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 11 Gaps: 0
 US-10-624-932C-2_COPY_817_897 (1-81) x ADN95100 (1-2635)
 Qy 1 GlnLysIleLeuSerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeu 20
 Db 1379 CAGAAGATAATTTCCAGCCTGGACCCACCTGTAGCGGGGTGCGACTGCGGACTCTG 1438
 Qy 21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40
 Db 1439 GCCCAGAACTCCACCTGGACGACATCTCAGCTCTTTTGGCTCCAGGCCAGCCACACA 1498
 Qy 41 AlaMetIleLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
 Db 1499 GCCATGATCTCTCAACCTGTGGAGGCGGACATTCCTCCCAACGGCACTCAGCCAGCTG 1558
 Qy 61 AlaAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla 80
 Db 1559 GCTGCAGCAGTGGCTGGACTGGCCAGCCAGACGCTGCCTCTTCACAGTGTGGAGGCT 1618
 Qy 81 Glu 81
 Db 1619 GAG 1621
 RESULT 4
 ABK52891
 ID ABK52891 standard; DNA; 2697 BP.
 XX
 AC ABK52891;
 XX
 DT 27-AUG-2002 (first entry)
 DE Human netrin binding membrane receptor UNC5H-1 DNA sequence #1.
 XX
 KW Netrin binding membrane receptor; receptor; UNC5H-1; gene; ds; human;
 KW neurotropic; neuroprotective; cytotatic; antiparkinsonian;
 KW cerebroprotective; cancer; central nervous system; CNS; stroke;
 XX Parkinson's disease; multiple sclerosis; Alzheimer's disease.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 1..2697
 FT /*tag= a
 FT /product= "Netrin binding membrane receptor UNC5H-1"
 XX
 PN WO200233080-A2.
 XX
 PD 25-APR-2002.
 XX
 PF 15-OCT-2001; 2001WO-EP011891.
 XX

PR 16-OCT-2000; 2000US-0240061P.
XX (FARB) BAYER AG.
XX Koehler RH;
XX WPI; 2002-463314/49.
DR P-PSDB; AAU97899.
XX Novel human netrin binding membrane receptor polypeptide and
PT polynucleotides for identifying modulating agents useful in treating
PT diseases e.g. Parkinson's disease, multiple sclerosis, stroke,
PT Alzheimer's disease.
XX Claim 1; Fig 1; 94pp; English.
XX This invention relates to the DNA and protein sequences of a novel
CC purified human netrin binding membrane receptor, UNC5H-1. The DNA
CC sequence of the invention is useful as a probe for detecting a nucleic
CC acid encoding the UNC5H-1 protein in a biological sample. The sequences
CC of the invention are useful to screen for agents which decrease the
CC activity of the UNC5H-1 protein. The sequences are also useful for
CC screening agents which regulate (modulate) the activity of the protein of
CC the invention. A pharmaceutical composition containing the protein of the
CC invention or a reagent that modulates the activity of the UNC5H-1 protein
CC may be useful for treating a UNC5H-1 dysfunction related disease such as
CC cancer or a central nervous system (CNS) disorders (e.g. Parkinson's
CC disease, multiple sclerosis, stroke and Alzheimer's disease). Fusion
CC proteins comprising the UNC5H-1 protein are useful for generating
CC antibodies and for in various assay systems, and the protein can be used
CC as a bait protein in a two-hybrid assay or three-hybrid assay. The method
CC of the invention is useful for detecting a coding sequence for the UNC5H-
CC 1 protein. The present sequence represents a DNA sequence encoding the
CC human netrin binding membrane receptor UNC5H-1 protein of the invention
XX
SQ Sequence 2697 BP; 503 A; 906 C; 807 G; 481 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.16e-43 Length: 2697
Score: 423.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x ABK52891 (1-2697)

QY 1 GlnLysIleLeuSerSerLeuAspProProCysArgArgGlyAlaAspTrrpArgThrLeu 20
DB 2449 CAGAAAGATTAATTCAGCCTGGACCACCCCTGTAGCGGGGTGGCGGAGCTGTG 2508

QY 21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40
DB 2509 GCCCAGAAATCCACCTGAGCAGCCATCTCAGCTTCTTTGGCTCCAGCCAGCCCA 2568

QY 41 AlaMetIleLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
DB 2569 GCCATGATCTCAACTGTGGGAGCGCGGCACTTCCCAACGGCAACTCAGCCAGCTG 2628

QY 61 AlaAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla 80
DB 2629 GCTGCAGCAGTGCTGGAGTGGCGCCAGCAGCAGCTGCGCTTTCACAGTGTGCGAGGCT 2688

QY 81 Glu 81
DB 2689 GAG 2691

RESULT 5
ID ABK37922
XX ABK37922 standard; CDNA; 2752 BP.
XX
XX ABK37922;
XX

DT 21-MAY-2002 (first entry)
XX cDNA encoding Human protein NOV1.
XX Human; NOVX; ss; gene; cardiomyopathy; atherosclerosis; diabetes;
KW cell signal processing disorder; metabolic disorder; obesity; infection;
KW anorexia; cancer-associated cachexia; cancer; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorders; dyslipidaemia; pain; asthma; hypertension;
KW osteoporosis; Crohn's disease; multiple sclerosis; angina pectoris;
KW myocardial infarction; ulcer; allergy; benign prostatic hypertrophy;
KW psychosis; neurological disorder; anxiety; schizophrenia;
KW manic depression; dementia; dyskinesia; Huntington's disease;
KW Gilles de la Tourette's syndrome; gene therapy.
XX
XX Homo sapiens.
XX WO200210216-A2.
XX 07-FEB-2002.
XX 30-JUL-2001; 2001WO-US024225.
XX 28-JUL-2000; 2000US-0221409P.
PR 04-AUG-2000; 2000US-0222840P.
PR 04-AUG-2000; 2000US-0223752P.
PR 04-AUG-2000; 2000US-0223762P.
PR 04-AUG-2000; 2000US-0223769P.
PR 04-AUG-2000; 2000US-0223770P.
PR 14-AUG-2000; 2000US-0225148P.
PR 15-AUG-2000; 2000US-0225392P.
PR 15-AUG-2000; 2000US-0225470P.
PR 16-AUG-2000; 2000US-0225697P.
PR 01-FEB-2001; 2001US-0263662P.
PR 05-APR-2001; 2001US-0281645P.
XX
XX (CURA-) CURAGEN CORP.
XX Padigaru M, Mezes P, Mishra V, Burgess C, Casman S, Grosse WM;
PI Alsobrook JP, Lepley DM, Gerlach VL, Macdougall JR, Smithson G;
XX WPI; 2002-180074/23.
DR P-PSDB; AAU85403.
XX
PT New isolated cytoplasmic, nuclear, membrane bound, or secreted
PT polypeptide, useful for treating cardiomyopathy, atherosclerosis,
PT infections, cancer, neurodegenerative, metabolic, hematopoietic and
PT immune disorders.
XX
PS Claim 9; Page 9-10; 213pp; English.
XX
CC The invention relates to an isolated cytoplasmic, nuclear, membrane
CC bound, or secreted polypeptide (NOVX, x= 1-14) their variants or mature
CC form. Also included are the nucleic acids encoding the NOVX proteins, a
CC vector comprising the nucleic acid, a cell comprising the vector, an anti-
CC NOVX antibody and modulators of NOVX. NOVX, the nucleic acid and the
CC antibody are useful for treating or preventing a NOVX-associated
CC disorder, where the disorder is selected from cardiomyopathy,
CC atherosclerosis, diabetes, a disorder related to cell signal processing
CC and metabolic pathway modulation, metabolic disorders, obesity,
CC infectious disease, anorexia, cancer-associated cachexia, cancer,
CC neurodegenerative disorders, Alzheimer's disease, Parkinson's disease,
CC immune disorders, haematopoietic disorders, and the various
CC dyslipidaemias, metabolic disturbances associated with obesity, the
CC metabolic syndrome X and wasting disorders associated with chronic
CC diseases, bacterial, fungal, protozoal and viral infections, pain,
CC bulimia, asthma, hypertension, urinary retention, osteoporosis, Crohn's
CC disease, multiple sclerosis, Albrit Hereditary Osteodystrophy, angina
CC pectoris, myocardial infarction, ulcer, allergy, benign prostatic
CC hypertrophy, and psychotic and neurological disorders, including anxiety,
CC schizophrenia, manic depression, delirium, dementia, and dyskinesias,
CC such as Huntington's disease and Gilles de la Tourette's syndrome. The
CC nucleic acid is useful in gene therapy. The present sequence encodes a

```
CC NOVX protein
XX SQ Sequence 2752 BP; 505 A; 937 C; 829 G; 481 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.2e-43 Length: 2752
Score: 423.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x ABK37922 (1-2752)

Qy 1 GlnlysllelleSerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrIeu 20
Db 2494 CAGAAGATAATTTCCAGCGCTGGACCCACCTGTAGCGGGTGGCGACTCGGCACTCTG 2553

Qy 21 AlaGlnlyLeuHleLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40
Db 2554 GCCCAGAAATCCACCTGGAGCGCATCTCAGCTTCITTTGGCTCCAGCCCGCCACCA 2613

Qy 41 AlaMetIleLeuAenLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
Db 2614 GCCATGATCTCAACCTGTGGAGCGGGGCACCTTCCCAACGGCAACCTCAGCCAGCTG 2673

Qy 61 AlalaAlaValAlaGlyIeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla 80
Db 2674 GCTGCGAGTGGTGGAGTGGCGAGCCAGCGTGGCCCTTTTCACAGTGTGCGAGGCT 2733

Qy 81 Glu 81
Db 2734 GAG 2736

RESULT 6
ADH71617
ID ADH71617 standard; DNA; 2752 BP.
XX AC ADH71617;
XX XX
XX 25-MAR-2004 (first entry)
XX DE Human gene of the invention NOV21e SEQ ID NO:513.
XX KW ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
XX KW anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;
XX KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
XX KW obesity; diabetes; infectious disease; metabolic syndrome X;
XX KW dyslipidaemia.
XX OS Homo sapiens.
XX XX
XX FN WO2003102155-A2.
XX PD 11-DEC-2003.
XX XX
XX PF 03-JUN-2003; 2003WO-US017430.
XX PR
XX PR 03-JUN-2002; 2002US-0385120P.
XX PR 04-JUN-2002; 2002US-0385784P.
XX PR 05-JUN-2002; 2002US-0386041P.
XX PR 05-JUN-2002; 2002US-0386047P.
XX PR 06-JUN-2002; 2002US-0386376P.
XX PR 06-JUN-2002; 2002US-0386453P.
XX PR 06-JUN-2002; 2002US-0386864P.
XX PR 06-JUN-2002; 2002US-0387016P.
XX PR 07-JUN-2002; 2002US-0386796P.
XX PR 07-JUN-2002; 2002US-0386816P.
XX PR 07-JUN-2002; 2002US-0386931P.
XX PR 07-JUN-2002; 2002US-0386942P.
XX PR 07-JUN-2002; 2002US-0386971P.
XX PR 07-JUN-2002; 2002US-0387262P.
XX PR 08-JUN-2002; 2002US-0296960P.

10-JUN-2002; 2002US-0387400P.
10-JUN-2002; 2002US-0387535P.
11-JUN-2002; 2002US-0387610P.
11-JUN-2002; 2002US-0387625P.
11-JUN-2002; 2002US-0387634P.
11-JUN-2002; 2002US-0387668P.
11-JUN-2002; 2002US-0387696P.
11-JUN-2002; 2002US-0387702P.
11-JUN-2002; 2002US-0387836P.
11-JUN-2002; 2002US-0387859P.
12-JUN-2002; 2002US-0387933P.
12-JUN-2002; 2002US-0387934P.
12-JUN-2002; 2002US-0387960P.
12-JUN-2002; 2002US-0388022P.
12-JUN-2002; 2002US-0388096P.
13-JUN-2002; 2002US-0389123P.
14-JUN-2002; 2002US-0389118P.
14-JUN-2002; 2002US-0389120P.
14-JUN-2002; 2002US-0389144P.
14-JUN-2002; 2002US-0389146P.
17-JUN-2002; 2002US-0389729P.
17-JUN-2002; 2002US-0389742P.
18-JUN-2002; 2002US-0389884P.
19-JUN-2002; 2002US-039006P.
19-JUN-2002; 2002US-0390209P.
21-JUN-2002; 2002US-0390763P.
17-JUN-2002; 2002US-0396706P.
06-AUG-2002; 2002US-0401628P.
09-AUG-2002; 2002US-0402156P.
09-AUG-2002; 2002US-0402256P.
09-AUG-2002; 2002US-0402389P.
12-AUG-2002; 2002US-0402786P.
12-AUG-2002; 2002US-0402816P.
12-AUG-2002; 2002US-0402821P.
12-AUG-2002; 2002US-0402832P.
13-AUG-2002; 2002US-0403458P.
13-AUG-2002; 2002US-0403531P.
13-AUG-2002; 2002US-0403532P.
13-AUG-2002; 2002US-0403533P.
15-AUG-2002; 2002US-0403617P.
26-AUG-2002; 2002US-0406182P.
27-AUG-2002; 2002US-0406355P.
27-AUG-2002; 2002US-0406240P.
12-SEP-2002; 2002US-0410084P.
20-SEP-2002; 2002US-0412528P.
23-SEP-2002; 2002US-0412731P.
30-SEP-2002; 2002US-0414801P.
30-SEP-2002; 2002US-0414839P.
30-SEP-2002; 2002US-0414840P.
30-SEP-2002; 2002US-0414954P.
09-OCT-2002; 2002US-0417186P.
09-OCT-2002; 2002US-0417406P.
23-OCT-2002; 2002US-0420639P.
28-OCT-2002; 2002US-0421156P.
31-OCT-2002; 2002US-0422690P.
01-NOV-2002; 2002US-0423130P.
05-NOV-2002; 2002US-0423798.
05-NOV-2002; 2002US-0423798P.
12-NOV-2002; 2002US-0425453P.

(CURA-) CURAGEN CORP.
Alesbrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
Catterton E, Crabtree-Bokor JR, Edinger SR, Ellerman K;
Ettenberg S, Gangoli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
Padigaru M, Patturajan M, Pena CEA, Peyman JA, Raha D, Raetelli L;
Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shinkets RA;
Smithson G, Spytek KA, Stone DU, Vernet CAM, Voss EZ, Zhong M;
Zhong H;
```

XX WP1; 2004-081935/08.
DR P-PSDB; ADH71618.
XX
XX PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
XX Example 21; SEQ ID NO 513; 1880pp; English.
XX
XX The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.
XX
SQ Sequence 2752 BP; 505 A; 937 C; 829 G; 481 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.2e-43 Length: 2752
Score: 423.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps:

US-10-624-932C-2_COPY_817_897 (1-81) x ADH71617 (1-2752)

QY 1 GlnLysIleLeuSerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeu 20
DB 2494 CAGAGATATTTCCAGCTGACCCACCTGTAGCGGGTGCAGACTGGCGGACTCTG 2553
QY 21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPheAlaSerIysProSerProThr 40
DB 2554 GCCCAGAAATCCACCTGCAGACGCACTCTCAGCTTCTTGGCTCCAAAGCCAGCCCA 2613
QY 41 AlaMetIleLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
DB 2614 GCCATGATCCTCAACTGTGGGAGCGCGGCACCTTCCCCAACGGCAACCTCAGCAGCTG 2673
QY 61 AlaAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla 80
DB 2674 GCTGACGACGTGGCTGGACTGGCCAGCAGACGCTGGCCCTCTTCACAGTGTTCGGAGGCT 2733
QY 81 Glu 81
DB 2734 GAG 2736

RESULT 7
ADH71633
ID ADH71633 standard; DNA; 2880 BP.
XX
XX AC ADH71633;
XX
XX DT 25-MAR-2004 (first entry)
XX
XX DE Human gene of the invention NOV21m SEQ ID NO:529.
XX
XX ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.

XX OS Homo sapiens.
XX PN WO2003102155-A2.
XX PD 11-DEC-2003.
XX
XX 03-JUN-2003; 2003WO-US017430.
XX
XX 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 06-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 06-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-0386798P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387931P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.

```

PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
XX
PA (CURA-) CURAGEN CORP.
XX
XX Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Craterton E, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangoli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VV, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigaru M, Patturajan M, Pena CE, Feyman JA, Rana D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;
XX
XX WPI; 2004-081935/08.
DR P-PSDB; ADH71634.
XX
XX New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
XX Example 21; SEQ ID NO 529; 1880pp; English.
XX
XX The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.
XX
XX SQ Sequence 2880 BP; 527 A; 984 C; 867 G; 502 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.27e-43 Length: 2880
Score: 423.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x ADH71633 (1-2880)

QY 1 GlnlysllelleSerSerleuAspProProCysArgArgGlyAlaAspTrrpArgThrleu 20
DB 2537 CAGAAAGATAAATTCAGCTGGACCCACCCCTGTAGCGGGGTGGCGACTGGGAGCTGTG 2596

QY 21 AlaGlnlyLeuHisLeuAspSerHisLeuSerPheAlaSerLysProSerProthr 40
DB 2597 GCCCAGAAACTCCACTGGACAGCCATCTCAGCTTCCTTGTGCTCAACGCCGCCCCACA 2656

QY 41 AlaMetIleLeuAsnLeuTrrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
DB 2657 GCCATGATCCTCAACCTGTGGGAGCGGGGCACTTCCGCAACGGCAACCTCAGCCAGCTG 2716
```

```

QY 61 AlalaalavalAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla 80
DB 2717 GCTGCAGCAGTGGCTGGACTGGGCCAGCCAGCTGGCCTCTTTCACAGTGTGGAGGCT 2776

QY 81 Glu 81
DB 2777 GAG 2779

RESULT 8
ABK49422
ID ABK49422 standard; DNA; 2881 BP.
XX
AC ABK49422;
XX
XX 15-JUL-2002 (first entry)
XX DNA encoding human UNC5-like protein NOV1.
XX Human; NOVX polypeptide; cardiomyopathy; atherosclerosis; cancer;
KW cell signal processing; metabolic pathway modulation; cancerous tissue;
KW antibody; diabetes; transgenic animal; UNC5-like protein; NOV1;
KW chromosome 13; Gene; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH CDS 87..2786
FT /*tag= a
FT /product= "Human UNC5-like protein NOV1"
XX
XX WO200229038-A2.
XX
XX 11-APR-2002.
XX
XX 04-OCT-2001; 2001WO-US031377.
XX
XX 04-OCT-2000; 2000US-0237862P.
XX (CURA-) CURAGEN CORP.
XX Herrmann JL, Rastelli L, Shimkets RA;
XX WPI; 2002-340104/37.
XX P-PSDB; AAU79939.
XX Novel isolated NOVX polypeptide, and encoded polynucleotide, useful for
XX treating cardiomyopathy, atherosclerosis, and cancer.
XX Claim 8; Page 7-8; 180pp; English.
XX
XX The present invention relates to a new NOVX polypeptide having a 900
CC (NOV1), 4349 (NOV2), 940 (NOV3), 798 (NOV4), 865 (NOV5), or 331 (NOV6)
CC residue amino acid sequence, as given in the specification. The novel
CC polypeptide, and its encoding polynucleotide, are used to treat
CC cardiomyopathy, atherosclerosis, cancer or a disease related to cell
CC signal processing and metabolic pathway modulation, in a human. Detecting
CC the polypeptide or polynucleotide is useful for identifying cancerous
CC tissue. The antibody can be used to treat diabetes or cancer. The host
CC cells can be used to produce non-human transgenic animals useful in drug
CC screening. The present nucleic acid sequence is that of the human UNC5-
CC like NOV1 gene located on chromosome 13. This sequence encodes the human
CC UNC5-like protein NOV1 of the invention
XX
XX SQ Sequence 2881 BP; 526 A; 985 C; 868 G; 502 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.27e-43 Length: 2881
Score: 423.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
```

US-10-624-932C-2_COPY_817_897 (1-81) x ABK49422 (1-2881)

QY 1 GlnLysIleLeuSerLeuAspProProCysArgArgGlyAlaAspTirArgThrLeu 20
 Db 2538 CAGAAGATAATTTCCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTG 2597

QY 21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40
 Db 2598 GCCCAGAAACTCCACCTGGACGCCATCTCAGCTCTTTGGCTCCAGCCGCCAGCCACCA 2657

QY 41 AlaMetIleLeuAsnLeuTirGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
 Db 2658 GCCATGATCTCAACCTGTGGAGCGCGGCACCTTCCCACAGCGCAACCTCAGCCAGCTG 2717

QY 61 AlaAlaAlaValAlaGlyLeuGlnProAspAlaGlyLeuPheThrValSerGluAla 80
 Db 2718 GCTGCAGCAGTGGCTGGACTGGGCCAGCCAGACGCTGGCCTCTTTCACAGTGTGCGAGGCT 2777

QY 81 Glu 81
 Db 2778 GAG 2780

RESULT 9
 ID ADG42568 standard; cDNA; 2881 BP.
 AC ADG42568;
 XX XX
 DT 26-FEB-2004 (first entry)
 XX XX
 DE Novel human NOV1 cDNA.
 XX XX
 KW cytostatic; gene therapy; NOVX-agonist; NOVX-antagonist; pharmaceutical;
 KW NOVX-associated disorder; cancer; human; gene; ss.
 OS Homo sapiens.
 OS US2003204052-A1.
 XX XX
 PD 30-OCT-2003.
 XX XX
 PF 04-OCT-2001; 2001US-00970944.
 XX XX
 PR 04-OCT-2000; 2000US-0237862P.
 XX XX
 PA (HERR/) HERRMANN J L.
 PA (RAST/) RASTELLI L.
 PA (SHIM/) SHIMKETS R A.
 XX XX
 PI Herrmann JL, Rastelli L, Shinkets RA;
 XX XX
 DR WPI; 2003-900673/82.
 DR P-PSDB; ADG42569.
 XX XX
 PT New NOVX gene or NOVX-specific antibody, useful for preparing a
 PT composition for treating or preventing a NOVX-associated disorder, e.g.,
 PT cancer.
 XX XX
 PS Claim 9; SEQ ID NO 1; 118pp; English.
 XX XX
 CC The invention describes a new isolated polypeptide comprising: a
 CC polypeptide or its mature form comprising a sequence not given in the
 CC specification; or a variant of (A), where one or more amino acid residues
 CC in the variant differs in no more than 15% from the amino acid sequence
 CC of the mature form. The pharmaceutical composition may be administered
 CC via oral, transdermal, rectal or parenteral route. The polypeptide,
 CC nucleic acid or antibody is useful for preparing a composition for
 CC treating or preventing a NOVX-associated disorder, e.g., cancer. This
 CC sequence encodes a human NOVX protein.
 XX XX
 SQ Sequence 2881 BP; 526 A; 987 C; 866 G; 502 T; 0 U; 0 Other;


```
XX PD 11-DEC-2003.
XX PF 03-JUN-2003; 2003WO-US017430.
XX PF 03-JUN-2002; 2002US-0385120P.
XX PF 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 06-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 06-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-0387096P.
PR 07-JUN-2002; 2002US-0387166P.
PR 07-JUN-2002; 2002US-0387933P.
PR 07-JUN-2002; 2002US-0388593P.
PR 07-JUN-2002; 2002US-0388697P.
PR 07-JUN-2002; 2002US-0388711P.
PR 07-JUN-2002; 2002US-0388726P.
PR 07-JUN-2002; 2002US-0388762P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388098P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389723P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396708P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402818P.
PR 12-AUG-2002; 2002US-0402821P.
PR 13-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406244P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.

PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-04231130P.
PR 05-NOV-2002; 2002US-04232798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
XX PA (CURA-) CURAGEN CORP.
XX PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangoli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev V, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigaru M, Patturajan M, Pena CEA, Peyman JA, Raba D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shinkets RA;
PI Smithson G, Spytek KA, Stone DU, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;
XX WI: 2004-081935/08.
XX P-PSDB, ADH71638.
XX DR New NOVX polypeptides and nucleic acid molecules useful for preventing or
XX PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
XX PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX PS Example 21; SEQ ID NO 533; 1880pp; English.
XX CC The invention relates to a novel isolated polypeptide (NOVX). A
XX CC polypeptide of the invention has cytostatic, immunomodulator,
XX CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
XX CC antilipraemic activity, and may have a use in gene therapy, and as a
XX CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
XX CC any of the 303 fully defined nucleotide sequences given in the
XX CC specification. The polypeptide is useful in the manufacture of a
XX CC medicament for treating a syndrome associated with a human disease. The
XX CC polypeptide, polynucleotide and antibody are useful in diagnosing,
XX CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
XX CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
XX CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
XX CC further used as hybridisation probes, in chromosome mapping, tissue
XX CC typing, preventive medicine, and pharmacogenomics. The present sequence
XX CC encodes a NOVX polypeptide of the invention.
XX SQ Sequence 2881 BP; 527 A; 985 C; 867 G; 502 T; 0 U; 0 Other;

Alignment Scores:
Pred. NO.: 1.27e-43 Length: 2881
Score: 423.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x ADH71637 (1-2881)

Qy 1 GlnlyseileSerSerLeuAspProCyeArgGlyAlaAspTrpArgThrLeu 20
Db 2338 CAGAAGATAATTTCCAGCTGGAGCCACCTCTGAGCGGGGTGCCGACTGCGGACTCTG 2597
Qy 21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40
Db 2598 GCCCAGAAACTCCACCTGGACGACCATCTCAGCTCTTTGCTCCAGCCAGCCCCACA 2657
Qy 41 AlaMetIleLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
Db 2658 GCCATGATCTCTCAACTGTGGAGCGCGGACCTTCCCAACGCGCAACTCAGCAGCTG 2717
Qy 61 AlaAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla 80
Db 2718 GCTGACGAGTGGCTGGACTGGGCGCAGCCAGACGCTGCGCTCTTTCCACAGTGTGGAGGCT 2777
```

Qy 81 Glu 81
Db 2778 GAG 2780
RESULT 12
ID ADH71641
XX ADH71641 standard; DNA; 2881 BP.
AC
XX ADH71641;
XX 25-MAR-2004 (first entry)
XX Human gene of the invention NOV21q SEQ ID NO:537.
DE
XX ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipaeamic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX
XX Homo sapiens.
OS
XX WO2003102155-A2.
XX
XX 11-DEC-2003.
XX
XX 03-JUN-2003; 2003WO-US017430.
PF
XX 03-JUN-2002; 2002US-0385120P.
XX 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 05-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 07-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387658P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390066P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.

PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 15-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.

XX (CURA-) CURAGEN CORP.

XX Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ,
Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K,
Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X,
Gusev VI, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR,
MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS,
Padigaru M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L,
Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA,
Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M,
Zhong H;
XX

XX WPI; 2004-081935/08.
DR P-PSDB; ADH71642.

XX New NOVX polypeptides and nucleic acid molecules useful for preventing or
treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

XX Example 21; SEQ ID NO 537; 1880pp; English.

XX The invention relates to a novel isolated polypeptide (NOVX). A
polypeptide of the invention has cytostatic, immunomodulator,
neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
antilipaeamic activity, and may have a use in gene therapy, and as a
vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
any of the 303 fully defined nucleotide sequences given in the
specification. The polypeptide is useful in the manufacture of a
medicament for treating a syndrome associated with a human disease. The
polypeptide, polynucleotide and antibody are useful in diagnosing.
treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
further used as hybridisation probes, in chromosome mapping, tissue
typing, preventive medicine, and pharmacogenomics. The present sequence
encodes a NOVX polypeptide of the invention.

XX SQ Sequence 2881 BP; 526 A; 986 C; 867 G; 502 T; 0 U; 0 Other;

Alignment Scores:

```
Pred. No.: 1.27e-43 Length: 2881
Score: 423.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-10-624-932c-2_COPY_817_897 (1-81) x ADH71641 (1-2881)

Qy 1 GlnLysIleSerLeuAspProProCysArgGlyAlaAspTriaArgThrLeu 20
2538 CAGAGATATTTCCAGCTGACCCACCTGTAGCGGGTGGCGGACTCTG 2597
Db

Qy 21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPheAlaSerLysProSerProThr 40
2598 GCCAGAAATCTCACCTGACAGCATCTCAGCTTCTTGCTCCAAAGCCAGCCACCA 2657
Dy

Qy 41 AlaMetIleLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
2658 GCCATGATCTCAACCTGTGGAGCGGGGCACTTCCCAACGGCAACCTCAGCCAGCTG 2717
Dy

Qy 61 AlaAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla 80
2718 GCTGAGCAGTGGCTGGACTGGCCAGCCAGACGCTGGCCTCTTCACAGTGTGGAGGCT 2777
Dy

Qy 81 Glu 81
2778 GAG 2780
Dy

RESULT 13
ADH71609
ID ADH71609 standard; DNA; 2881 BP.
XX
AC ADH71609;
XX
XX
DT 25-MAR-2004 (first entry)
XX
XX
DE Human gene of the invention NOV21a SEQ ID NO:505.
XX
KW ds; Gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipaeamic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX
XX Homo sapiens.
XX
XX WO2003102155-A2.
XX
XX 11-DEC-2003.
XX
XX 03-JUN-2003; 2003WO-US017430.
XX
PR 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 06-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 06-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-038796P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386943P.
PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387950P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 13-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390008P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 21-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 27-AUG-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-0423798.
PR 05-NOV-2002; 2002US-0423798.
PR 12-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
XX
XX (CURA-) CURAGEN CORP.
XX
PI Alsbrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigaru M, Patturajan M, Pena CEA, Peyman JA, Raha D, Raetelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shinkets RA;
PI Smithson G, Spytek KA, Stone DU, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;
XX
XX WPI; 2004-081935/08.
XX P-PSDB; ADH71610.
XX
XX New NOVX polypeptides and nucleic acid molecules useful for preventing or
```

PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX Example 21; SEQ ID NO 505; 1880pp; English.

XX The invention relates to a novel isolated polypeptide (NOVX). A
XX polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing.
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.

SQ Sequence 2881 BP; 526 A; 985 C; 868 G; 502 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.27e-43 Length: 2881
Score: 423.00 Matches: 81
Percent Similarity: 100.00% Conservations: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x ADH71609 (1-2881)

Qy 1 GlnYslllelleSerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrIleu 20
Db 2538 CAGAAGATAATTCAGCGCTGGACCCACCTGTAGCGGGTGGCGACTGCTG 2597
Qy 21 AlaGlnYsleuHsLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40
Db 2598 GCCCAGAACTCCACCTGGAGCGCACTCAGCTTCCTCCAGCCAGCCGCCACA 2657
Qy 41 AlaMetlleLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
Db 2658 GCCATGATCTCAACCTGTGGAGCGCGGCACCTCCCAACGGCAACCTCAGCCAGCTG 2717
Qy 61 AlalalavalAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla 80
Db 2718 GCTGAGCAGTGGCTGGACTGGCGCAGCCAGACGCTGGCCTCTTTCACAGTGTGGAGGCT 2777

Qy 81 Glu 81

Db 2778 GAG 2780

RESULT 14

ADH71629

ID ADH71629 standard; DNA; 2881 BP.

XX ADH71629;

XX 25-MAR-2004 (first entry)

XX Human gene of the invention NOV21k SEQ ID NO:525.

XX ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.

XX Homo sapiens.

XX WO2003102155-A2.

XX

PD 11-DEC-2003.
XX 03-JUN-2003; 2003WO-US017430.
XX 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 06-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 06-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-0386796P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 15-AUG-2002; 2002US-0403617P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.

PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Alsebrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Cateron E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Etkenberg S, Gangoli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Guev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI MacLachlan T, Malyankar UM, Mexick AJ, Millet I, Mishra VS;
PI Padigaru M, Patcurajan M, Pena CE, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Szytek KA, Stone DJ, Vernhet CAM, Voss EZ, Zhong M;
PI Zhong H;
XX
XX WPI; 2004-081935/08.
DR P-PSDB; ADH71630.
DR
XX
XX New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
XX Example 21; SEQ ID NO 525; 1880pp; English.
XX
XX The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.
XX
SQ Sequence 2881 BP; 526 A; 986 C; 868 G; 501 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.27e-43 Length: 2881
Score: 423.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps:

US-10-624-932C-2_COPY_817_897 (1-81) x ADH71629 (1-2881)

Qy 1 GlnYvlllelSerLeuAspProCysArgArgGlyAlaAspTrpArgThrLeu 20
Db 2538 CAGAGATAAATTCAGCTGGACCCCTGTAGCGGGGTGCGACTGGCGGACTGTG 2597

Qy 21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPheAlaSerLysProSerProThr 40
Db 2598 GCCAGAAATCCACCTGACGAGCATCTCAGCTTCTTTGCTCCAGCCGCCCCACA 2657

Qy 41 AlaMetlleLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
Db 2658 GCCATGATCCTCAACCTGTGGAGCGGGGACATTTCCCAACGGCAACCTCAGCCAGCTG 2717

Qy 61 AlaAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla 80
Db 2718 GCTGCAGCAGTGCGCTGGAGTGGGCCAGCCAGCAGCTGCGCTCTTTCACAGTGTGGAGGCT 2777

Qy 81 Glu 81
Db 2778 GAG 2780
RESULT 15
ADH71631
ID ADH71631 standard; DNA; 2881 BP.
XX
XX AC ADH71631;
XX
XX DT 25-MAR-2004 (first entry)
XX
XX DE Human gene of the invention NOV211 SEQ ID NO:527.
XX
XX KW ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX
XX OS Homo sapiens.
XX
XX PN WO2003102155-A2.
XX
XX PD 11-DEC-2003.
XX
XX PF 03-JUN-2003; 2003WO-US017430.
XX
XX PR 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 06-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 06-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-0386796P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 11-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390066P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 8, 2005, 23:51:22 ; Search time 129.111 Seconds
(without alignments)
1026.543 Million cell updates/sec

Title: US-10-624-932C-2_COPY_817_897

Perfect score: 423
Sequence: 1 QKIISLDPPCRGADWRTL.....AAVAGLQPDAGLFTVSEAE 81

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool_h/US10624932/runat_08092005_161706_15822/app_query.fasta_1.1386
-DB=Issued_Patents_NA -QWMT=fastcap -SUFFIX=rni -MINMATCH=0.1 -LOOPEXT=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10624932 @CIGN 1.1 187 @runat 08092005_161706_15822 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=10 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:
1: /cgn2_6/ptodata/1/ina/5A COMB.seq:
2: /cgn2_6/ptodata/1/ina/5B COMB.seq:
3: /cgn2_6/ptodata/1/ina/6A COMB.seq:
4: /cgn2_6/ptodata/1/ina/6B COMB.seq:
5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq:
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	410	96.9	3014	2 US-08-808-982-1	Sequence 1, Appli
2	410	96.9	3014	3 US-09-306-902A-1	Sequence 1, Appli
3	376	88.9	1787	2 US-08-808-982-2	Sequence 2, Appli
4	376	88.9	1787	3 US-09-306-902A-2	Sequence 2, Appli
5	357.5	84.5	19326	4 US-09-949-016-16776	Sequence 16776, A
6	221	52.2	3008	2 US-09-949-016-4794	Sequence 4794, Ap
7	198	46.8	2831	2 US-08-808-982-3	Sequence 3, Appli
8	198	46.8	2831	3 US-09-306-902A-3	Sequence 3, Appli
9	190	44.9	1968	4 US-09-969-532-31	Sequence 31, Appli
10	190	44.9	2001	4 US-09-969-532-29	Sequence 29, Appli
11	190	44.9	2010	4 US-09-969-532-27	Sequence 27, Appli
12	190	44.9	2043	4 US-09-969-532-25	Sequence 25, Appli

13	190	44.9	2661	4 US-09-969-532-15	Sequence 15, Appli
14	190	44.9	2694	4 US-09-969-532-13	Sequence 13, Appli
15	190	44.9	2703	4 US-09-969-532-11	Sequence 11, Appli
16	190	44.9	2736	4 US-09-969-532-9	Sequence 9, Appli
17	190	44.9	3411	4 US-09-969-532-33	Sequence 33, Appli
18	141	33.3	1507	4 US-08-270-767-1278	Sequence 1278, Ap
19	141	33.3	1507	4 US-08-270-767-16560	Sequence 16560, A
20	133	31.4	114139	4 US-09-949-016-16536	Sequence 16536, A
c 21	99	23.4	601	4 US-09-949-016-170040	Sequence 170040,
c 22	99	23.4	601	4 US-09-949-016-170041	Sequence 170041,
23	81	19.1	4935	2 US-08-631-097-3	Sequence 3, Appli
24	81	19.1	5886	3 US-08-810-712-9	Sequence 9, Appli
25	71.5	16.9	3625	4 US-09-023-655-1180	Sequence 1180, Ap
26	71	16.8	28933	4 US-09-949-016-16095	Sequence 16095, A
27	71	16.8	31414	4 US-09-949-016-12717	Sequence 12717, A
c 28	70	16.5	1519	4 US-09-474-699-8	Sequence 8, Appli
c 29	70	16.5	12385	3 US-09-823-862-3	Sequence 3, Appli
c 30	70	16.5	14706	4 US-09-949-016-16122	Sequence 16122, A
31	69.5	16.4	1287	4 US-09-799-451-469	Sequence 469, App
32	69.5	16.4	95109	4 US-09-949-016-16027	Sequence 16027, A
33	69.5	16.4	162914	4 US-09-949-016-15578	Sequence 15578, A
c 34	68.5	16.2	1929	3 US-09-040-229B-7	Sequence 7, Appli
35	68.5	16.2	3971	4 US-09-876-176-1	Sequence 1, Appli
36	68.5	16.2	4108	4 US-09-919-172-15	Sequence 15, Appli
c 37	68	16.1	351	4 US-09-894-844-32	Sequence 32, Appli
38	68	16.1	80269	4 US-09-949-016-15681	Sequence 15681, A
39	68	16.1	84425	4 US-09-949-016-17402	Sequence 17402, A
40	68	16.1	4403765	3 US-09-103-840A-2	Sequence 2, Appli
c 41	68	16.1	4411529	3 US-09-103-840A-1	Sequence 1, Appli
42	67.5	16.0	3469	4 US-09-560-385A-23	Sequence 23, Appli
43	67.5	16.0	3511	4 US-09-560-385A-19	Sequence 19, Appli
44	67.5	16.0	3585	4 US-09-560-385A-21	Sequence 21, Appli
45	67.5	16.0	3621	4 US-09-560-385A-17	Sequence 17, Appli

ALIGNMENTS

RESULT 1

US-08-808-982-1
; Sequence 1, Application US/08808982
; Patent No. 5939271
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; APPLICANT: Leonardo, E. David
; APPLICANT: Hink, Lindsay
; APPLICANT: Masu, Masayuki
; APPLICANT: Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,982
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:

```
;
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 3014 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
US-08-808-982-1
Alignment Scores:
Pred. No.: 1.63e-46 Length: 3014
Score: 410.00 Matches: 78
Percent Similarity: 97.53% Conservative: 1
Best Local Similarity: 96.30% Mismatches: 2
Query Match: 96.93% Indels: 0
DB: 2 Gaps: 0
US-10-624-932C-2_COPY_817_897 (1-81) x US-08-808-982-1 (1-3014)
Qy 1 GlnlylleiSerSerLeuAspProProCysArgArgGlyAlaAspTTPArgThrLeu 20
Db 2449 CAAAGATCATCGCAGTCTGGACCCCTGCAGCGCGCGCGCGACTGGAGAACTCTA 2508
Qy 21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40
Db 2509 GCCCAGAAATTCACCTGGACAGCATCTTAGCTTTTGGCTTCCAAGCCCGAGCCCTACA 2568
Qy 41 AlaMetlleLeuAnLeuTTPGluAlaArgHisPheProAnGlyAsnLeuSerGlnLeu 60
Db 2569 GCCATGATCTCTCAACCTATGGGAGGCACGGCACTTCCCAACCGCAACCTCGGCAGCTG 2628
Qy 61 AlaAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla 80
Db 2629 GCACAGCTGTGGCGGAGTGGGCAACCAACCATGCTGGCCCTCTTCACGGTGTGGAGGCC 2688
Qy 81 Glu 81
Db 2689 GAG 2691
RESULT 2
US-09-306-902A-1
; Sequence 1, Application US/09306902A
; Patent No. 6277585
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindsey
; Masu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/306,902A
; FILING DATE: 07-May-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
;
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 3014 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-306-902A-1
Alignment Scores:
Pred. No.: 1.63e-46 Length: 3014
Score: 410.00 Matches: 78
Percent Similarity: 97.53% Conservative: 1
Best Local Similarity: 96.30% Mismatches: 2
Query Match: 96.93% Indels: 0
DB: 3 Gaps: 0
US-10-624-932C-2_COPY_817_897 (1-81) x US-09-306-902A-1 (1-3014)
Qy 1 GlnlylleiSerSerLeuAspProProCysArgArgGlyAlaAspTTPArgThrLeu 20
Db 2449 CAAAGATCATCGCAGTCTGGACCCCTGCAGCGCGCGCGCGACTGGAGAACTCTA 2508
Qy 21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40
Db 2509 GCCCAGAAATTCACCTGGACAGCATCTTAGCTTTTGGCTTCCAAGCCCGAGCCCTACA 2568
Qy 41 AlaMetlleLeuAnLeuTTPGluAlaArgHisPheProAnGlyAsnLeuSerGlnLeu 60
Db 2569 GCCATGATCTCTCAACCTATGGGAGGCACGGCACTTCCCAACCGCAACCTCGGCAGCTG 2628
Qy 61 AlaAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla 80
Db 2629 GCACAGCTGTGGCGGAGTGGGCAACCAACCATGCTGGCCCTCTTCACGGTGTGGAGGCC 2688
Qy 81 Glu 81
Db 2689 GAG 2691
RESULT 3
US-08-808-982-2
; Sequence 2, Application US/08808982
; Patent No. 5939271
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; APPLICANT: Hink, Lindsey
; APPLICANT: Masu, Masayuki
; APPLICANT: Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,982
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
```


TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1787 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-808-982-2

Alignment Scores:
Pred. No.: 4.06e-42 Length: 1787
Score: 376.00 Matches: 77
Percent Similarity: 92.77% Conservative: 0
Best Local Similarity: 92.77% Mismatches: 4
Query Match: 88.89% Indels: 2
DB: 2 Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x US-08-808-982-2 (1-1787)

Qy 1 GlnlysllelleSerSerLeuAspProProCysArgArgGlyAlaAspTTPArgThrLeu 20
Db 1420 CAGAGATAATTTCCAGCTGGACCCACCTGTAGCGGGGTGCGACTGCGGACTCTG 1479
Qy 21 AlaGlnlyLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40
Db 1480 GCCCAGAAATCCACCTGCAGCCATCTCAGCTTCTTTGGCTTCCAGCCGAGCCACCA 1539
Qy 41 AlaMetlleLeuAenLeuTTPGluAlaArgHisPheProAenGlyAenLeuSerGlnLeu 60
Db 1540 GCCATGATCTCCACCTGTGGAGCGCGGCACCTTCCCAACGGCACTCAGCCAGCTG 1599
Qy 61 AlaAlaAlaValAlaGlyLeuGlyClnProAspAlaGlyLeu-PheThrVal-SerGluA 80
Db 1600 GCTCAGCAGTGGCTGGGACTGGCCAGCAGACGGTGGCTTCTTTCACAGTGTTCGGAGG 1659
Qy 80 laGlu 81
Db 1660 CTGAG 1664

RESULT 4

US-09-306-902A-2
Sequence 2, Application US/09306902A
Patent No. 627585
GENERAL INFORMATION:

APPLICANT: Tessier-Lavigne, Marc

Leonardo, E. David

Hink, Lindsey

Masu, Masayuki

Kazuko, Keino-Masu

TITLE OF INVENTION: Netrin Receptors

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/306,902A

FILING DATE: 07-May-1999

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: UC96-217

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1787 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cdna
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-306-902A-2

Alignment Scores:
Pred. No.: 4.06e-42 Length: 1787
Score: 376.00 Matches: 77
Percent Similarity: 92.77% Conservative: 0
Best Local Similarity: 92.77% Mismatches: 4
Query Match: 88.89% Indels: 2
DB: 3 Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x US-09-306-902A-2 (1-1787)

Qy 1 GlnlysllelleSerSerLeuAspProProCysArgArgGlyAlaAspTTPArgThrLeu 20
Db 1420 CAGAGATAATTTCCAGCTGGACCCACCTGTAGCGGGGTGCGACTGCGGACTCTG 1479
Qy 21 AlaGlnlyLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40
Db 1480 GCCCAGAAATCCACCTGCAGCCATCTCAGCTTCTTTGGCTTCCAGCCGAGCCACCA 1539
Qy 41 AlaMetlleLeuAenLeuTTPGluAlaArgHisPheProAenGlyAenLeuSerGlnLeu 60
Db 1540 GCCATGATCTCCACCTGTGGAGCGCGGCACCTTCCCAACGGCACTCAGCCAGCTG 1599
Qy 61 AlaAlaAlaValAlaGlyLeuGlyClnProAspAlaGlyLeu-PheThrVal-SerGluA 80
Db 1600 GCTCAGCAGTGGCTGGGACTGGCCAGCAGACGGTGGCTTCTTTCACAGTGTTCGGAGG 1659
Qy 80 laGlu 81
Db 1660 CTGAG 1664

RESULT 5

US-09-949-016-16776/c
Sequence 16776, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 16776

LENGTH: 19326

TYPE: DNA

ORGANISM: Human

US-09-949-016-16776

Alignment Scores:

Pred. No.: 4.42e-38 Length: 19326

Score: 357.50 Matches: 81

Percent Similarity: 50.94% Conservative: 0

Best Local Similarity: 50.94% Mismatches: 0

```
Query Match: 84.52% Indels: 78
DB: 4 Gaps: 1

US-10-624-932C-2_COPY_817_897 (1-81) x US-09-949-016-16776 (1-19326)
Qy 1 GlnlysllelleSerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeu 20
Db 18788 CAGAGATATTTTCAGCCTGGACCCACCTGTAGGGGGGTGCGACTGGCGACTCTG 18729
Qy 21 AlaGlnlyslleuHisLeuAsp----- 27
Db 18728 GCCCAGAAATCCACTGGACAGGTGGCGGGAGAGGGGCGACAGAGGGCCCTGCGCAGGCC 18669
Qy 27 ----- 27
Db 18668 ACCGACAGTCTGCCCCGGCGGGGTGGGTGGAGGAGGAGGCCCTGTGGGGGCTG 18609
Qy 27 ----- 27
Db 18608 TGCCGCATCTACTAGTGGCGGGGAGTCATTGTGTTGGCTTCGGGGAGGCCCTGCCCT 18549
Qy 27 ----- 27
Db 18548 GGGGTGGGCCAGGGGGGAGAGGTGTGACGTGGGGCCAGGCCAGGCTGTGACGGGCC 18489
Qy 28 -----8erHisLeuSerPhePheAlaSerlyseProSerProThrAlaMetI1 43
Db 18488 CCCTCCCTCCACAGCCATCTCAGCTCTTTTGGCTTCAAGGCCAGGCCACAGCCATGAT 18429
Qy 43 eLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeuAlaAla 63
Db 18428 CCTCACTGTGGAGGGCGGCATCTTCCCAACGGCACTTCAGCCAGCTGGCTGCAGC 18369
Qy 63 aValAlaGlyLeuGlnProAspAlaGlyLeuPheThrValSerGluAlaGlu 81
Db 18368 AGTGGCTGGAGTGGGCCAGCCAGACGGTGGCTCTTCACAGTGTCCGAGGCTGAG 18314

RESULT 6
US-09-949-016-4794
; Sequence 4794, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMERISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4794
; LENGTH: 3008
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4794

Alignment Scores:
Pred. No.: 2,77e-20 Length: 3008
Score: 221.00 Matches: 42
Percent Similarity: 74.07% Conservativeness: 18
Best Local Similarity: 51.85% Mismatches: 21
Query Match: 52.25% Indels: 0
DB: 4 Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x US-09-949-016-4794 (1-3008)
Qy 1 GlnlysllelleSerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeu 20
```

```
Db 2064 CAGAAGCTCTGTAGCAGCTGGATGCCCCAGAGAGGCCATGACTGGAGGATGCTG 2123
Qy 21 AlaGlnlyslleuHisLeuAspSerHisLeuSerPhePheAlaSerlyseProSerProThr 40
Db 2124 GCCCATAAGCTGAACCTGGACAGGTACTTGAATTTACTTTGCCACCAATCCAGCCCACT 2183
Qy 41 AlaMetIleLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
Db 2184 GGGGTAATCTCGATCTTTGGGAAGCACAGAACTTCCAGATGGAAACCTCGAGCATGCTG 2243
Qy 61 AlaAlaAlaValAlaGlyLeuGlnProAspAlaGlyLeuPheThrValSerGluAla 80
Db 2244 GCAGCTCTCTGGGAAGAATGGGAAGACATGAACCGTGTGTCTTAGCAGCAGAGAAGG 2303
Qy 81 Glu 81
Db 2304 CAG 2306

RESULT 7
US-08-808-982-3
; Sequence 3, Application US/08808982
; Patent No. 5939271
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; APPLICANT: Leonardo, E. David
; APPLICANT: Hink, Lindsey
; APPLICANT: Masu, Masayuki
; APPLICANT: Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,982
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NOS: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2831 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-808-982-3

* Alignment Scores:
Pred. No.: 3,95e-17 Length: 2831
Score: 198.00 Matches: 38
Percent Similarity: 76.06% Conservativeness: 16
Best Local Similarity: 53.52% Mismatches: 17
Query Match: 46.81% Indels: 0
DB: 2 Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x US-08-808-982-3 (1-2831)
```

Qy 1 GlnYsIlleSerSerLeuAspProProCysArgArgGlyAlaAspTIPArgThrLeu 20
Db 2583 CAGAGAGCTGCAACAGCGCTGACGCCCAACTCAGCGGGCAATGACTGGCGGCTGTG 2642
Qy 21 AlaGlnYsLeuHleSerSerHisLeuSerPhePheAlaSerLysProSerProThr 40
Db 2643 GCACAGAGCTCTCCATGACCGGTACTTGAACCTTCTGCGCCACCAAGCTAGTCCCA 2702
Qy 41 AlaMetIleLeuAsnLeuTIPGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
Db 2703 GCGGTGATCTTAGACCTCTGGGAAGCTCGGCAGCAGGATGATGGGGACCTCAACAGCCTG 2762
Qy 61 AlaAlaAlaValAlaGlyLeuGlyGlnProAsp 71
Db 2763 GCCAGTGCCTTGGAGAGATGGCAAGAGTGAG 2795

RESULT 8
US-09-306-902A-3
; Sequence 3, Application US/09306902A
; Patent No. 6277585
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindsay
; Masu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/306,902A
; FILING DATE: 07-May-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2831 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-306-902A-3

Alignment Scores:
Pred. No.: 3,95e-17 Length: 2831
Score: 198.00 Matches: 38
Percent Similarity: 76.08% Conservative: 16
Best Local Similarity: 53.52% Mismatches: 17
Query Match: 46.81% Indels: 0
Gaps: 3

US-10-624-932C-2_COPY_817_897 (1-81) x US-09-306-902A-3 (1-2831)

Qy 1 GlnYsIlleSerSerLeuAspProProCysArgArgGlyAlaAspTIPArgThrLeu 20
Db 2583 CAGAGAGCTGCAACAGCGCTGACGCCCAACTCAGCGGGCAATGACTGGCGGCTGTG 2642

Db 2583 CAGAGAGCTGCAACAGCGCTGACGCCCAACTCAGCGGGCAATGACTGGCGGCTGTG 2642
Qy 21 AlaGlnYsLeuHleSerSerHisLeuSerPhePheAlaSerLysProSerProThr 40
Db 2643 GCACAGAGCTCTCCATGACCGGTACTTGAACCTTCTGCGCCACCAAGCTAGTCCCA 2702
Qy 41 AlaMetIleLeuAsnLeuTIPGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
Db 2703 GCGGTGATCTTAGACCTCTGGGAAGCTCGGCAGCAGGATGATGGGGACCTCAACAGCCTG 2762
Qy 61 AlaAlaAlaValAlaGlyLeuGlyGlnProAsp 71
Db 2763 GCCAGTGCCTTGGAGAGATGGCAAGAGTGAG 2795

RESULT 9
US-09-969-532-31
; Sequence 31, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-31

Alignment Scores:
Pred. No.: 3,04e-16 Length: 1968
Score: 190.00 Matches: 36
Percent Similarity: 70.37% Conservative: 21
Best Local Similarity: 44.44% Mismatches: 24
Query Match: 44.92% Indels: 0
Gaps: 4

US-10-624-932C-2_COPY_817_897 (1-81) x US-09-969-532-31 (1-1968)

Qy 1 GlnYsIlleSerSerLeuAspProProCysArgArgGlyAlaAspTIPArgThrLeu 20
Db 1681 CAGCGATTTGCTGTACATTTGATACCCCAATGCAAGGCAAGGATCGCAGATGTTA 1740
Qy 21 AlaGlnYsLeuHleSerSerHisLeuSerPhePheAlaSerLysProSerProThr 40
Db 1741 GCACAGAAAAACAGCATCAACAGGAATTTATCTTTATTCGCTACACAAAGTAGCCCATCT 1800
Qy 41 AlaMetIleLeuAsnLeuTIPGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
Db 1801 GCTGTCAATTTGAACCTGTGGGAAGCTCGTCATCAGCATGATGGTGATCTTGACCTCCCTG 1860
Qy 61 AlaAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla 80
Db 1861 GCTGTGCTTGAAGAGATTTGGGAGGACACACAGCAAACTCTCAACATTTCAAGATCC 1920

Alignment Scores:
Pred. No.: 81 Glu 81
Score: 1921 CAG 1923
Percent Similarity: 76.08% Conservative: 16
Best Local Similarity: 53.52% Mismatches: 17
Query Match: 46.81% Indels: 0
Gaps: 3

US-09-969-532-29
; Sequence 29, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin

```
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 2001
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-29

Alignment Scores:
Pred. No.: 3,13e-16 Length: 2001
Score: 190.00 Matches: 36
Percent Similarity: 70.37% Conservative: 21
Best Local Similarity: 44.44% Mismatches: 24
Query Match: 44.92% Indels: 0
DB: 4 Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x US-09-969-532-29 (1-2001)
Qy 1 GlnlystlelleSerSerLeuAspProProCysArgGlyAlaAspTtpArgThrLeu 20
Db 1714 CAGCGGATTTGTGTACATTTGATACCCCAATGCCAAGGCAAGGACTGGCAGATGTTA 1773
Qy 21 AlaGlnlystlelleSerSerLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40
Db 1774 GCACAGAAAACAGCATCAACAGGAATTTATCTTATTTTCGCTACACAAAGTAGCCCATCT 1833
Qy 41 AlaMetlleLeuAnLeuTtpGluAlaArgHisPheProAnGlyAsnLeuSerGlnLeu 60
Db 1834 GCTGTCAATTTGAACCTGTGGAGAGCTCGTCATCAGCATGATGTTGATCTTGCCTCG 1893
Qy 61 AlaAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla 80
Db 1894 GCCTGTGCCCTTGAAGAGATTGGGAGGACACACACAGAAACTCTCAAAACATTTCAAGATCC 1953
Qy 81 Glu 81
Db 1954 CAG 1956

RESULT 11
US-09-969-532-27
; Sequence 27, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-27

Alignment Scores:
Pred. No.: 3,13e-16 Length: 2010
Score: 190.00 Matches: 36
Percent Similarity: 70.37% Conservative: 21
Best Local Similarity: 44.44% Mismatches: 24
Query Match: 44.92% Indels: 0
DB: 4 Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x US-09-969-532-27 (1-2010)
```

```
Qy 1 GlnlystlelleSerSerLeuAspProProCysArgGlyAlaAspTtpArgThrLeu 20
Db 1723 CAGCGGATTTGTGTACATTTGATACCCCAATGCCAAGGCAAGGACTGGCAGATGTTA 1782
Qy 21 AlaGlnlystlelleSerSerHisLeuSerPhePheAlaSerLysProSerProThr 40
Db 1783 GCACAGAAAACAGCATCAACAGGAATTTATCTTATTTTCGCTACACAAAGTAGCCCATCT 1842
Qy 41 AlaMetlleLeuAnLeuTtpGluAlaArgHisPheProAnGlyAsnLeuSerGlnLeu 60
Db 1843 GCTGTCAATTTGAACCTGTGGAGAGCTCGTCATCAGCATGATGTTGATCTTGCCTCG 1902
Qy 61 AlaAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla 80
Db 1903 GCCTGTGCCCTTGAAGAGATTGGGAGGACACACACAGAAACTCTCAAAACATTTCAAGATCC 1962
Qy 81 Glu 81
Db 1963 CAG 1965

RESULT 12
US-09-969-532-25
; Sequence 25, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 2043
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-25

Alignment Scores:
Pred. No.: 3,2e-16 Length: 2043
Score: 190.00 Matches: 36
Percent Similarity: 70.37% Conservative: 21
Best Local Similarity: 44.44% Mismatches: 24
Query Match: 44.92% Indels: 0
DB: 4 Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x US-09-969-532-25 (1-2043)
Qy 1 GlnlystlelleSerSerLeuAspProProCysArgGlyAlaAspTtpArgThrLeu 20
Db 1756 CAGCGGATTTGTGTACATTTGATACCCCAATGCCAAGGCAAGGACTGGCAGATGTTA 1815
Qy 21 AlaGlnlystlelleSerSerHisLeuSerPhePheAlaSerLysProSerProThr 40
Db 1816 GCACAGAAAACAGCATCAACAGGAATTTATCTTATTTTCGCTACACAAAGTAGCCCATCT 1875
Qy 41 AlaMetlleLeuAnLeuTtpGluAlaArgHisPheProAnGlyAsnLeuSerGlnLeu 60
Db 1876 GCTGTCAATTTGAACCTGTGGAGAGCTCGTCATCAGCATGATGTTGATCTTGCCTCG 1935
Qy 61 AlaAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla 80
Db 1936 GCCTGTGCCCTTGAAGAGATTGGGAGGACACACACAGAAACTCTCAAAACATTTCAAGATCC 1995
Qy 81 Glu 81
Db 1996 CAG 1998

RESULT 13
```

```
US-09-969-532-15
; Sequence 15, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 2661
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-15

Alignment Scores:
Pred. No.: 4.66e-16 Length: 2661
Score: 190.00 Matches: 36
Percent Similarity: 70.37% Conservativeness: 21
Best Local Similarity: 44.44% Mismatches: 24
Query Match: 44.92% Indels: 0
DB: 4 Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x US-09-969-532-15 (1-2661)
Qy 1 GlnlylIleSerSerLeuAspProCysArgArgGlyAlaAspTTPArgThrLeu 20
Db 2374 CAGCGGATTTGTGTACATTTGATACCCCAATGCCAAAGGCAAGGACTGGCAGATGTTA 2433
Qy 21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40
Db 2434 GCACAGAAAAACAGCATCAACAGGAAATTTATCTTATTCGCTACACAAAGTAGCCCATCT 2493
Qy 41 AlaMetIleLeuAsnLeuTTPGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
Db 2494 GCTGTCAATTTGAACCTTGGAGAGATTGGGAGGACATCATCAGCATGATGGTGATCTTTGACTCCCTG 2553
Qy 61 AlaAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla 80
Db 2554 GCCTGTGCCCTTGAAGAGATTGGGAGGACACACACAGAAACTCTCAAAACATTTCAAGATCC 2613
Qy 81 Glu 81
Db 2614 CAG 2616

RESULT 14
US-09-969-532-13
; Sequence 13, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 2694
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-13

Alignment Scores:
Pred. No.: 4.74e-16 Length: 2694
```

```
Score: 190.00 Matches: 36
Percent Similarity: 70.37% Conservativeness: 21
Best Local Similarity: 44.44% Mismatches: 24
Query Match: 44.92% Indels: 0
DB: 4 Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x US-09-969-532-13 (1-2694)
Qy 1 GlnlylIleSerSerLeuAspProCysArgArgGlyAlaAspTTPArgThrLeu 20
Db 2407 CAGCGGATTTGTGTACATTTGATACCCCAATGCCAAAGGCAAGGACTGGCAGATGTTA 2466
Qy 21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40
Db 2467 GCACAGAAAAACAGCATCAACAGGAAATTTATCTTATTCGCTACACAAAGTAGCCCATCT 2526
Qy 41 AlaMetIleLeuAsnLeuTTPGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
Db 2527 GCTGTCAATTTGAACCTTGGAGAGATTGGGAGGACATCATCAGCATGATGGTGATCTTTGACTCCCTG 2586
Qy 61 AlaAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla 80
Db 2587 GCCTGTGCCCTTGAAGAGATTGGGAGGACACACACAGAAACTCTCAAAACATTTCAAGATCC 2646
Qy 81 Glu 81
Db 2647 CAG 2649

RESULT 15
US-09-969-532-11
; Sequence 11, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 2703
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-11

Alignment Scores:
Pred. No.: 4.77e-16 Length: 2703
Score: 190.00 Matches: 36
Percent Similarity: 70.37% Conservativeness: 21
Best Local Similarity: 44.44% Mismatches: 24
Query Match: 44.92% Indels: 0
DB: 4 Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x US-09-969-532-11 (1-2703)
Qy 1 GlnlylIleSerSerLeuAspProCysArgArgGlyAlaAspTTPArgThrLeu 20
Db 2416 CAGCGGATTTGTGTACATTTGATACCCCAATGCCAAAGGCAAGGACTGGCAGATGTTA 2475
Qy 21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40
Db 2476 GCACAGAAAAACAGCATCAACAGGAAATTTATCTTATTCGCTACACAAAGTAGCCCATCT 2535
Qy 41 AlaMetIleLeuAsnLeuTTPGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
Db 2536 GCTGTCAATTTGAACCTTGGAGAGATTGGGAGGACATCATCAGCATGATGGTGATCTTTGACTCCCTG 2595
Qy 61 AlaAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla 80
Db 2596 GCTGTCAATTTGAACCTTGGAGAGATTGGGAGGACATCATCAGCATGATGGTGATCTTTGACTCCCTG 2655
```

Db 2596 GCCTGTGCCCTTGAAGAGATTGGGAGGACACACACGAACTCTCAAACATTTTCAGAAATCC 2655
Qy 81 Glu 81
:::
Db 2656 CAG 2658

Search completed: September 9, 2005, 09:52:08
Job time : 144.111 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 9, 2005, 04:41:16 ; Search time 808.309 Seconds
(without alignments)
658.098 Million cell updates/sec

Title: US-10-624-932C-2_COPY_817_897

Perfect score: 423

Sequence: 1 QKISSLDPPCRRGADWRTL.....AAVAGLGQDPAGLFTVSEAE 81

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 7351250 seqs, 3283620254 residues

Total number of hits satisfying chosen parameters: 14702500

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model
-O=/cgn2_1/usPTO_spool_h/US10624932/runat_08092005_161709_15882/app_query.fasta_1.1366
-DB=Published Applications NA -QPMF=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNIT8=bits -START=1 -END=-1 -MATRIX=DIOSUM62
-TRANS=human40.cdi -LIST=45 -DOCALLGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10624932 @cgn 1 1 989 @runat 08092005_161709_15882
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US05_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US10J_PUBCOMB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US10K_PUBCOMB.seq.*
23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	423	100.0	2752	10	US-09-918-779-1	Sequence 1, Appli
2	423	100.0	2752	18	US-10-624-932-1	Sequence 1, Appli
3	423	100.0	2881	10	US-09-970-944-1	Sequence 1, Appli
4	423	100.0	3561	20	US-10-643-795A-77	Sequence 77, Appli
5	423	100.0	3561	21	US-10-948-518-77	Sequence 77, Appli
6	423	100.0	3580	17	US-10-311-623-13	Sequence 13, Appli
7	410	96.9	2697	16	US-10-240-154-15	Sequence 15, Appli
8	410	96.9	3014	10	US-09-933-261-1	Sequence 1, Appli
9	410	96.9	3014	14	US-10-256-702-1	Sequence 1, Appli
10	393	92.9	1269	14	US-10-103-313-36	Sequence 36, Appli
11	376	88.9	1787	10	US-09-933-261-2	Sequence 2, Appli
12	376	88.9	1787	14	US-10-256-702-2	Sequence 2, Appli
13	368	87.0	1321	18	US-10-296-115-365	Sequence 365, App
14	364	86.1	574	9	US-09-764-861-20	Sequence 20, Appli
15	364	86.1	574	10	US-09-764-861-20	Sequence 20, Appli
16	364	86.1	574	14	US-10-103-313-192	Sequence 192, App
17	364	86.1	574	14	US-10-115-928-20	Sequence 20, Appli
c 18	357.5	84.5	9582	9	US-09-764-861-62	Sequence 62, Appli
c 19	357.5	84.5	9582	10	US-09-764-861-62	Sequence 62, Appli
c 20	357.5	84.5	9582	14	US-10-115-928-62	Sequence 62, Appli
c 21	351.5	83.1	18772	9	US-09-764-861-63	Sequence 63, Appli
c 22	351.5	83.1	18772	10	US-09-764-861-63	Sequence 63, Appli
c 23	351.5	83.1	18772	14	US-10-115-928-63	Sequence 63, Appli
c 24	327	77.3	600	22	US-10-972-079-78338	Sequence 78338, A
c 25	327	77.3	600	22	US-10-972-079-78339	Sequence 78339, A
c 26	304	71.9	341	9	US-09-867-701-3673	Sequence 3673, Ap
c 27	234	55.3	599	22	US-10-972-079-78337	Sequence 78337, A
c 28	201	47.5	866	21	US-10-764-420-2213	Sequence 2213, Ap
c 29	198	46.8	2831	10	US-09-933-261-3	Sequence 3, Appli
c 30	198	46.8	2831	14	US-10-256-702-3	Sequence 3, Appli
c 31	191	45.2	2406	17	US-10-108-260A-239	Sequence 239, App
c 32	191	45.2	2860	17	US-10-087-684-1	Sequence 1, Appli
c 33	191	45.2	2860	17	US-10-087-684-3	Sequence 3, Appli
c 34	191	45.2	2860	17	US-10-218-779-1	Sequence 1, Appli
c 35	191	45.2	2860	17	US-10-218-779-3	Sequence 3, Appli
c 36	191	45.2	2895	18	US-10-037-417-37	Sequence 37, Appli
c 37	191	45.2	2995	11	US-09-972-211-55	Sequence 55, Appli
c 38	191	45.2	2995	18	US-10-096-625-55	Sequence 55, Appli
c 39	191	45.2	3485	9	US-09-816-828-18	Sequence 18, Appli
c 40	191	45.2	3501	17	US-10-295-027-1123	Sequence 1123, Ap
c 41	191	45.2	3884	14	US-10-028-072-145	Sequence 145, App
c 42	191	45.2	3884	14	US-10-140-808-145	Sequence 145, App
c 43	191	45.2	3884	14	US-10-121-049-145	Sequence 145, App
c 44	191	45.2	3884	14	US-10-123-904-145	Sequence 145, App
c 45	191	45.2	3884	14	US-10-140-470-145	Sequence 145, App

ALIGNMENTS

RESULT 1
US-09-918-779-1
; Sequence 1, Application US/09918779
; Publication No. US20030064369A1
; GENERAL INFORMATION:
; APPLICANT: Taupier, Raymond
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Rastelli, Luca
; APPLICANT: Spaderna, Steven
; APPLICANT: Shmukets, Richard
; APPLICANT: Zethusen, Bryan
; APPLICANT: Spytek, Kimberly
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Gusev, Vladimir
; APPLICANT: Grosse, William

APPLICANT: Alsobrook, John
APPLICANT: Lepley, Denise
APPLICANT: Burgess, Catherine
APPLICANT: Gerlach, Valerie
APPLICANT: Ellerman, Karen
APPLICANT: MacDougall, John
APPLICANT: Stone, David
APPLICANT: Smithson, Glenda

TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same

FILE REFERENCE: 21402-074 US

CURRENT APPLICATION NUMBER: US/09/918,779

PRIOR FILING DATE: 2001-07-30

PRIOR FILING DATE: 2000-07-28

PRIOR APPLICATION NUMBER: 60/221,409

PRIOR FILING DATE: 2000-07-28

PRIOR APPLICATION NUMBER: 60/222,840

PRIOR FILING DATE: 2000-08-04

PRIOR APPLICATION NUMBER: 60/223,752

PRIOR FILING DATE: 2000-08-08

PRIOR APPLICATION NUMBER: 60/223,762

PRIOR FILING DATE: 2000-08-08

PRIOR APPLICATION NUMBER: 60/223,770

PRIOR FILING DATE: 2000-08-08

PRIOR APPLICATION NUMBER: 60/223,769

PRIOR FILING DATE: 2000-08-08

PRIOR APPLICATION NUMBER: 60/225,146

PRIOR FILING DATE: 2000-08-14

PRIOR APPLICATION NUMBER: 60/225,392

PRIOR FILING DATE: 2000-08-15

PRIOR APPLICATION NUMBER: 60/225,470

PRIOR FILING DATE: 2000-08-15

PRIOR APPLICATION NUMBER: 60/225,697

PRIOR FILING DATE: 2000-08-16

PRIOR APPLICATION NUMBER: 60/263,662

PRIOR FILING DATE: 2001-02-01

PRIOR APPLICATION NUMBER: 60/281,645

PRIOR FILING DATE: 2001-04-05

NUMBER OF SEQ ID NOS: 61

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 2752

TYPE: DNA

ORGANISM: Homo sapiens

US-09-918-779-1

Alignment Scores: 3.97e-49 Length: 2752

Pred. No.: 423.00 Matches: 81

Score: 100.00% Conservative: 0

Percent Similarity: 100.00% Mismatches: 0

Best Local Similarity: 100.00% Indels: 0

Query Match: 100.00% Gaps: 0

DB: 10

US-10-624-932c-2_copy_817_897 (1-81) x US-09-918-779-1 (1-2752)

Qy 1 GlnLysLeuSerLeuAspProCysArgArgGlyAlaAspTrpArgThrLeu 20

Db 2494 CAGAAGATAATTTCCAGCTGGACCCACCTCTGAGGGGGTGGCGACTGCGGACTCTG 2553

Qy 21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40

Db 2554 GCCCAGAACTCCACCTGGACAGCCATCTCAGCTTCTTGGCTCCAGCCCGAGCCACCA 2613

Qy 41 AlaMetLeuAnLeuTrpGluAlaArgHisPheProAsnGlyAnLeuSerGlnLeu 60

Db 2614 GCCATGATCTCCACCTGTGGAGCGCGGCACTTCCCAACGCGCAACCTCAGCGAGCTG 2673

Qy 61 AlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla 80

Db 2674 GCTGCAGCAGTGGTGGACTGGGCGCCAGCCAGACGCTGGCCCTCTTCACAGTGTGCGAGGCT 2733

Qy 81 Glu 81

Db 2734 GAG 2736

RESULT 2

US-10-624-932-1

; Sequence 1, Application US/10624932

; Publication No. US20040096877A1

; GENERAL INFORMATION:

; APPLICANT: Taupier, Raymond

; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Rastelli, Luca

; APPLICANT: Spaderna, Steven

; APPLICANT: Shimkets, Richard

; APPLICANT: Zerhusen, Bryan

; APPLICANT: Spytek, Kimberly

; APPLICANT: Shenoy, Suresh

; APPLICANT: Li, Li

; APPLICANT: Gusev, Vladimir

; APPLICANT: Grosse, William

; APPLICANT: Alsobrook, John

; APPLICANT: Lepley, Denise

; APPLICANT: Burgess, Catherine

; APPLICANT: Gerlach, Valerie

; APPLICANT: Ellerman, Karen

; APPLICANT: MacDougall, John

; APPLICANT: Stone, David

; APPLICANT: Smithson, Glenda

TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same

FILE REFERENCE: 21402-074 US

CURRENT APPLICATION NUMBER: US/10/624,932

PRIOR FILING DATE: 2003-07-21

PRIOR APPLICATION NUMBER: 09/918,779

PRIOR FILING DATE: 2001-07-03

PRIOR APPLICATION NUMBER: 60/221,409

PRIOR FILING DATE: 2000-07-28

PRIOR APPLICATION NUMBER: 60/222,840

PRIOR FILING DATE: 2000-08-04

PRIOR APPLICATION NUMBER: 60/223,752

PRIOR FILING DATE: 2000-08-08

PRIOR APPLICATION NUMBER: 60/223,762

PRIOR FILING DATE: 2000-08-08

PRIOR APPLICATION NUMBER: 60/223,770

PRIOR FILING DATE: 2000-08-08

PRIOR APPLICATION NUMBER: 60/223,769

PRIOR FILING DATE: 2000-08-08

PRIOR APPLICATION NUMBER: 60/225,146

PRIOR FILING DATE: 2000-08-14

PRIOR APPLICATION NUMBER: 60/225,392

PRIOR FILING DATE: 2000-08-15

PRIOR APPLICATION NUMBER: 60/225,470

PRIOR FILING DATE: 2000-08-15

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 61

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 2752

TYPE: DNA

ORGANISM: Homo sapiens

US-10-624-932-1

Alignment Scores: 3.97e-49 Length: 2752

Pred. No.: 423.00 Matches: 81

Score: 100.00% Conservative: 0

Percent Similarity: 100.00% Mismatches: 0

Best Local Similarity: 100.00% Indels: 0

Query Match: 100.00% Gaps: 0

DB: 18

US-10-624-932c-2_COPY_817_897 (1-81) x US-10-624-932-1 (1-2752)

Qy 1 GlnLysLeuSerLeuAspProCysArgArgGlyAlaAspTrpArgThrLeu 20

Db 2494 CAGAAGATAATTTCCAGCTGGACCCACCTCTGAGGGGGTGGCGACTGCGGACTCTG 2553

Qy 21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40

Db 2554 GCCCAGAAATCTCCACTGGACAGCCATCTCAGCTTTCTTGGCTCCAGCCAGCCCCACA 2613
Qy 41 AlaMetIleLeuAsnLeuTrpGluAlaAArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
Db 2614 GCCATGATCTCTCAACTGTGGAGGCGGGCACTTCCCAACGGCAACTCAGCCAGCTG 2673
Qy 61 AlaAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValserGluAla 80
Db 2674 GCTGCAGCAGTGGCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCCACAGTGTGGAGGCT 2733
Qy 81 Glu 81
Db 2734 GAG 2736

RESULT 3

; Sequence 1, Application US/09970944
; Publication No. US20030204052A1
; GENERAL INFORMATION:
; APPLICANT: Herrman, John L
; APPLICANT: Rastelli, Luca
; APPLICANT: Shinkets, Richard A
; TITLE OF INVENTION: No. US20030204052A1el Proteins and Nucleic Acids Encoding Same an
; TITLE OF INVENTION: Antibodies Directed Against these Proteins
; FILE REFERENCE: 21402-138
; CURRENT APPLICATION NUMBER: US/09/970,944
; PRIOR FILING DATE: 2002-05-02
; PRIOR FILING DATE: 2002-03-862
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1

; LENGTH: 2881
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-970-944-1

Alignment Scores:
Pred. No.: 4,21e-49 Length: 2881
Score: 423.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x US-09-970-944-1 (1-2881)

Qy 1 GlnLysIleLeuSerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeu 20
Db 2538 CAGAAGATAATTTCCAGCCTGGACCCACCTGTAGCGGGGTGCGCACTGGCGGACTCTG 2597
Qy 21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPheAlaSerLysProSerProThr 40
Db 2598 GCCCAGAAATCTCCACTGGACAGCCATCTCAGCTTCTTTGGCTCCAGCCAGCCCCACA 2657
Qy 41 AlaMetIleLeuAsnLeuTrpGluAlaAArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
Db 2658 GCCATGATCTCTCAACTGTGGAGGCGGGCACTTCCCAACGGCAACTCAGCCAGCTG 2717
Qy 61 AlaAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValserGluAla 80
Db 2718 GCTGCAGCAGTGGCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCCACAGTGTGGAGGCT 2777
Qy 81 Glu 81
Db 2778 GAG 2780

RESULT 4

US-10-643-795A-77
; Sequence 77, Application US/10643795A
; Publication No. US20040241703A1
; GENERAL INFORMATION:

; APPLICANT: FREDERIC J. DESAUVAGE
; APPLICANT: GRETCHEN FRANTZ
; APPLICANT: KENNETH J. HILLAN
; APPLICANT: PAUL POLAKIS
; APPLICANT: ANDREW POLSON
; APPLICANT: VICTORIA SMITH
; APPLICANT: SUSAN D. SPENCER
; APPLICANT: THOMAS D. WU
; APPLICANT: ZEMIN ZHANG
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR

; FILE REFERENCE: P5026R1-US
; CURRENT APPLICATION NUMBER: US/10/643,795A

; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405,645
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/413,192
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: US 60/419,008
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/426,847
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/484,959
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 158
; SEQ ID NO 77

; LENGTH: 3561
; TYPE: DNA

; ORGANISM: Homo sapien
US-10-643-795A-77

Alignment Scores:
Pred. No.: 5,5e-49 Length: 3561
Score: 423.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 20 Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x US-10-643-795A-77 (1-3561)

Qy 1 GlnLysIleLeuSerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeu 20
Db 2284 CAGAAGATAATTTCCAGCCTGGACCCACCTGTAGCGGGGTGCGCACTGGCGGACTCTG 2343
Qy 21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPheAlaSerLysProSerProThr 40
Db 2344 GCCCAGAAATCTCCACTGGACAGCCATCTCAGCTTCTTTGGCTCCAGCCAGCCCCACA 2403
Qy 41 AlaMetIleLeuAsnLeuTrpGluAlaAArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
Db 2404 GCCATGATCTCTCAACTGTGGAGGCGGGCACTTCCCAACGGCAACTCAGCCAGCTG 2463
Qy 61 AlaAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValserGluAla 80
Db 2464 GCTGCAGCAGTGGCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCCACAGTGTGGAGGCT 2523
Qy 81 Glu 81
Db 2524 GAG 2526

RESULT 5

US-10-948-518-77
; Sequence 77, Application US/10948518
; Publication No. US20050064492A1
; GENERAL INFORMATION:
; APPLICANT: FREDERIC J. DESAUVAGE
; APPLICANT: GRETCHEN FRANTZ
; APPLICANT: KENNETH J. HILLAN
; APPLICANT: PAUL POLAKIS
; APPLICANT: ANDREW POLSON

```
; APPLICANT: VICTORIA SMITH
; APPLICANT: SUSAN D. SPENCER
; APPLICANT: THOMAS D. WU
; APPLICANT: ZEMIN ZHANG
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF TUMOR
; FILE REFERENCE: P5026R1-US
; CURRENT APPLICATION NUMBER: US/10/948,518
; CURRENT FILING DATE: 2004-09-22
; PRIOR APPLICATION NUMBER: US/10/643,795
; PRIOR FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405,645
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/413,192
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: US 60/419,008
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/426,847
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/484,959
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 158
; SEQ ID NO 77
; LENGTH: 3561
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-948-518-77

Alignment Scores:
Pred. No.: 5.5e-49 Length: 3561
Score: 423.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-10-624-932c-2_COPY_817_897 (1-81) x US-10-948-518-77 (1-3561)
Qy 1 GlnlysllelleSerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeu 20
Db 2284 CAGAAGATAATTTCCAGCTGGACCCACCTGTAGGCGGGTGGCGGACTCTG 2343
Qy 21 AlaGlnlysllelleSerSerLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40
Db 2344 GCCAGAAATCCACCTGGACAGCATCTCAGCTTCTTTGCTCCAAAGCCAGCCCCACA 2403
Qy 41 AlaMetlleLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
Db 2404 GCCATGATCTTCACCTGTGGAGGGCGGCGGACTTCCCAAGCGGACCTCAGCGAGCTG 2463
Qy 61 AlaAlaAlaValAlaGlyLeuGlnProAspAlaGlyLeuPheThrValSerGluAla 80
Db 2464 GCTGCAGCAGTGGCTGGAGTGGCGCAGCCAGCAGCTGGCCCTCTTCACAGTGTGGAGGCT 2523
Qy 81 Glu 81
Db 2524 GAG 2526

RESULT 6
US-10-311-623-13
; Sequence 13, Application US/10311623
; Publication No. US20040023244A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; GRIFFIN, Jennifer A.
; APPLICANT: KALLICK, Deborah A.; TRIBOULEY, Catherine M.
; APPLICANT: YUE, Henry; NGUYEN, Daniel B.
; APPLICANT: TANG, Y. Tom; LAL, Preeti G.
; APPLICANT: POLICKY, Jennifer L.; AZIMZAI, Yalda
; APPLICANT: LU, Dying Aina M.; GRAUL, Richard C.
; APPLICANT: YAO, Monique G.; BURFORD, Neil
; APPLICANT: HAFALIA, April J. A.; BAUGHN, Mariah R.
```

```
; APPLICANT: BANDMAN, Olga; ARVIZU, Chandra S.
; APPLICANT: YANG, Junming; XU, Yuming
; APPLICANT: GANDHI, Ameena R.; WARREN, Bridget A.
; APPLICANT: DING, Li; SANJANWALA, Madhusudan M.
; APPLICANT: DUGGAN, Brendan M.; LU, Yan
; TITLE OF INVENTION: RECEPTORS
; FILE REFERENCE: PF-0793 USN
; CURRENT APPLICATION NUMBER: US/10/311,623
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 01/19942
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/214,027
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: US 60/228,045
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/255,104
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PERL Program
; SEQ ID NO 13
; LENGTH: 3580
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040023244A1 6052371CB1
US-10-311-623-13

Alignment Scores:
Pred. No.: 5.54e-49 Length: 3580
Score: 423.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-10-624-932c-2_COPY_817_897 (1-81) x US-10-311-623-13 (1-3580)
Qy 1 GlnlysllelleSerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeu 20
Db 2284 CAGAAGATAATTTCCAGCTGGACCCACCTGTAGGCGGGTGGCGGACTCTG 2343
Qy 21 AlaGlnlysllelleSerSerLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40
Db 2344 GCCAGAAATCCACCTGGACAGCATCTCAGCTTCTTTGCTCCAAAGCCAGCCCCACA 2403
Qy 41 AlaMetlleLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
Db 2404 GCCATGATCTTCACCTGTGGAGGGCGGCGGACTTCCCAAGCGGACCTCAGCGAGCTG 2463
Qy 61 AlaAlaAlaValAlaGlyLeuGlnProAspAlaGlyLeuPheThrValSerGluAla 80
Db 2464 GCTGCAGCAGTGGCTGGAGTGGCGCAGCCAGCAGCTGGCCCTCTTCACAGTGTGGAGGCT 2523
Qy 81 Glu 81
Db 2524 GAG 2526

RESULT 7
US-10-240-154-15
; Sequence 15, Application US/10240154
; Publication No. US20030175741A1
; GENERAL INFORMATION:
; APPLICANT: Cochran et al.
; TITLE OF INVENTION: SCHIZOPHRENIA RELATED GENES
; FILE REFERENCE: CRFW-P01-006
; CURRENT APPLICATION NUMBER: US/10/240,154
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: PCT/GB01/01486
; PRIOR FILING DATE: 2001-04-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
```

```
; LENGTH: 2697
; TYPE: DNA
; ORGANISM: Rattus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2697)
US-10-240-154-15

Alignment Scores:
Pred. No.: 2,7e-47 Length: 2697
Score: 410.00 Matches: 78
Percent Similarity: 97.53% Conservatives: 1
Best Local Similarity: 96.30% Mismatches: 2
Query Match: 96.93% Indels: 0
DB: 16 Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x US-10-240-154-15 (1-2697)
Qy 1 GlnylslelleSerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeu 20
Db 2449 CAAAAGATCATCGCCAGTCTGGACCCACCTTGCAGCGGGCGCGACTGGAGAACTCTA 2508
Qy 21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPheAlaSerLysProSerProThr 40
Db 2509 GCCCAGAAATTCACCTTGGACAGCCATCTTAGCTTCTTTGGCTCCAAAGCCAGCCCTACA 2568
Qy 41 AlaMetlleLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
Db 2569 GCCATGATCTCAACCTATGGAGGACGACGACACTTCCCAACGGCAACTCGGCAGCTG 2628
Qy 61 AlaAlaAlaValAlaGlyLeuGlnProAspAlaGlyLeuPheThrValSerGluAla 80
Db 2629 GCAGCAGCTGTGGCGGAGTGGCCAAACAGATGCTGGCCTCTTTCACGGTGTGGAGGCC 2688
Qy 81 Glu 81
Db 2689 GAG 2691

RESULT 8
US-09-933-261-1
; Sequence 1, Application US/09933261
; Publication No. US20030040046A1
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindsay
; Masu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/933,261
; FILING DATE: 20-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/808,982
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
```

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3014 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-933-261-1

Alignment Scores:
Pred. No.: 3.11e-47 Length: 3014
Score: 410.00 Matches: 78
Percent Similarity: 97.53% Conservatives: 1
Best Local Similarity: 96.30% Mismatches: 2
Query Match: 96.93% Indels: 0
DB: 10 Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x US-09-933-261-1 (1-3014)
Qy 1 GlnylslellelleSerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeu 20
Db 2449 CAAAAGATCATCGCCAGTCTGGACCCACCTTGCAGCGGGCGCGACTGGAGAACTCTA 2508
Qy 21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPheAlaSerLysProSerProThr 40
Db 2509 GCCCAGAAATTCACCTTGGACAGCCATCTTAGCTTCTTTGGCTCCAAAGCCAGCCCTACA 2568
Qy 41 AlaMetlleLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
Db 2569 GCCATGATCTCAACCTATGGAGGACGACGACACTTCCCAACGGCAACTCGGCAGCTG 2628
Qy 61 AlaAlaAlaValAlaGlyLeuGlnProAspAlaGlyLeuPheThrValSerGluAla 80
Db 2629 GCAGCAGCTGTGGCGGAGTGGCCAAACAGATGCTGGCCTCTTTCACGGTGTGGAGGCC 2688
Qy 81 Glu 81
Db 2689 GAG 2691

RESULT 9
US-10-256-702-1
; Sequence 1, Application US/10256702
; Publication No. US20030059859A1
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindsay
; Masu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/256,702
; FILING DATE: 27-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/933,261
```

```
;
; FILING DATE: 20-Aug-2001
; APPLICATION NUMBER: 08/808,982
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3014 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-256-702-1

Alignment Scores:
Pred. No.: 3,11e-47 Length: 3014
Score: 410.00 Matches: 78
Percent Similarity: 97.53% Conservative: 1
Best Local Similarity: 96.30% Mismatches: 2
Query Match: 96.93% Indels: 0
DB: 14 Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x US-10-256-702-1 (1-3014)

Qy 1 GlnLysIleSerLeuAspProCysArgGlyAlaAspTTPArgThrLeu 20
Db 2449 CAAAGATCATCGCGAGTGTGAGCCACCTTGACGGCGCGCGACTGGAGAACTCTA 2508

Qy 21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPheAlaSerLysProSerProThr 40
Db 2509 GCCCAGAAATTCACCTGGACAGGCATCTTAGCTTCTTTGGCTCCAAGCCAGCCCTACA 2568

Qy 41 AlaMetIleLeuAenLeuTTPGluAlaArgHisPheProAenGlyAenLeuSerGlnLeu 60
Db 2569 GCCATGATCTCTCAACCTATGGAGGCGACGGCACATTCCTCCCAACGGCAACCTGGCCAGCTG 2628

Qy 61 AlaAlaAlaValAlaGlyLeuGlnProAspAlaGlyLeuPheThrValSerGluAla 80
Db 2629 GCACGAGCTGTGGCGGAGTGGGCGCAACCATGCTGGCTTTCACGGTGTGGAGGCC 2688

Qy 81 Glu 81
Db 2689 GAG 2691

RESULT 10
US-10-103-313-36
; Sequence 36, Application US/10103313
; Publication No. US20030082758A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P0207C1
; CURRENT APPLICATION NUMBER: US/10/103,313
; CURRENT FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 653
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 1269
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-103-313-36

Alignment Scores:
Pred. No.: 2.69e-45 Length: 1269
Score: 393.00 Matches: 74
Percent Similarity: 100.00% Conservative: 0

;
; FILING DATE: 20-Aug-2001
; APPLICATION NUMBER: 08/808,982
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3014 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-624-932C-2_COPY_817_897 (1-81) x US-10-103-313-36 (1-1269)

Qy 8 AspProCysArgGlyAlaAspTTPArgThrLeuAlaGlnLysLeuHisLeuAsp 27
Db 9 GACCCACCTGTAGCGGGGTGGCGACTGGCGGACTCTGGCCCAAGAACTCCACCTGGAC 68

Qy 28 SerHisLeuSerPheAlaSerLysProSerProThrAlaMetIleLeuAenLeuTTP 47
Db 69 AGCATCTCAGCTTCTTTGGCTTCAAGCCACGCCCCACGCGCATGATCTCAACCTGTGG 128

Qy 48 GluAlaArgHisPheProAenGlyAenLeuSerGlnLeuAlaAlaValAlaGlyLeu 67
Db 129 GAGCGCGGCACTTCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTG 188

Qy 68 GlyGlnProAspAlaGlyLeuPheThrValSerGluAlaGlu 81
Db 189 GGCAGCCAGACGCTGGCTTCTTTCACAGTGTGGAGGCTGAG 230

RESULT 11
US-09-933-261-2
; Sequence 2, Application US/09933261
; Publication No. US20030040046A1
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindsey
; Masu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/933,261
; FILING DATE: 20-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/808,982
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1787 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-933-261-2

Alignment Scores:
Pred. No.: 1.07e-42 Length: 1787
Score: 376.00 Matches: 77
```


